

R-HEMBA1006446//Homo sapiens mRNA for cadherin-6, complete cds//1.6e-05:487:58//Hs.32963:D31784  
R-HEMBA1006461//ESTs//5.1e-78:393:97//Hs.142677:R95895  
R-HEMBA1006467//ESTs, Weakly similar to putative p150 [H.sapiens]//3.0e-17:342:63//Hs.111730:AA604403  
R-HEMBA1006471//ESTs//3.8e-66:370:92//Hs.14063:T77441  
5 R-HEMBA1006474  
R-HEMBA1006483//Human G protein-coupled receptor (STRL22) mRNA, complete cds//4.2e-40:365:78//Hs.46468:U45984  
R-HEMBA1006485//H.sapiens mRNA for aminopeptidase//2.5e-92:517:91//Hs.132243:Y07701  
R-HEMBA1006486//EST//7.0e-47:240:76//Hs.161917:AA483223  
10 R-HEMBA1006489//ESTs//2.1e-93:440:99//Hs.125264:AA873350  
R-HEMBA1006492//ESTs//0.00034:52:90//Hs.163219:AA810720  
R-HEMBA1006494//EST//1.8e-06:192:67//Hs.141401:H93387  
R-HEMBA1006497//ESTs//6.2e-45:232:97//Hs.118015:N33117  
R-HEMBA1006502//Complement component 5 receptor 1 (C5a ligand)//8.7e-16:135:72//Hs.2161:M62505  
15 R-HEMBA1006507//Homo sapiens mRNA for KIAA0666 protein, partial cds//3.9e-117:570:96//Hs.153858:AB014566  
R-HEMBA1006521//ESTs//9.9e-99:496:96//Hs.64906:AA677300  
R-HEMBA1006530//ESTs//0.18:260:60//Hs.24970:AI057628  
R-HEMBA1006535//GS1 PROTEIN//0.52:267:62//Hs.78991:M86934  
20 R-HEMBA1006540//EST//0.016:143:66//Hs.148189:AA897331  
R-HEMBA1006546//Homo sapiens mRNA for KIAA0582 protein, partial cds//2.2e-48:287:91//Hs.79507:AB011154  
R-HEMBA10065597//ESTs, Moderately similar to neurodegeneration-associated protein 1 [R.norvegicus]//1.8e-109:547:96//Hs.21122:AA191594  
R-HEMBA1006562//EST//1.1e-13:327:63//Hs.149641:AI283064  
25 R-HEMBA1006566//ESTs//2.6e-59:311:97//Hs.146014:R51876  
R-HEMBA1006569//ESTs//4.7e-89:458:96//Hs.42861:W74725  
R-HEMBA1006579//ESTs//2.9e-19:110:99//Hs.126191:AA873876  
R-HEMBA1006583//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//9.5e-29:276:76//Hs.144563:AF057280  
30 R-HEMBA1006595//ESTs//1.3e-96:487:96//Hs.43228:N67390  
R-HEMBA1006597//Small inducible cytokine A5 (RANTES)//9.8e-44:291:85//Hs.155464:AF088219  
R-HEMBA1006612  
R-nnnnnnnnnnnn//ESTs//1.2e-25:225:80//Hs.138852:AA284247  
R-HEMBA1006624//ESTs//1.9e-93:454:98//Hs.72531:AA773630  
35 R-HEMBA1006631//Human mRNA for KIAA0033 gene, partial cds//7.5e-60:286:90//Hs.22271:D26067  
R-HEMBA1006635//ESTs, Moderately similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!! [H.sapiens]//2.7e-91:426:100//Hs.139469:AI299889  
R-HEMBA1006639//ESTs, Highly similar to POLYADENYLATE-BINDING PROTEIN [Homo sapiens]//3.4e-37:186:  
100//Hs.109818:AA411185  
40 R-HEMBA1006643//ESTs//1.8e-35:189:97//Hs.139640:AA846777  
R-HEMBA1006648//Homo sapiens integrin-linked kinase (ILK) mRNA, complete cds//8.1e-108:567:94//Hs.6196:  
U40282  
R-HEMBA1006652//ESTs//7.6e-100:536:93//Hs.142613:AA129427  
R-HEMBA1006653//ESTs//2.0e-33:181:87//Hs.153599:AI282511  
45 R-HEMBA1006665//EST//1.2e-13:141:72//Hs.145596:AI263102  
R-HEMBA1006674//ESTs//3.1e-32:212:83//Hs.95115:AA206594  
R-HEMBA1006676//ESTs//2.6e-95:510:93//Hs.39140:AI041842  
R-HEMBA1006682//EST//1.4e-05:277:62//Hs.145762:AI269435  
R-HEMBA1006695//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//1.9e-32:  
50 261:79//Hs.77579:AF013263  
R-HEMBA1006696//ESTs//4.5e-95:448:99//Hs.155694:AI032695  
R-HEMBA1006708//ESTs, Weakly similar to Miller-Dieker lissencephaly gene [H.sapiens]//1.1e-92:483:94//Hs.  
6525:AI205313  
R-HEMBA1006709//ESTs//3.4e-25:207:80//Hs.88617:AA872062  
55 R-HEMBA1006717  
R-HEMBA1006737//EST//5.9e-30:317:75//Hs.140568:AA826002  
R-HEMBA1006744//Interleukin 10//3.7e-41:419:74//Hs.2180:M57627  
R-HEMBA1006754//ESTs//1.2e-46:276:83//Hs.141254:AI334099

R-HEMBA1006758//ESTs//0.00043:48:100//Hs.157265:AA489646  
 R-HEMBA1006767//EST//0.094:120:65//Hs.159873:R92763  
 R-HEMBA1006779//EST//9.3e-45:298:85//Hs.149580:AI281881  
 R-HEMBA1006780//ESTs//1.6e-46:423:77//Hs.141602:N63562  
 5 R-HEMBA1006789//ESTs//7.6e-55:245:95//Hs.6459:AI092936  
 R-HEMBA1006795//ESTs//8.6e-47:315:78//Hs.140491:W52705  
 R-HEMBA1006796//ESTs//0.26:175:65//Hs.103280:AI334978  
 R-HEMBA1006807//Homo sapiens DEC-205 mRNA, complete cds//5.7e-47:461:75//Hs.153563:AF011333  
 R-HEMBA1006821//ESTs//3.5e-12:222:68//Hs.150439:AI016305  
 10 R-HEMBA1006824//Homo sapiens mRNA, clone:RES4-16//6.7e-51:298:90//Hs.121493:D25272  
 R-HEMBA1006832//ESTs//0.0050:108:70//Hs.12853:T65556  
 R-HEMBA1006849//Human mRNA for KIAA0118 gene, partial cds//2.1e-49:367:83//Hs.154326:D42087  
 R-HEMBA1006865//ESTs//0.85:112:63//Hs.116430:AA644665  
 15 R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0772 protein, complete cds//1.8e-67:611:74//Hs.15519:AB018315  
 R-HEMBA1006885//ESTs//2.4e-66:347:96//Hs.100624:N95453  
 R-HEMBA1006900//ESTs//2.7e-91:466:96//Hs.32984:R89739  
 R-HEMBA1006921//ESTs//2.2e-33:170:100//Hs.152277:AA593117  
 20 R-HEMBA1006926//ESTs, Weakly similar to ZK1053.6 [C.elegans]//2.9e-28:213:84//Hs.9096:AA029400  
 R-HEMBA1006929//ESTs//4.0e-13:210:66//Hs.100895:AA479308  
 R-HEMBA1006936//ESTs//3.9e-05:60:93//Hs.8737:W22712  
 R-HEMBA1006938//EST//0.0021:244:62//Hs.144237:W52382  
 R-HEMBA1006941//Homo sapiens mRNA for putative thioredoxin-like protein//6.5e-77:371:98//Hs.42644:  
 AJ010841  
 25 R-HEMBA1006949//ESTs//1.2e-67:335:98//Hs.25780:R51321  
 R-HEMBA1006973//ESTs//0.029:242:61//Hs.146074:N34457  
 R-HEMBA1006976//EST//0.70:206:61//Hs.147092:AI189827  
 R-HEMBA1006993//Human mRNA for KIAA0327 protein, complete cds//2.6e-47:368:80//Hs.149323:AB002325  
 R-HEMBA1006996//ESTs//0.027:326:58//Hs.105008:AA451679  
 30 R-HEMBA1007002//ESTs//0.13:116:66//Hs.26928:Z41440  
 R-HEMBA1007017//ESTs//4.3e-47:208:87//Hs.155243:N70293  
 R-HEMBA1007018//ESTs, Moderately similar to LIC-2 [R.norvegicus]//2.8e-112:558:96//Hs.107905:AI248363  
 R-HEMBA1007045  
 35 R-HEMBA1007051//ESTs//2.5e-39:321:80//Hs.146811:AA410788  
 R-HEMBA1007052//EST//3.4e-41:377:74//Hs.44634:N34839  
 R-HEMBA1007062//ESTs//1.2e-92:439:99//Hs.162882:AA807140  
 R-HEMBA1007066//ESTs//0.85:204:61//Hs.22795:AI208272  
 R-HEMBA1007073//ESTs//6.6e-52:362:85//Hs.30821:AI096866  
 R-HEMBA1007078//EST, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//7.2e-  
 40 40:163:83//Hs.152369:AA504818  
 R-HEMBA1007085//ESTs//8.1e-103:519:96//Hs.90638:AI348087  
 R-HEMBA1007087//ESTs//3.1e-51:354:86//Hs.6449:W95025  
 R-HEMBA1007112//EST//0.090:328:59//Hs.136623:AA633597  
 R-HEMBA1007113//Homo sapiens mRNA, clone:RES4-16//1.1e-47:427:76//Hs.121493:D25272  
 45 R-HEMBA1007129//ESTs//6.1e-13:314:65//Hs.137538:AA769438  
 R-HEMBA1007147  
 R-HEMBA1007149//ESTs//9.7e-103:540:94//Hs.127240:AA149818  
 R-HEMBA1007151//ESTs//8.2e-102:505:96//Hs.24948:AA977674  
 50 R-nnnnnnnnnnnn//Homo sapiens epsin 2b mRNA, complete cds//1.6e-104:529:94//Hs.22396:AF062085  
 R-HEMBA1007178//ESTs//2.2e-57:366:90//Hs.21648:AI302954  
 R-HEMBA1007194//ESTs//9.0e-68:336:98//Hs.49760:AA741051  
 R-HEMBA1007203//Homo sapiens mRNA for KIAA0214 protein, complete cds//1.7e-62:332:95//Hs.3363:D86987  
 R-HEMBA1007206//Human c-yes-1 mRNA//4.5e-49:390:80//Hs.75680:M15990  
 55 R-HEMBA1007224//Homo sapiens mRNA for KIAA0797 protein, partial cds//7.4e-98:471:97//Hs.27197:  
 AB018340  
 R-HEMBA1007251//ESTs//1.6e-78:377:99//Hs.98912:AA436864  
 R-HEMBA1007256//ESTs//3.5e-20:127:79//Hs.137352:AA024934  
 R-HEMBA1007267//Homo sapiens KIAA0395 mRNA, partial cds//8.8e-48:343:83//Hs.43681:AL022394

R-HEMBA1007273//ESTs//1.0e-98:472:98//Hs.122610:AA807062  
R-HEMBA1007279//ESTs//3.3e-107:558:94//Hs.126480:AI221207  
R-HEMBA1007281//EST//0.074:244:63//Hs.29304:R73543  
R-HEMBA1007288//EST//9.4e-43:344:81//Hs.162112:AA524804  
5 R-HEMBA1007300//ESTs//0.096:371:57//Hs.102680:N52990  
R-HEMBA1007301  
R-HEMBA1007319//ESTs//7.7e-113:570:96//Hs.29263:AI337917  
R-HEMBA1007320//ESTs, Moderately similar to hypothetical protein 2 [H.sapiens]//5.5e-15:311:64//Hs.142764:  
AA205569  
10 R-HEMBA1007322//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//5.7e-49:383:83//Hs.139107:  
K00629  
R-HEMBA1007327//Human melanoma antigen recognized by T-cells (MART-1) mRNA//1.9e-42:371:79//Hs.  
15 154069:U06452  
R-HEMBA1007341//EST//3.0e-17:291:68//Hs.150788:AI301848  
R-HEMBA1007342//EST//2.7e-11:263:67//Hs.145259:AI218684  
15 R-HEMBA1007347//Homo sapiens DEC-205 mRNA, complete cds//9.7e-47:368:82//Hs.153563:AF011333  
R-HEMBB1000005//ESTs, Weakly similar to putative p150 [H.sapiens]//3.3e-44:341:71//Hs.111730:AA604403  
R-HEMBB1000008//Homo sapiens tumor necrosis factor superfamily member LIGHT mRNA, complete cds//3.2e-  
40:292:83//Hs.129708:AF064090  
20 R-HEMBB1000018//H.sapiens mRNA for urea transporter//5.0e-49:311:87//Hs.66710:X96969  
R-HEMBB1000024//ESTs//7.5e-21:234:76//Hs.157049:AI345418  
R-HEMBB1000025//ESTs//2.2e-36:371:78//Hs.56562:AA056332  
R-HEMBB1000030//ESTs//3.2e-76:373:97//Hs.140190:AA701449  
25 R-HEMBB1000036//ESTs, Highly similar to HYPOTHETICAL 43.2 KD PROTEIN C34E10.1 IN CHROMOSOME  
III [Caenorhabditis elegans]//6.0e-92:477:95//Hs.4877:AA418465  
R-HEMBB1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds//2.5e-92:467:97//  
Hs.20815:AF084928  
R-HEMBB1000039//ESTs//1.8e-43:361:71//Hs.108206:N64702  
R-HEMBB1000044//EST//7.6e-70:367:95//Hs.140860:R42954  
30 R-HEMBB1000048//EST//1.5e-45:262:91//Hs.157627:AI357802  
R-HEMBB1000050//ESTs//0.039:91:74//Hs.163189:AA236903  
R-HEMBB1000054//ESTs//3.0e-104:550:94//Hs.152395:AA533107  
R-HEMBB1000055//ESTs, Moderately similar to UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX SUB-  
UNIT VI REQUIRING PROTEIN [H.sapiens]//1.1e-72:350:99//Hs.116490:AA659584  
35 R-HEMBB1000059//ESTs//1.7e-10:200:70//Hs.163954:N57939  
R-HEMBB1000083//Homo sapiens mRNA for GCP170, complete cds//6.0e-41:337:80//Hs.4953:D63997  
R-HEMBB1000089//Human mRNA for KIAA0355 gene, complete cds//3.5e-39:487:70//Hs.153014:AB002353  
R-HEMBB1000099//ESTs//5.7e-37:353:75//Hs.22910:W18193  
40 R-HEMBB1000103//Homo sapiens mRNA for KIAA0640 protein, partial cds//6.5e-18:298:69//Hs.153026:  
AB014540  
R-HEMBB1000113//EST//8.2e-94:437:100//Hs.136893:AA805239  
R-HEMBB1000119//Homo sapiens ASMTL gene//1.2e-84:428:95//Hs.6315:Y15521  
R-HEMBB1000136//ESTs//0.043:262:59//Hs.61304:AA025692  
R-HEMBB1000141//ESTs//5.0e-38:254:79//Hs.141658:N77915  
45 R-HEMBB1000144//ESTs//9.6e-05:235:60//Hs.61700:AA033951  
R-HEMBB1000173//EST//9.6e-44:258:76//Hs.161917:AA483223  
R-HEMBB1000175//ESTs//4.8e-98:475:97//Hs.149740:AI199558  
R-HEMBB1000198//ESTs//1.0:123:62//Hs.116602:AA665965  
R-HEMBB1000215//Human mRNA for KIAA0355 gene, complete cds//2.2e-46:302:86//Hs.153014:AB002353  
50 R-HEMBB1000217//ESTs//2.2e-105:496:99//Hs.65973:AI339364  
R-HEMBB1000218//Homo sapiens DNA fragmentation factor 40 kDa subunit (DFF40) mRNA, complete cds//1.1e-  
48:292:79//Hs.133089:AF064019  
R-HEMBB10002267//ESTs, Weakly similar to HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME  
II [C.elegans]//5.1e-73:449:89//Hs.16803:AA843214  
55 R-HEMBB1000240//ESTs//1.1e-109:536:97//Hs.13528:AA523106  
R-HEMBB1000244//Small inducible cytokine A5 (RANTES)//9.5e-42:323:83//Hs.155464:AF088219  
R-HEMBB1000250//EST//8.8e-12:284:64//Hs.145960:AI276783  
R-HEMBB1000258//EST//4.5e-14:315:66//Hs.162551:AA584782

R-HEMBB1000264  
R-HEMBB1000266//ESTs, Weakly similar to similar to the beta transducin family [C.elegans]//2.7e-102:556:93//  
Hs.16079:AA083522  
R-HEMBB1000272//ESTs//4.3e-91:480:94//Hs.107467:H11385  
5 R-HEMBB1000274//Homo sapiens mRNA for KIAA0557 protein, partial cds//7.9e-24:198:72//Hs.101414:  
AB011129  
R-HEMBB1000284//ESTs//4.8e-64:389:91//Hs.118043:N50458  
R-HEMBB1000307//Human mRNA for KIAA0355 gene, complete cds//3.6e-43:288:87//Hs.153014:AB002353  
R-HEMBB1000312//ESTs//6.0e-23:272:73//Hs.121354:AA758601  
10 R-HEMBB1000317//ESTs//7.5e-90:424:99//Hs.150042:AI298034  
R-HEMBB1000318//Small inducible cytokine A5 (RANTES)//3.3e-41:318:80//Hs.155464:AF088219  
R-HEMBB1000335//ESTs//3.7e-15:324:65//Hs.85077:AA968576  
R-HEMBB1000336//ESTs//6.4e-76:402:95//Hs.17207:H92480  
15 R-HEMBB-1000337//ESTs//2.1e-80:391:97//Hs.118990:AI378084  
R-HEMBB1000338//Small inducible cytokine A5 (RANTES)//4.0e-39:274:85//Hs.155464:AF088219  
R-HEMBB1000339//EST//5.8e-41:336:79//Hs.151873:AA205736  
R-HEMBB1000341//ESTs//3.8e-19:310:68//Hs.37573:H59651  
R-HEMBB1000343//EST//1.1e-77:396:95//Hs.162664:AA605020  
20 R-HEMBB1000354//Human mRNA for KIAA0186 gene, complete cds//1.7e-15:293:65//Hs.36232:D80008  
R-HEMBB1000369//ESTs//1.6e-21:234:73//Hs.111583:AA463590  
R-HEMBB1000374//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//2.3e-56:335:77//Hs.  
92381:AB007956  
R-HEMBB1000376//H.sapiens mRNA for urea transporter//2.7e-50:525:74//Hs.66710:X96969  
R-HEMBB1000391//ESTs//6.6e-50:316:88//Hs.142259:AA828840  
25 R-HEMBB1000399//Homo sapiens mRNA for cell cycle checkpoint protein//3.8e-109:531:97//Hs.16184:AJ001642  
R-HEMBB1000402//H.sapiens mRNA for MACH-alpha-2 protein//2.7e-35:369:72//Hs.19949:X98173  
R-HEMBB1000404//ESTs//0.088:298:59//Hs.61607:AA032026  
R-HEMBB1000420//EST//2.2e-78:376:98//Hs.160787:AI336591  
R-HEMBB1000434//Human mrna for KIAA0118 gene, partial cds//3.9e-50:302:89//Hs.154326:D42087  
30 R-HEMBB1000438//ESTs, Weakly similar to !!!! ALU CLASS B WARNING ENTRY !!!! [H.sapiens]//0.30:214:63//  
Hs.142209:AA873303  
R-HEMBB1000441//Human c-yes-1 mRNA//2.2e-46:280:90//Hs.75680:M15990  
R-HEMBB1000449//ESTs//7.8e-59:332:92//Hs.87013:AA130221  
R-HEMBB1000455//EST//4.8e-14:421:65//Hs.68832:AA088438  
35 R-HEMBB1000472//ESTs//1.1e-104:505:98//Hs.132824:AI033396  
R-HEMBB1000480//Human mRNA for KIAA0392 gene, partial cds//2.5e-49:295:90//Hs.40100:AB002390  
R-HEMBB1000487//EST//0.78:87:68//Hs.134601:AI081506  
R-HEMBB1000490//Small inducible cytokine A5 (RANTES)//4.0e-39:320:80//Hs.155464:AF088219  
R-HEMBB1000491//Homo sapiens PYRIN (MEFV) mRNA, complete cds//3.7e-50:312:76//Hs.113283:AF018080  
40 R-HEMBB1000493//ESTs//7.1e-18:150:82//Hs.142068:AA176125  
R-HEMBB1000510//EST//1.4e-45:139:97//Hs.152260:AA489703  
R-HEMBB1000518//Human mRNA for KIAA0118 gene, partial cds//4.8e-50:415:78//Hs.154326:D42087  
R-HEMBB1000523//Homo sapiens PYRIN (MEFV) mRNA, complete cds//2.7e-57:497:78//Hs.113283:AF018080  
R-HEMBB1000530//ESTs//2.7e-73:425:90//Hs.141254:AI334099  
45 R-HEMBB1000550//EST//2.9e-11:113:79//Hs.161503:N68662  
R-HEMBB1000554//Human huntingtin interacting protein (HIP1) mRNA, complete cds//8.2e-13:92:81//Hs.97206:  
AF052288  
R-HEMBB1000556//ESTs//1.1e-94:529:92//Hs.33476:N36986  
R-HEMBB1000564//ESTs//1.3e-19:128:91//Hs.142058:N34258  
50 R-HEMBB1000573//ESTs//1.6e-86:494:90//Hs.120979:AI160709  
R-HEMBB1000575//ESTs//1.6e-45:232:74//Hs.141019:AA287618  
R-HEMBB1000586//ESTs//5.1e-42:281:83//Hs.138852:AA284247  
R-HEMBB1000589//ESTs//1.0e-10:184:71//Hs.142677:R95895  
R-HEMBB1000591//ESTs//3.2e-40:406:75//Hs.138787:H73704  
55 R-HEMBB1000592//ESTs//1.8e-97:455:99//Hs.94229:W65391  
R-HEMBB1000598//Human anti secretory factor-1 mRNA, complete cds//1.8e-46:305:85//Hs.148495:AF050199  
R-HEMBB1000623//ESTs//8.3e-47:277:92//Hs.6045:W67125  
R-HEMBB1000630//ESTs//5.1e-106:538:96//Hs.13422:AI082249

R-HEMBB1000631//ESTs//5.1e-100:508:96//Hs.110379:N58152  
R-HEMBB1000632//ESTs//6.2e-44:371:80//Hs.132722:AA618531  
R-HEMBB1000637//Human mRNA for KIAA0080 gene, partial cds//6.4e-49:254:86//Hs.74554:D38522  
R-HEMBB1000638//EST//2.2e-38:371:76//Hs.162236:AA551582  
5 R-HEMBB1000643//ESTs//0.0049:191:62//Hs.55445:W31963  
R-HEMBB1000649//ESTs, Moderately similar to hTAFII68 [H.sapiens]//4.0e-76:399:95//Hs.124106:AA948100  
R-HEMBB1000652//ESTs//1.5e-14:271:64//Hs.163954:N57939  
R-HEMBB1000665//ESTs//4.2e-12:109:87//Hs.41407:W94988  
R-HEMBB1000671//ESTs//2.8e-68:439:87//Hs.140491:W52705  
10 R-HEMBB1000673//EST//0.58:46:82//Hs.142286:AA338293  
R-HEMBB1000684//ESTs//8.5e-20:307:72//Hs.122825:AA765454  
R-nnnnnnnnnnnn//Homo sapiens neuroan1 mRNA, complete cds//6.5e-52:287:93//Hs.158300:AF040723  
R-HEMBB1000705//Small inducible cytokine A5 (RANTES)//4.6e-24:165:78//Hs.155464:AF088219  
R-HEMBB1000706//EST//1.2e-10:211:65//Hs.105524:AA521412  
15 R-HEMBB1000709//ESTs, Weakly similar to putative p150 [H.sapiens]//3.9e-50:245:99//Hs.111730:AA604403  
R-HEMBB1000725//Human mRNA for KIAA0308 gene, partial cds//0.11:350:59//Hs.10351:AB002306  
R-HEMBB1000726//EST//5.3e-49:303:88//Hs.149580:AI281881  
R-HEMBB100073 8//Homo sapiens mRNA, clone:RES4-16//2.5e-49:302:89//Hs.121493:D25272  
R-HEMBB1000749//ESTs//1.6e-49:331:86//Hs.152788:AA630925  
20 R-HEMBB1000763//ESTs//9.7e-104:474:95//Hs.77480:AA100522  
R-HEMBB1000770//EST//1.0e-75:359:99//Hs.136564:AA642445  
R-HEMBB1000781//ESTs//5.3e-66:317:99//Hs.28827:AI125541  
R-HEMBB1000789//ESTs//5.9e-83:394:99//Hs.120842:AA435771  
R-HEMBB1000790//PLATELET GLYCOPROTEIN V PRECURSORY//1.3e-37:193:75//Hs.73734:Z23091  
25 R-HEMBB1000794//ESTs//7.1e-98:490:96//Hs.105743:AA532718  
R-HEMBB1000807//ESTs//2.6e-22:145:92//Hs.53913:AA908961  
R-HEMBB1000810//Small inducible cytokine A5 (RANTES)//1.8e-34:206:79//Hs.155464:AF088219  
R-HEMBB1000821//ESTs//2.4e-90:425:99//Hs.118659:AI052447  
R-HEMBB1000822//ESTs//1.7e-45:288:89//Hs.24130:R27124  
30 R-HEMBB1000826//Small inducible cytokine A5 (RANTES)//2.9e-51:245:82//Hs.155464:AF088219  
R-HEMBB1000827//EST//2.8e-40:295:84//Hs.149580:AI281881  
R-HEMBB1000831//ESTs//4.0e-59:291:98//Hs.62675:AA044176  
R-HEMBB1000835//ESTs//7.3e-21:124:82//Hs.102671:N52545  
R-HEMBB1000840//ATPase, Na<sup>+</sup>/K<sup>+</sup> transporting, beta 2 polypeptide//1.3e-43:163:84//Hs.78854:AF007876  
35 R-HEMBB1000848//Homo sapiens mRNA for KIAA0565 protein, complete cds//9.5e-41:367:78//Hs.129740:AB011137  
R-HEMBB1000852//EST//1.2e-09:188:70//Hs.127869:AA968599  
R-HEMBB1000870//Cytochrome P450, 51 (lanosterol 14-alpha-demethylase)//1.0e-41:483:73//Hs.2379:U23942  
R-HEMBB1000876//EST//0.0022:211:63//Hs.125552:AA884141  
40 R-HEMBB1000883//ESTs//1.4e-65:343:95//Hs.98269:H27247  
R-HEMBB1000887//ESTs//4.0e-22:212:79//Hs.138965:AI004740  
R-HEMBB1000888//EST//8.2e-07:196:64//Hs.118276:W15258  
R-HEMBB1000890//ISLET AMYLOID POLYPEPTIDE PRECURSORY//1.1e-46:327:83//Hs.51048:X68830  
R-HEMBB1000893//EST//4.7e-34:242:85//Hs.149580:AI281881  
45 R-HEMBB1000908//EST//0.95:27:100//Hs.142568:AA285066  
R-HEMBB1000910//ESTs//1.9e-36:318:78//Hs.141140:AA715983  
R-HEMBB1000913//Human mRNA for KIAA0327 protein, complete cds//2.5e-33:367:73//Hs.149323:AB002325  
R-HEMBB1000915//ESTs//0.00018:188:61//Hs.44847:AI222742  
R-HEMBB1000917//Homo sapiens KIAA0414 mRNA, partial cds//3.7e-41:228:84//Hs.127649:AB007874  
50 R-HEMBB1000927//ESTs//2.2e-62:307:98//Hs.97044:AA365784  
R-HEMBB1000947//ESTs, Weakly similar to F26E4.13 [C.elegans]//3.3e-60:350:91//Hs.49163:AA532881  
R-HEMBB1000959//Human Line-1 repeat mRNA with 2 open reading frames//8.1e-84:546:86//Hs.23094:MI9503  
R-HEMBB1000973//ESTs//6.8e-95:445:99//Hs.105859:AI419354  
R-HEMBB1000975//ESTs//1.2e-39:197:100//Hs.26176:AI032007  
55 R-HEMBB1000981//EST//7.7e-58:284:98//Hs.60179:AA007242  
R-HEMBB1000985//ESTs//1.2e-103:524:95//Hs.43102:AA131369  
R-HEMBB1000991//EST//0.99:58:72//Hs.100246:T23625  
R-HEMBB1000996//Homo sapiens LIM protein mRNA, complete cds//1.3e-41:482:70//Hs.154103:AF061258

	R-HEMBB1001004//ESTs//5.7e-70:362:95//Hs.6434:W27112
5	R-HEMBB1001008//ESTs, Weakly similar to hypothetical L1 protein [H.sapiens]//2.3e-25:339:71//Hs.129992:H58762
	R-HEMBB1001011//ESTs//4.0e-53:325:92//Hs.33268:AI191214
	R-HEMBB1001014//ESTs//1.3e-46:323:83//Hs.163980:AA715814
	R-HEMBB1001020//Homo sapiens PYRIN (MEFV) mRNA, complete cds//3.0e-46:305:76//Hs.113283:AF018080
10	R-HEMBB1001024//ESTs//8.5e-47:374:80//Hs.141602:N63562
	R-HEMBB1001037//ESTs//2.6e-47:282:91//Hs.155384:Z78385
	R-HEMBB1001047//EST//6.2e-33:232:74//Hs.160146:AI049975
	R-HEMBB1001051//ESTs//3.7e-79:385:98//Hs.95290:AA046107
	R-HEMBB1001056//Homo sapiens mRNA for KIAA0618 protein, complete cds//1.1e-87:497:91//Hs.15832:AB014518
15	R-HEMBB1001058//Homo sapiens mRNA for KIAA0475 protein, complete cds//2.2e-26:125:81//Hs.5737:AB007944
	R-HEMBB1001060//ESTs//1.9e-37:541:69//Hs.141534:N64785
	R-HEMBB1001063//ESTs//4.7e-42:269:88//Hs.55855:AA621381
	R-HEMBB1001068//Homo sapiens liprin-beta2 mRNA, partial cds//9.1e-107:512:97//Hs.12953:AF034803
	R-HEMBB1001096//Human HsLIM15 mRNA for HsLiml5, complete cds//1.2e-20:233:70//Hs.37181:D64108
20	R-HEMBB1001102//Human mRNA for KIAA0355 gene, complete cds//9.1e-40:299:82//Hs.153014:AB002353
	R-HEMBB1001105//Homo sapiens PYRIN (MEFV) mRNA, complete cds//4.8e-46:296:87//Hs.113283:AF018080
	R-HEMBB1001114//ESTs//6.2e-44:293:86//Hs.70279:AA757426
	R-HEMBB1001117//ESTs//1.1e-80:471:90//Hs.61935:T75092
	R-HEMBB1001119//ESTs//4.0e-38:213:84//Hs.109140:AI289942
	R-HEMBB1001126
25	R-HEMBB1001133//Human SS-A/Ro ribonucleoprotein autoantigen 60 kd subunit mRNA, complete cds//1.6e-24:285:73//Hs.554:M25077
	R-HEMBB1001137//ESTs//4.6e-10:66:100//Hs.74924:AI332962
	R-HEMBB1001142//EST//6.4e-48:315:85//Hs.149580:AI281881
30	R-HEMBB1001151
	R-HEMBB1001153//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.3e-65:331:96//Hs.154179:AA579197
	R-HEMBB1001169//Oxytocin receptor//1.5e-25:165:73//Hs.2820:X64878
	R-nnnnnnnnnnnnnn//ESTs//3.5e-41:233:93//Hs.129218:AA991162
35	R-HEMBB1001177
	R-HEMBB1001182//ESTs//1.9e-86:455:95//Hs.6937:AA524349
	R-HEMBB1001199
	R-HEMBB1001208//ESTs//3.3e-43:216:99//Hs.121806:N71183
	R-HEMBB1001209//ESTs//6.7e-80:409:96//Hs.141185:R99549
40	R-HEMBB1001210//ESTs//2.2e-46:290:88//Hs.103329:D11573
	R-HEMBB1001218//Kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monoclonal and antibody IA4))//3.1e-44:298:87//Hs.103458:X53795
	R-HEMBB1001221//ESTs//9.4e-75:353:100//Hs.151504:AA550817
	R-HEMBB1001234//ESTs, Highly similar to 65 KD YES-ASSOCIATED PROTEIN [Gallus gallus]//3.8e-80:400:96//Hs.71873:AA148213
45	R-HEMBB1001242//ESTs//1.6e-63:404:87//Hs.25534:AA149560
	R-HEMBB1001249//ESTs//3.8e-34:360:70//Hs.150727:AI292236
	R-HEMBB1001253//EST//0.0011:84:77//Hs.124579:AA853987
	R-HEMBB1001254//ESTs//4.5e-95:444:99//Hs.161059:AI431268
50	R-HEMBB1001267//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//1.3e-50:524:73//Hs.159897:AB007970
	R-HEMBB1001271//Human mRNA for KIAA0118 gene, partial cds//4.0e-45:323:84//Hs.154326:D42087
	R-HEMBB1001282//EST//2.9e-78:401:96//Hs.72871:AA169412
	R-HEMBB1001288//ESTs, Highly similar to HYPOTHETICAL 27.3 KD PROTEIN ZK353.7 IN CHROMOSOME III [Caenorhabditis elegans]//2.6e-104:515:97//Hs.16606:W81021
55	R-HEMBB1001289//ESTs//7.8e-45:440:75//Hs.44702:AI148840
	R-HEMBB1001294//ESTs//1.9e-100:476:99//Hs.109017:AI057112
	R-HEMBB1001302
	R-HEMBB1001304//ESTs//4.0e-92:431:99//Hs.113750:AI091154

R-HEMBB1001314//Interleukin 10//6.3e-41:334:79//Hs.2180:M57627  
R-HEMBB1001315//Interleukin 10//1.9e-43:285:87//Hs.2180:M57627  
R-HEMBB1001317//Human cytochrome P450-IIB (hIIB3) mRNA, complete cds//8.4e-45:357:81//Hs.110194:  
M29873  
5 R-HEMBB1001326//ESTs//0.85:174:62//Hs.133487:AI393754  
R-HEMBB1001331//ESTs, Weakly similar to DFS70 [H.sapiens]//6.5e-61:313:96//Hs.43071:AA206222  
R-HEMBB1001335//EST//5.2e-80:381:99//Hs.116769:AA630365  
R-HEMBB1001337//ESTs//2.7e-84:404:99//Hs.148966:AI242639  
R-HEMBB1001339//ESTs//2.1e-97:485:96//Hs.88357:AA262470  
10 R-HEMBB1001346  
R-HEMBB1001348//ESTs//1.1e-43:295:85//Hs.163604:R94354  
R-HEMBB1001356//EST//6.0e-11:89:88//Hs.152366:AA486721  
R-HEMBB1001364//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.0e-  
12:129:79//Hs.9792:AA027055  
15 R-HEMBB1001366//Human mRNA for KIAA0118 gene, partial cds//1.2e-50:550:72//Hs.154326:D42087  
R-HEMBB1001367//ESTs//1.2e-19:165:82//Hs.146314:R99617  
R-HEMBB1001369//Small inducible cytokine A5 (RANTES)//1.9e-25:217:80//Hs.155464:AF088219  
R-HEMBB1001380//ESTs//4.0e-08:216:63//Hs.143763:AI174205  
R-HEMBB1001384//ESTs//6.6e-110:547:96//Hs.6671:AI341699  
20 R-HEMBB1001387//ESTs//1.1e-104:497:98//Hs.87654:AA853970  
R-HEMBB1001394//ESTs//6.4e-73:428:89//Hs.139922:AA281350  
R-HEMBB1001410//Alcohol dehydrogenase 7 sigma subunit (class IV)//0.88:365:58//Hs.389:X76342  
R-HEMBB1001424//ESTs//1.3e-88:466:94//Hs.42174:AA194644  
R-HEMBB1001426//ESTs//2.2e-45:337:82//Hs.37573:H59651  
25 R-HEMBB1001429//EST//3.8e-59:543:76//Hs.158803:AI376846  
R-HEMBB1001436//ESTs//3.7e-69:332:99//Hs.156518:AA724317  
R-HEMBB1001443//ESTs//4.8e-54:270:98//Hs.21898:AI088201  
R-HEMBB1001449//ESTs//3.2e-43:170:84//Hs.150727:AI292236  
R-HEMBB1001454//ESTs//9.1e-46:304:86//Hs.139190:N55515  
30 R-HEMBB1001458//ESTs//3.2e-98:478:97//Hs.50144:N67293  
R-HEMBB1001463//Homo sapiens KIAA0421 mRNA, partial cds//4.3e-50:440:78//Hs.41742:AB007881  
R-HEMBB1001464//ESTs, Weakly similar to K01H12.1 [C.elegans]//0.25:222:61//Hs.13275:AI341468  
R-HEMBB1001482//ESTs, Moderately similar to zinc finger protein [R.norvegicus]//0.80:53:83//Hs.26799:W74481  
R-HEMBB1001500//EST//1.4e-13:310:67//Hs.162663:AA604515  
35 R-HEMBB1001521//Homo sapiens mRNA for KIAA0737 protein, complete cds//2.5e-29:186:92//Hs.17630:  
AB018280  
R-HEMBB1001527//ESTs, Weakly similar to HYPOTHETICAL 92.1 KD PROTEIN ZK1098.3 IN CHROMOSOME  
III [Caenorhabditis elegans]//4.7e-51:404:81//Hs.141429:AA631915  
R-HEMBB1001531//ESTs//3.3e-13:250:67//Hs.139158:AA226159  
40 R-HEMBB1001535//H.sapiens mRNA for sigma 3B protein//1.9e-39:291:82//Hs.154782:X99459  
R-HEMBB1001536//Human mRNA for KIAA0355 gene, complete cds//5.0e-44:318:83//Hs.153014:AB002353  
R-HEMBB1001537//Homo sapiens KIAA0409 mRNA, pardal cds//3.2e-47:318:80//Hs.5158:AB007869  
R-HEMBB1001555//ESTs//2.6e-13:182:71//Hs.112671:AI377274  
R-HEMBB1001562//ESTs//1.7e-43:316:83//Hs.151365:AA643962  
45 R-HEMBB1001564//EST//1.3e-35:141:81//Hs.162197:AA53521  
R-HEMBB1001565//Human mRNA for KIAA0331 gene, complete cds//5.1e-18:152:85//Hs.146395:AB002329  
R-HEMBB1001585//ESTs//1.1e-32:190:84//Hs.33354:AA179944  
R-HEMBB1001586//ESTs//4.9e-94:447:99//Hs.124084:AA843219  
R-HEMBB1001588//EST//8.3e-27:363:69//Hs.141603:N66015  
50 R-HEMBB1001603//ESTs//1.2e-101:482:99//Hs.12403:AI090184  
R-HEMBB1001618//ESTs//5.8e-35:437:70//Hs.136868:AA805044  
R-HEMBB1001619//EST//1.7e-38:476:70//Hs.139093:AA166888  
R-HEMBB1001630//Homo sapiens mRNA, clone:RES4-16//5.7e-41:193:90//Hs.121493:D25272  
R-HEMBB1001635//ESTs//9.5e-34:304:82//Hs.140444:AI002082  
55 R-HEMBB1001637//ESTs//1.0e-42:443:74//Hs.21978:AA009633  
R-HEMBB1001641//EST//2.4e-06:67:86//Hs.162398:AA572813  
R-HEMBB1001653//ESTs//4.8e-80:381:99//Hs.140502:AA806438  
R-HEMBB1001665//ESTs//2.3e-44:372:79//Hs.132818:AI038577

R-HEMBB1001668//ESTs//0.73:212:62//Hs.8928:N32572  
R-HEMBB1001673//Homo sapiens mRNA for KIAA0646 protein, complete cds//5.9e-117:573:97//Hs.24439:  
AB014546  
R-HEMBB1001684//ESTs, Moderately similar to Tbcl [M.musculus]//5.4e-106:523:97//Hs.26939:AA804534  
5 R-HEMBB1001685//ESTs, Moderately similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]//1.9e-  
43:292:86//Hs.96337:AA225358  
R-HEMBB1001695//ESTs//3.7e-101:539:94//Hs.78289:R60867  
R-HEMBB1001704//EST//0.96:248:57//Hs.163025:AA703038  
R-HEMBB1001706//ESTs//1.3e-39:308:81//Hs.141318:N71080  
10 R-HEMBB1001707//ESTs, Moderately similar to hypothetical protein 2 [H.sapiens]//4.9e-32:277:73//Hs.142764:  
AA205569  
R-HEMBB1001717//ESTs//1.6e-34:225:87//Hs.57883:AA218645  
R-HEMBB1001735//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//  
8.6e-11:158:71//Hs.141263:H64113  
15 R-HEMBB1001736//ESTs//0.0035:223:60//Hs.21354:AA203403  
R-HEMBB1001747//EST//9.9e-55:293:81//Hs.112866:AA620488  
R-HEMBB1001749//ESTs//2.5e-13:95:91//Hs.139888:N25287  
R-HEMBB1001753//ESTs//2.6e-07:141:70//Hs.144604:AI052059  
R-HEMBB1001756//EST//2.6e-06:165:64//Hs.121195:AA757211  
20 R-HEMBB1001760//LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR//1.3e-24:264:74//Hs.70008:  
L00352  
R-HEMBB1001762//ESTs//2.1e-81:447:93//Hs.152766:AA211369  
R-HEMBB1001785//ESTs//0.040:390:58//Hs.116651:AA993406  
R-HEMBB1001797//ESTs//2.1e-90:428:99//Hs.8958:AA169253  
25 R-HEMBB1001802//Desmin//9.9e-95:497:93//Hs.119104:M63391  
R-HEMBB1001812//ESTs//1.2e-12:91:78//Hs.138852:AA284247  
R-HEMBB1001816//Human Line-1 repeat mRNA with 2 open reading frames//5.9e-13:143:76//Hs.23094:M19503  
R-HEMBB1001831//Homo sapiens PAM COOH-terminal interactor protein 1 (PCIP1) mRNA, complete cds//5.5e-  
106:498:98//Hs.159396:AF056209  
30 R-HEMBB1001836//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//9.6e-39:288:73//Hs.  
67619:AB007957  
R-HEMBB1001839  
R-HEMBB1001850//EST//0.020:119:68//Hs.32767:H38125  
R-HEMBB1001863//ESTs//4.5e-17:226:72//Hs.157253:AI357539  
35 R-HEMBB1001867//ESTs//2.3e-16:254:68//Hs.123664:AA806106  
R-HEMBB1001868//EST//9.8e-30:155:100//Hs.160572:AA888397  
R-HEMBB1001869//ESTs//2.8e-42:376:78//Hs.141973:N21434  
R-HEMBB1001872//EST//0.85:156:64//Hs.119501:AA487980  
R-HEMBB1001874//EST//0.64:107:70//Hs.147482:AI215572  
40 R-HEMBB1001875//EST//0.079:199:59//Hs.121810:AA775240  
R-HEMBB1001880//Thromboxane A2 receptor//9.0e-47:297:88//Hs.89887:D38081  
R-HEMBB1001899//ESTs//6.3e-68:323:100//Hs.121538:AA609310  
R-HEMBB1001905//ESTs//4.4e-19:227:73//Hs.146173:AA906191  
R-HEMBB1001906//ESTs//1.6e-90:463:95//Hs.28266:H46725  
45 R-HEMBB1001908//Homo sapiens EVI5 homolog mRNA, complete cds//3.7e-27:557:64//Hs.26929:AF008915  
R-HEMBB1001910//EST//6.0e-37:308:78//Hs.162197:AA535216  
R-HEMBB1001911//Homo sapiens tapasin (NGS-17) mRNA, complete cds//8.0e-58:367:79//Hs.5247:AF029750  
R-HEMBB1001915//ESTs//3.1e-73:395:93//Hs.17054:AI139897  
R-HEMBB1001921//Human mRNA for KIAA0392 gene, partial cds//2.7e-50:323:88//Hs.40100:AB002390  
50 R-HEMBB1001922//H.sapiens mRNA for novel member of serine-arginine domain protein, SRrp129//7.4e-38:531:  
70//Hs.153086:Y11251  
R-HEMBB1001925//Human mRNA for KIAA0327 protein, complete cds//9.5e-19:199:77//Hs.149323:AB002325  
R-HEMBB1001930//EST//1.9e-18:136:78//Hs.132635:AI032875  
R-HEMBB1001944//EST//0.034:228:57//Hs.93664:N23366  
55 R-HEMBB1001945//ESTs//1.8e-83:439:95//Hs.7341:N57875  
R-HEMBB1001947//ESTs//5.6e-109:533:97//Hs.48855:AA134589  
R-HEMBB1001950//ESTs//1.5e-107:583:93//Hs.8033:N94998  
R-HEMBB1001952//ESTs//3.1e-40:283:85//Hs.146811:AA410788

R-HEMBB1001953//Human mRNA for KIAA0080 gene, partial cds//6.2e-50:284:83//Hs.74554:D38522  
 R-HEMBB1001957//EST//4.8e-50:382:81//Hs.149580:AI281881  
 R-HEMBB1001962//ESTs//1.5e-20:143:88//Hs.11924:W26972  
 R-HEMBB1001967//Homo sapiens mRNA for KIAA0575 protein, complete cds//2.3e-61:296:88//Hs.153468:  
 5 AB011147  
 R-HEMBB1001973//ESTs//1.4e-48:303:88//Hs.132722:AA618531  
 R-HEMBB1001983//ESTs//2.6e-72:374:95//Hs.141022:H06475  
 R-HEMBB1001988//ESTs//2.0e-31:204:88//Hs.142531:N91572  
 R-HEMBB1001990//ESTs//9.4e-115:574:96//Hs.44426:AA173223  
 10 R-HEMBB1001996  
 R-HEMBB1001997//ESTs//7.6e-78:380:98//Hs.32682:H37798  
 R-HEMBB1002002//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//3.0e-18:222:71//Hs.103948:  
 K00627  
 R-HEMBB1002005//EST//2.2e-41:339:80//Hs.160833:AI345334  
 15 R-HEMBB1002009//EST//2.9e-44:245:94//Hs.28788:R66896  
 R-HEMBB1002015//EST//0.0027:198:63//Hs.160868:AI359052  
 R-HEMBB1002042//ESTs//1.1e-75:529:84//Hs.106919:AA523900  
 R-HEMBB1002043//ESTs//7.9e-40:292:83//Hs.70279:AA757426  
 R-HEMBB1002044//ESTs//2.1e-92:460:94//Hs.115897:AA156638  
 20 R-HEMBB1002045//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.6e-75:301:85//Hs.113283:AF018080  
 R-HEMBB1002049//ESTs//3.8e-77:409:94//Hs.122624:R82638  
 R-HEMBB1002050//ESTs//8.7e-45:330:82//Hs.44702:AI148840  
 R-HEMBB1002068//ESTs//8.3e-70:333:99//Hs.134807:AI090671  
 R-HEMBB1002069//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//1.5e-75:486:81//Hs.  
 25 129735:AF010144  
 R-HEMBB1002092//ESTs//6.5e-46:331:83//Hs.22910:W18193  
 R-HEMBB1002094//EST//3.6e-45:280:88//Hs.149580:AI281881  
 R-HEMBB1002115  
 R-HEMBB1002139//ESTs//4.2e-45:318:85//Hs.107657:AA126814  
 30 R-HEMBB1002142//Homo sapiens haemopoietic progenitor homeobox HPX42B (HPX42B) mRNA, complete cds//  
 1.4e-45:281:88//Hs.125231:AF068006  
 R-HEMBB1002152//EST//4.3e-39:250:89//Hs.156552:AA833553  
 R-HEMBB1002189//H.sapiens mRNA for translin associated protein X//1.4e-47:328:85//Hs.96247:X95073  
 R-HEMBB1002190//ESTs//8.3e-05:122:70//Hs.41974:AF039185  
 35 R-HEMBB1002193//Human sky mRNA for Sky, complete cds//8.9e-24:398:69//Hs.301:U18934  
 R-HEMBB1002217//EST//6.6e-50:303:89//Hs.149580:AI281881  
 R-HEMBB1002218//ESTs//2.3e-19:150:86//Hs.136031:W95841  
 R-HEMBB1002232//ESTs//8.9e-47:445:77//Hs.163971:N27584  
 R-HEMBB1002247//EST//6.6e-09:236:65//Hs.130578:AI004631  
 40 R-HEMBB1002249//ESTs//5.2e-16:325:64//Hs.156253:AI334807  
 R-HEMBB1002254//Human Line-1 repeat mRNA with 2 open reading frames//3.8e-99:590:88//Hs.23094:M19503  
 R-HEMBB1002255//Human mRNA for KIAA0365 gene, partial cds//5.6e-45:342:83//Hs.84123:AB002363  
 R-HEMBB1002266//ESTs//4.4e-98:472:98//Hs.65366:AI189112  
 R-HEMBB1002280//EST//2.9e-41:247:90//Hs.161917:AA483223  
 45 R-HEMBB1002300//ESTs//8.4e-19:229:75//Hs.138463:N72305  
 R-HEMBB1002306//Homo sapiens KIAA0432 mRNA, complete cds//0.0021:138:67//Hs.155174:AB007892  
 R-HEMBB1002327//EST//0.042:249:61//Hs.121097:AA714637  
 R-HEMBB1002329//ESTs//1.7e-94:453:99//Hs.7114:R24312  
 R-HEMBB1002340//ESTs//5.8e-15:163:77//Hs.26378:H10228  
 50 R-HEMBB1002342//Homo sapiens mRNA for putative thioredoxin-like protein//0.85:46:84//Hs.42644:AJ010841  
 R-HEMBB1002358//ESTs//2.0e-52:319:81//Hs.140255:AA708322  
 R-HEMBB1002359//ESTs//2.7e-106:517:97//Hs.13634:AI051613  
 R-HEMBB1002364//Human mRNA for KIAA0080 gene, partial cds//5.3e-37:360:65//Hs.74554:D38522  
 R-HEMBB1002371//Catalase//3.3e-22:235:77//Hs.76359:X04085  
 55 R-HEMBB1002381//Homo sapiens (JH8) mRNA, partial cds//1.0e-08:120:78//Hs.142296:AF072467  
 R-HEMBB1002383//ESTs//3.5e-108:520:98//Hs.45140:D80055  
 R-HEMBB1002387  
 R-HEMBB1002415//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.3e-23:

168:77//Hs.133526:N21103  
R-HEMBB1002425//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//3.2e-57:304:90//Hs.144563:  
AF057280  
R-HEMBB1002442//ESTs//2.7e-48:289:87//Hs.155243:N70293  
5 R-HEMBB1002453//Human mRNA for KIAA0355 gene, complete cds//6.2e-45:292:87//Hs.153014:AB002353  
R-HEMBB1002457//Human mRNA for KIAA0118 gene, partial cds//2.7e-46:546:71//Hs.154326:D42087  
R-HEMBB1002458//EST//1.8e-72:343:100//Hs.162006:AA508089  
R-HEMBB1002477//ESTs//1.6e-38:215:93//Hs.18240:AA460083  
R-HEMBB1002489//ESTs//1.2e-101:534:94//Hs.7981:H15176  
10 R-HEMBB1002492//ESTs//5.0e-14:350:62//Hs.99205:AA204969  
R-HEMBB1002495//ESTs//2.1e-19:147:86//Hs.163747:AA174017  
R-HEMBB1002502//ESTs, Weakly similar to p40 [H.sapiens]//1.2e-68:336:98//Hs.141515:T41142  
R-HEMBB1002509//ESTs//2.7e-97:459:99//Hs.127638:AI014615  
15 R-HEMBB1002510//ESTs, Weakly similar to located at OATL1 [H.sapiens]//2.2e-48:265:95//Hs.48827:AA873278  
R-HEMBB1002520//EST//7.2e-40:198:84//Hs.140493:AA804538  
R-HEMBB1002522//Human putative transmembrane receptor IL-1Rrp mRNA, complete cds//0.50:142:69//Hs.  
159301:U43672  
R-HEMBB1002531//EST//0.024:147:61//Hs.148305:AA909605  
R-HEMBB1002534//EST//3.1e-22:168:84//Hs.146794:AI149478  
20 R-HEMBB1002545//ESTs//9.2e-90:421:99//Hs.118317:AI033259  
R-HEMBB1002550//ESTs, Weakly similar to similar to S. cerevisiae LAG1 [C.elegans]//5.1e-22:210:81//Hs.11896:  
T68813  
R-HEMBB1002556//ISLET AMYLOID POLYPEPTIDE PRECURSORY//1.9e-45:344:82//Hs.51048:X68830  
R-HEMBB1002579//ESTs//4.6e-47:326:85//Hs.155184:AA573189  
25 R-HEMBB1002582//ESTs//0.00036:91:76//Hs.140039:AA047045  
R-HEMBB1002590//ESTs//1.0e-37:210:84//Hs.36658:N91138  
R-HEMBB1002596//Human mRNA for KIAA0118 gene, partial cds//2.2e-46:297:87//Hs.154326:D42087  
R-HEMBB1002600//EST//2.5e-17:147:84//Hs.121918:AA777424  
R-HEMBB1002601//ESTs//7.8e-68:358:95//Hs.101489:R66923  
30 R-HEMBB1002603//EST//1.1e-47:281:90//Hs.149580:AI281881  
R-HEMBB1002607//ESTs//5.4e-75:379:97//Hs.29438:H42896  
R-HEMBB1002610//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//6.2e-07:  
140:70//Hs.155456:AA707265  
R-HEMBB1002613//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0508//8.5e-47:278:83//Hs.  
159187:AB007977  
R-HEMBB1002614//ESTs//3.4e-81:383:99//Hs.13012:AI094150  
R-HEMBB1002617//Homo sapiens protease-activated receptor 4 mRNA, complete cds//7.4e-19:151:80//Hs.  
137574:AF055917  
R-HEMBB1002623//ESTs//1.6e-45:288:87//Hs.138852:AA284247  
40 R-HEMBB1002635//Small inducible cytokine A5 (RANTES)//5.5e-39:278:81//Hs.155464:AF088219  
R-HEMBB1002664//EST//8.9e-49:315:87//Hs.149580:AI281881  
R-HEMBB1002677//ESTs//0.65:159:62//Hs.163517:AI419775  
R-HEMBB1002683//H.sapiens mRNA for delta 4-3-oxosteroid 5 beta-reductase//8.6e-54:543:75//Hs.2638:  
Z28339  
45 R-HEMBB1002684//ESTs//3.0e-18:148:87//Hs.158270:AA776646  
R-HEMBB1002686//ESTs//6.1e-80:419:96//Hs.103002:W02753  
R-HEMBB1002692//ESTs//3.3e-58:451:82//Hs.141254:AI334099  
R-HEMBB1002697//ESTs//6.2e-86:423:98//Hs.129812:AA769487  
R-HEMBB1002699//EST//5.6e-46:322:84//Hs.140231:AI054398  
50 R-HEMBB1002702//ESTs//5.6e-36:412:72//Hs.154993:AA142842  
R-HEMBB1002705//POLYPOSIS LOCUS PROTEIN 1//0.024:412:58//Hs.74648:M73547  
R-HEMBB1002712//ESTs//9.0e-96:451:99//Hs.136806:AA805682  
R-MAMMA1000009//ESTs//3.0e-78:392:96//Hs.163947:AA678701  
R-MAMMA1000019//Small inducible cytokine A5 (RANTES)//1.5e-47:247:87//Hs.155464:AF088219  
55 R-MAMMA1000020//Zinc finger protein 2 (A1-5)//4.9e-49:384:80//Hs.155533:X60152  
R-MAMMA1000025//Homo sapiens KIAA0441 mRNA, complete cds//4.7e-11:154:71//Hs.32511:AB007901  
R-MAMMA1000043//Homo sapiens mRNA for KIAA0761 protein, partial cds//2.0e-58:277:84//Hs.93121:  
AB018304

R-MAMMA1000045//ESTs//1.0e-38:225:92//Hs.142567:AA287165  
R-MAMMA1000055//EST//0.14:91:67//Hs.144061:AA996350  
R-MAMMA1000057//Fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, Bombay phenotype included)//3.8e-77:545:83//Hs.69747:M35531  
5 R-MAMMA1000069//ESTs//8.0e-108:546:96//Hs.44856:N37065  
R-MAMMA1000084//Homo sapiens clone 23632 mRNA sequence//7.3e-43:313:83//Hs.46918:AF052099  
R-MAMMA1000085//ESTs, Highly similar to PUTATIVE CYSTEINYLY-TRNA SYNTHETASE C29E6.06C [Schizosaccharomyces pombe]//7.7e-104:546:94//Hs.7779:AA045241  
R-MAMMA1000092//EST, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//4.2e-10 22:287:71//Hs.136063:U51713  
R-MAMMA1000103//LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR//8.4e-49:334:86//Hs.70008:L00352  
R-MAMMA1000117//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.1e-08:96:80//Hs.115088:AA230172  
15 R-MAMMA1000129//EST//2.8e-64:310:99//Hs.136394:AA523577  
R-MAMMA1000133  
R-MAMMA1000134//ESTs//1.1e-21:152:87//Hs.163747:AA174017  
R-MAMMA1000139//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//6.3e-40:288:78//Hs.159897:AB007970  
20 R-MAMMA1000143//EST//5.0e-52:314:89//Hs.149580:AI281881  
R-MAMMA1000155//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//1.5e-59:562:75//Hs.77579:AF013263  
R-MAMMA1000163//ESTs//2.8e-92:457:96//Hs.114413:AA884787  
R-MAMMA1000171//Homo sapiens mRNA for putative lipoic acid synthetase, partial//2.5e-39:173:83//Hs.53531:  
25 AJ224162  
R-MAMMA1000173//ESTs, Highly similar to SRC SUBSTRATE P80/85 PROTEINS [Gallus gallus]//2.4e-07:63:90//Hs.90367:AI357069  
R-MAMMA1000175//EST//0.66:217:58//Hs.146444:AI127611  
R-MAMMA1000183//ESTs//6.7e-30:341:73//Hs.125254:AA872054  
30 R-MAMMA1000198//EST//2.8e-45:185:88//Hs.149580:AI281881  
R-MAMMA1000221//ESTs, Weakly similar to circadian clock protein [M.musculus]//1.4e-41:272:90//Hs.68398:AA421103  
R-MAMMA1000227//EST//2.4e-39:388:76//Hs.144175:H70425  
R-MAMMA1000241//EST//0.0027:263:61//Hs.37532:H57946  
35 R-MAMMA1000251//Homo sapiens mRNA for KIAA0772 protein, complete cds//5.3e-47:322:86//Hs.15519:AB018315  
R-MAMMA1000254//Homo sapiens tumor necrosis factor superfamily member LIGHT mRNA, complete cds//2.2e-43:315:83//Hs.129708:AF064090  
R-MAMMA1000257//EST//1.6e-62:330:93//Hs.141728:W73041  
40 R-MAMMA1000264//Von Hippel-Lindau syndrome//2.3e-31:141:81//Hs.78160:AF010238  
R-MAMMA1000266//ESTs//3.4e-34:150:81//Hs.163980:AA715814  
R-MAMMA1000270//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0508//2.7e-57:304:78//Hs.159187:AB007977  
R-MAMMA1000277//Thiopurine S-methyltransferase//3.7e-27:380:71//Hs.51124:AF019369  
45 R-MAMMA1000278//ESTs//5.2e-99:504:95//Hs.8494:W72694  
R-MAMMA1000279//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//3.1e-58:295:83//Hs.92381:AB007956  
R-MAMMA1000284//EST//4.1e-10:151:73//Hs.60742:AA017066  
R-MAMMA1000287  
50 R-MAMMA1000302//Homo sapiens KIAA0432 mRNA, complete cds//1.0:50:84//Hs.155174:AB007892  
R-MAMMA1000307//Human mRNA for KIAA0033 gene, partial cds//1.8e-48:468:76//Hs.22271:D26067  
R-MAMMA1000309//ESTs//1.7e-94:491:94//Hs.135106:AI335251  
R-MAMMA1000312//ESTs//8.9e-74:377:96//Hs.133163:AI051434  
R-MAMMA1000313//EST//8.3e-19:294:62//Hs.127400:AA954491  
55 R-MAMMA1000331//ESTs, Moderately similar to envelope protein [H.sapiens]//8.6e-54:278:97//Hs.139170:AA662998  
R-MAMMA1000339//EST//6.8e-44:169:89//Hs.149580:AI281881  
R-MAMMA1000340//Homo sapiens mRNA for KIAA0625 protein, partial cds//0.82:204:61//Hs.154919:AB014525

R-MAMMA1000348//ESTs//3.3e-34:320:75//Hs.139158:AA226159  
R-MAMMA1000356//ESTs, Highly similar to URIDYLATE KINASE [Saccharomyces cerevisiae]//0.42:172:61//Hs.11463:AA535912  
R-MAMMA1000360//Human mRNA for KIAA0118 gene, partial cds//3.8e-43:212:82//Hs.154326:D42087  
5 R-MAMMA1000361//ESTs//3.1e-17:188:68//Hs.164036:AA845659  
R-MAMMA1000372//ESTs//1.0e-46:307:85//Hs.145032:AA343523  
R-MAMMA1000385//ESTs//8.2e-97:467:98//Hs.152282:AA412065  
R-MAMMA1000388//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds//8.6e-14:106:  
92//Hs.32170:AB015132  
10 R-MAMMA1000395//ESTs//1.9e-57:292:96//Hs.11365:AB01060  
R-MAMMA1000402//ESTs, Moderately similar to RETROVIRUS-RELATED POL POLYPROTEIN [Mus musculus]  
//9.1e-47:316:81//Hs.138698:N38973  
R-MAMMA1000410//Archain//1.8e-40:443:74//Hs.33642:X81198  
15 R-MAMMA1000413//Homo sapiens mRNA for KIAA0792 protein, complete cds//1.3e-27:304:72//Hs.119387:  
AB007958  
R-MAMMA1000414//ESTs//2.9e-27:181:87//Hs.141254:AI334099  
R-MAMMA1000416//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//1.5e-58:  
282:82//Hs.97203:U83171  
R-MAMMA1000421//Thromboxane A2 receptor//4.9e-48:372:80//Hs.89887:D38081  
20 R-MAMMA1000422//ESTs//0.077:240:62//Hs.123136:AA631067  
R-MAMMA1000423//Human mRNA for KIAA0392 gene, partial cds//1.3e-48:375:81//Hs.40100:AB002390  
R-MAMMA1000424//Human melanoma antigen recognized by T-cells (MART-1) mRNA//1.4e-44:418:75//Hs.  
154069:U06452  
R-MAMMA1000429//ESTs//3.9e-113:565:96//Hs.5076:N53461  
25 R-MAMMA1000431//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//8.6e-68:  
302:85//Hs.97203:U83171  
R-MAMMA1000444//Calcium modulating ligand//5.5e-44:344:81//Hs.13572:AF068179  
R-MAMMA1000446//ESTs//1.0:236:60//Hs.126958:AI147447  
R-MAMMA1000458  
30 R-MAMMA1000468//ESTs//4.4e-51:271:96//Hs.6839:AA055176  
R-MAMMA1000472//ESTs//5.4e-39:146:86//Hs.141581:AA315361  
R-MAMMA1000478//ESTs//2.3e-74:365:98//Hs.140591:AA828959  
R-MAMMA1000483//ESTs//9.9e-23:235:75//Hs.163592:AA280886  
R-MAMMA1000490//EST//2.1e-80:500:87//Hs.142137:AA213759  
35 R-MAMMA1000500//Small inducible cytokine A5 (RANTES)//4.7e-43:283:86//Hs.155464:AF088219  
R-MAMMA1000501//ESTs//4.2e-37:250:86//Hs.141323:N80390  
R-MAMMA1000516//Human mRNA for KIAA0392 gene, partial cds//5.1e-46:459:75//Hs.40100:AB002390  
R-MAMMA1000522//ESTs//9.5e-16:226:70//Hs.116673:AA669267  
R-MAMMA1000559//ESTs//5.2e-34:244:84//Hs.150727:AI292236  
40 R-MAMMA1000565//EST//2.7e-38:386:76//Hs.162404:AA573131  
R-MAMMA1000567//EST//0.33:49:79//Hs.147754:AI220561  
R-MAMMA1000576//ESTs//4.9e-57:348:89//Hs.108921:N31211  
R-MAMMA1000583//Homo sapiens KIAA0412 mRNA, partial cds//1.3e-52:373:77//Hs.6200:AB007872  
R-MAMMA1000585//ESTs//5.1e-40:337:78//Hs.130815:AA936548  
45 R-MAMMA1000594//Small inducible cytokine A5 (RANTES)//3.0e-45:225:80//Hs.155464:AF088219  
R-MAMMA1000597//ESTs//2.0e-98:461:99//Hs.43212:AA993042  
R-MAMMA1000605//CD4 receptor {exons 1 and 2} [human, T-lymphocyte, mRNA, 3429 nt]//1.5e-50:500:73//Hs.  
116007:S79267  
R-MAMMA1000612//ESTs, Highly similar to HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN IN  
50 SIS1-MRPL2 INTERGENIC REGION [Saccharomyces cerevisiae]//8.6e-108:559:94//Hs.29203:AI344105  
R-MAMMA1000616//EST//0.071:169:60//Hs.144096:AI032180  
R-MAMMA1000621//ESTs//1.0e-90:477:94//Hs.26073:R96361  
R-MAMMA1000623  
R-MAMMA1000625//ESTs//3.4e-98:556:91//Hs.119482:AI361002  
55 R-MAMMA1000643//EST//4.9e-74:379:96//Hs.137447:AA342203  
R-MAMMA1000664//Homo sapiens mRNA for putative lipoic acid synthetase, partial//3.2e-43:400:76//Hs.53531:  
AJ224162  
R-MAMMA1000669//EST//6.9e-53:368:84//Hs.149580:AI281881

R-MAMMA1000670//ESTs, Highly similar to HYPOTHETICAL PROTEIN IN TONB 3'REGION [Klebsiella pneumoniae]/8.4e-98:464:98//Hs.31431:AI022065  
R-MAMMA1000672//ESTs//2.0e-80:382:99//Hs.106747:AI080476  
R-MAMMA1000684//ESTs//6.2e-72:357:98//Hs.67896:AA865212  
5 R-MAMMA1000696//Human mRNA for KIAA0345 gene, complete cds//3.3e-52:216:75//Hs.98938:AB002343  
R-MAMMA1000707//EST//7.0e-11:195:68//Hs.147002:AI184644  
R-MAMMA1000713//Homo sapiens DEC-205 mRNA, complete cds//1.5e-45:485:74//Hs.153563:AF011333  
R-MAMMA1000714//ESTs, Moderately similar to hypothetical protein 2 [H.sapiens]//1.2e-29:158:79//Hs.142764:  
AA205569  
10 R-MAMMA1000718//ESTs//3.1e-45:264:88//Hs.152413:AA780515  
R-MAMMA1000720//ESTs//7.4e-44:244:87//Hs.111742:R39329  
R-MAMMA1000723//Homo sapiens mRNA for alpha(I,2)fucosyltransferase, complete cds//5.6e-52:350:82//Hs.  
46328:D87942  
R-MAMMA1000731//ESTs//1.1e-19:420:66//Hs.35036:H95267  
15 R-MAMMA1000732//EST//2.9e-20:229:74//Hs.135400:AI056893  
R-MAMMA1000733//ESTs, Weakly similar to HYPOTHETICAL 92.1 KD PROTEIN ZK1098.3 IN CHROMOSOME  
III [Caenorhabditis elegans]//1.2e-35:371:74//Hs.141429:AA631915  
R-MAMMA1000734//Homo sapiens SEC63 (SEC63) mRNA, complete cds//2.1e-58:253:98//Hs.31575:AF100141  
R-MAMMA1000738//ESTs, Weakly similar to similar to Achlya ambisexualis antheridial steroid receptor [C.ele-  
20 gans]//2.3e-116:557:98//Hs.71472:AA632288  
R-MAMMA1000744//ESTs//0.015:143:67//Hs.135382:AI224205  
R-MAMMA1000746//Human Line-1 repeat mRNA with 2 open reading frames//2.3e-90:568:86//Hs.23094:M19503  
R-MAMMA1000752//Interleukin 10//2.8e-43:339:80//Hs.2180:M57627  
R-MAMMA1000760//EST//5.0e-44:306:86//Hs.162404:AA573131  
25 R-MAMMA1000761//EST//5.0e-41:187:85//Hs.162335:AA564256  
R-MAMMA1000775//Human mRNA for KIAA0355 gene, complete cds//3.0e-46:465:76//Hs.153014:AB002353  
R-MAMMA1000776//ESTs//1.9e-43:429:73//Hs.141742:W22204  
R-MAMMA1000778//ESTs//1.8e-31:445:70//Hs.111723:H57439  
R-MAMMA1000782//EST//0.0019:102:68//Hs.120686:AA747150  
30 R-MAMMA1000798//ESTs//1.4e-13:267:69//Hs.140156:AA704163  
R-MAMMA1000802//Clathrin, light polypeptide (Lcb)//1.5e-45:358:76//Hs.73919:X81637  
R-MAMMA1000831//ESTs//1.3e-1,04:510:97//Hs.17494:AA572675  
R-MAMMA1000839//EST//2.9e-51:307:89//Hs.149580:AI281881  
R-MAMMA1000841//ESTs//1.3e-34:412:72//Hs.121256:AA757902  
35 R-MAMMA1000842//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//9.4e-  
44:363:79//Hs.96337:AA225358  
R-MAMMA1000843//ESTs//2.2e-106:525:97//Hs.152016:AA603097  
R-MAMMA1000845//ESTs//1.6e-66:327:98//Hs.156900:AA468955  
R-MAMMA1000851//ESTs//3.7e-14:115:86//Hs.140590:R76251  
40 R-MAMMA1000855//Human mRNA for KIAA0392 gene, partial cds//5.7e-47:281:91//Hs.40100:AB002390  
R-MAMMA1000856//EST//1.8e-16:150:79//Hs.136811:AA789212  
R-MAMMA1000862//EST//3.2e-05:93:73//Hs.161205:AI419311  
R-MAMMA1000863//ESTs//1.0e-46:446:73//Hs.153432:AA098922  
R-MAMMA1000865//Homo sapiens clone 23632 mRNA sequence//3.0e-39:324:80//Hs.46918:AF052099  
45 R-MAMMA1000867//ESTs//9.8e-16:193:76//Hs.152340:AA521399  
R-MAMMA1000875//EST//3.1e-24:301:72//Hs.132635:AI032875  
R-MAMMA1000876//ESTs//9.9e-48:246:97//Hs.112165:AA621243  
R-MAMMA1000877//ESTs//1.4e-38:324:79//Hs.141024:H07128  
R-MAMMA1000880//Homo sapiens mRNA for KIAA0594 protein, partial cds//3.2e-40:542:68//Hs.154872:  
50 AB011166  
R-MAMMA1000883//ESTs//1.0:207:60//Hs.47199:N51107  
R-MAMMA1000897//ESTs//2.6e-78:383:97//Hs.41067:AI310215  
R-MAMMA1000905//Human mRNA for KIAA0331 gene, complete cds//9.7e-53:307:91//Hs.146395:AB002329  
R-MAMMA1000906//ESTs//8.0e-25:206:83//Hs.141825:AA017093  
55 R-MAMMA1000908//ESTs//4.4e-32:176:96//Hs.38559:AA701634  
R-MAMMA1000914//ESTs//0.032:150:63//Hs.119162:AA399989  
R-MAMMA1000921//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIP<sub>K</sub>) mRNA,  
complete cds//7.7e-38:269:74//Hs.108966:U48696

R-MAMMA1000931//ESTs//1.2e-80:457:91//Hs.122319:AA782335  
R-MAMMA1000940//ESTs//3.3e-43:329:82//Hs.35254:AI133727  
R-MAMMA1000941//ESTs//7.5e-55:306:84//Hs.163936:AA632281  
R-MAMMA1000942//ESTs//2.5e-83:405:98//Hs.116491:AA650428  
5 R-MAMMA1000943//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//9.3e-79:567:  
80//Hs.1361:M55053  
R-MAMMA1000956//EST//5.7e-53:256:100//Hs.162209:AA536178  
R-MAMMA1000957//Kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen,  
10 antigen detected by monoclonal and antibody IA4)//7.5e-49:340:85//Hs.103458:X53795  
R-MAMMA1000962//Homo sapiens mRNA for KIAA0575 protein, complete cds//2.0e-48:216:85//Hs.153468:  
AB011147  
R-MAMMA1000968//EST//6.2e-46:302:86//Hs.149580:AI281881  
R-MAMMA1000975//ESTs//1.4e-85:428:96//Hs.141742:W22204  
R-MAMMA1000979//Homo sapiens mRNA for KIAA0761 protein, partial cds//8.0e-39:338:79//Hs.93121:  
15 AB018304  
R-MAMMA1000987//EST//2.8e-41:249:90//Hs.149580:AI281881  
R-MAMMA1000998//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//3.9e-50:  
445:77//Hs.77579:AF013263  
R-MAMMA1001003//Sialophorin (gpL115, leukosialin, CD43)//4.1e-51:282:82//Hs.80738:X52075  
20 R-MAMMA1001008//ESTs, Weakly similar to renin [H.sapiens]//1.9e-82:405:97//Hs.25863:AA630313  
R-MAMMA1001021//Homo sapiens DEC-205 mRNA, complete cds//3.0e-44:309:86//Hs.153563:AF011333  
R-MAMMA1001024//ESTs//6.8e-35:333:78//Hs.107657:AA126814  
R-MAMMA1001030//ESTs//1.6e-110:552:96//Hs.59483:AA524536  
R-MAMMA1001035//ESTs//1.0e-45:273:85//Hs.138856:H47461  
25 R-MAMMA1001038//Human mRNA for KIAA0392 gene, partial cds//3.0e-50:298:91//Hs.40100:AB002390  
R-nnnnnnnnnnnnnn//ESTs//3.6e-86:445:95//Hs.122625:R68650  
R-MAMMA1001050//EST//2.2e-54:387:85//Hs.149580:AI281881  
R-MAMMA1001059//ESTs, Moderately similar to RNA helicase [M.musculus]//1.7e-13:273:65//Hs.98738:  
AI015487  
30 R-MAMMA1001067//ESTs//1.3e-38:324:78//Hs.20190:AA525532  
R-MAMMA1001073//ESTs//5.2e-106:554:94//Hs.12336:W63748  
R-MAMMA1001074//Human mRNA for KIAA0355 gene, complete cds//1.2e-38:544:68//Hs.153014:AB002353  
R-MAMMA1001075//ESTs//2.0e-98:463:99//Hs.18341:N38944  
R-MAMMA1001078//Human Line-1 repeat mRNA with 2 open reading frames//1.7e-84:556:85//Hs.23094:M19503  
35 R-MAMMA1001082//ESTs//2.4e-71:356:97//Hs.152302:T90222  
R-MAMMA1001091//ESTs//4.7e-83:429:95//Hs.154412:AA310926  
R-MAMMA1001092//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//  
6.4e-34:262:82//Hs.129727:AF035587  
R-MAMMA1001105//Human putative RNA binding protein RNPL mRNA, complete cds//4.2e-27:232:76//Hs.  
40 61840:U28686  
R-MAMMA1001110//ESTs//1.6e-17:128:87//Hs.161314:AI421576  
R-MAMMA1001126//CD4 receptor {exons 1 and 2} [human, T-lymphocyte, mRNA, 3429 nt]//8.8e-53:462:78//Hs.  
116007:S79267  
R-MAMMA1001133//Homo sapiens tapasin (NGS-17) mRNA, complete cds//1.8e-59:460:81//Hs.5247:AF029750  
45 R-MAMMA1001139//ESTs//1.3e-62:341:94//Hs.18819:R01029  
R-MAMMA1001143//ESTs//3.0e-48:383:80//Hs.152340:AA521399  
R-MAMMA1001145//Calcium modulating ligand//5.1e-48:403:79//Hs.13572:AF068179  
R-MAMMA1001154//EST//6.8e-35:313:75//Hs.162404:AA573131  
R-MAMMA1001161//Homo sapiens tapasin (NGS-17) mRNA, complete cds//1.1e-58:409:84//Hs.5247:AF029750  
50 R-MAMMA1001162//ESTs, Highly similar to t-BOP [M.musculus]//2.1e-91:430:99//Hs.129982:AI420970  
R-MAMMA1001181//ESTs//5.0e-112:557:96//Hs.118181:W02251  
R-MAMMA1001186//ESTs//3.8e-85:410:99//Hs.163811:W44959  
R-MAMMA1001191//ESTs//0.018:57:87//Hs.141253:AA226519  
R-MAMMA1001198//ESTs, Weakly similar to involved in signaling by the epidermal growth factor receptor [M.  
55 musculus]//2.6e-80:358:96//Hs.163827:AA074202  
R-MAMMA1001202//ESTs//7.0e-43:230:95//Hs.79788:AA527348  
R-MAMMA1001203//Clathrin, light polypeptide (Lcb)//2.8e-65:348:79//Hs.73919:X81637  
R-MAMMA1001206//EST//0.098:84:72//Hs.162941:AA635148

R-MAMMA1001215//ESTs//1.3e-43:156:86//Hs.155243:N70293  
R-MAMMA1001220//ESTs//8.9e-17:276:68//Hs.116518:AA653202  
R-MAMMA1001222//ESTs//0.49:112:66//Hs.24668:AA897315  
R-MAMMA1001243//EST//0.99:143:62//Hs.68522:C20701  
5 R-MAMMA1001244//ESTs//2.2e-06:79:83//Hs.123163:AA809619  
R-MAMMA1001249//ESTs//4.2e-68:343:97//Hs.147139:AI191307  
R-MAMMA1001256//ESTs, Moderately similar to hypothetical protein 2 [H.sapiens]//4.7e-31:221:77//Hs.142764:  
AA205569  
R-MAMMA1001259//ESTs//1.3e-43:266:90//Hs.6193:AA045149  
10 R-MAMMA1001260//Homo sapiens mRNA for KIAA0661 protein, complete cds//2.0e-21:226:75//Hs.65238:  
AB014561  
R-MAMMA1001268//H.sapiens HCG II mRNA//2.4e-53:181:85//Hs.146333:X81001  
R-MAMMA1001271//ESTs, Highly similar to PUTATIVE SERINE/THREONINE-PROTEIN KINASE EMK [Mus mus-  
culus]//1.1e-108:546:95//Hs.18999:N30643  
15 R-MAMMA1001274//Homo sapiens mRNA for KIAA0572 protein, partial cds//4.4e-32:188:94//Hs.14409:  
AB011144  
R-MAMMA1001280//EST//0.0015:170:62//Hs.116770:AA630371  
R-MAMMA1001292//ESTs//5.6e-102:481:99//Hs.94810:AA811876  
R-MAMMA1001296//Homo sapiens mRNA for KIAA0563 protein, complete cds//2.2e-27:348:70//Hs.15731:  
20 AB011135  
R-MAMMA1001298//ESTs//1.4e-44:375:79//Hs.70279:AA757426  
R-MAMMA1001305//Human G protein-coupled receptor (STRL22) mRNA, complete cds//4.0e-43:300:85//Hs.  
46468:U45984  
R-MAMMA1001322//Homo sapiens stress-activated protein kinase 4 mRNA, complete cds//8.8e-12:188:70//Hs.  
25 55771:AF004709  
R-MAMMA1001324//ESTs//5.3e-68:297:88//Hs.121228:AA709471  
R-MAMMA1001330//ESTs//1.6e-57:429:83//Hs.70279:AA757426  
R-MAMMA1001341//Homo sapiens 4F5S mRNA, complete cds//4.8e-27:285:75//Hs.32567:AF073519  
R-MAMMA1001343//ESTs//8.1e-51:273:93//Hs.162208:AA536127  
30 R-MAMMA1001346//ESTs//1.0:122:65//Hs.33028:AA482478  
R-MAMMA1001383//ESTs//1.4e-45:377:80//Hs.114671:N39322  
R-MAMMA1001388//EST//7.7e-47:361:80//Hs.162197:AA535216  
R-MAMMA1001397//EST//8.7e-48:337:83//Hs.149580:AI281881  
R-MAMMA1001408//EST//1.2e-38:251:87//Hs.162677:AA604831  
35 R-MAMMA1001411//ESTs//4.3e-93:435:99//Hs.105460:AA780275  
R-MAMMA1001419//Homo sapiens translation initiation factor 4e mRNA, complete cds//1.6e-19:117:96//Hs.  
19122:AF038957  
R-MAMMA1001420//ESTs//7.3e-96:507:95//Hs.55299:AI335267  
R-MAMMA1001435//ESTs//5.0e-97:459:99//Hs.144843:AI222168  
40 R-MAMMA1001442//ESTs//7.1e-28:167:83//Hs.141019:AA287618  
R-MAMMA1001446//Homo sapiens KIAA0432 mRNA, complete cds//6.2e-19:328:67//Hs.155174:AB007892  
R-MAMMA1001452//EST//5.6e-44:487:75//Hs.161476:N57542  
R-MAMMA1001465  
45 R-MAMMA1001476//Homo sapiens yolk sac permease-like molecule 3 (YSPL3) mRNA, complete cds//0.79:182:  
66//Hs.136529:AF058317  
R-MAMMA1001487//Homo sapiens KIAA0395 mRNA, partial cds//1.1e-35:328:78//Hs.43681:AL022394  
R-MAMMA1001501//ESTs//4.6e-100:472:98//Hs.123660:AA813065  
R-MAMMA1001502//Human mRNA for KIAA0080 gene, partial cds//5.6e-15:220:69//Hs.74554:D38522  
R-MAMMA1001510  
50 R-MAMMA1001522//ESTs//3.2e-16:214:75//Hs.152816:AA634242  
R-MAMMA1001547//H.sapiens mRNA for urea transporter//2.3e-45:282:89//Hs.66710:X96969  
R-MAMMA1001551//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIP5K) mRNA,  
complete cds//1.9e-56:489:76//Hs.108966:U48696  
R-MAMMA1001575//ESTs//4.3e-92:440:98//Hs.162882:AA807140  
55 R-MAMMA1001576//ESTs, Highly similar to TUBULIN GAMMA CHAIN [Homo sapiens]//1.9e-111:549:96//Hs.  
21635:AI417305  
R-MAMMA1001590//ESTs//1.1e-63:324:96//Hs.142217:AA278441  
R-MAMMA1001600//ESTs//5.6e-15:159:78//Hs.138633:H98792

EP 1 074 617 A2

	R-MAMMA1001604
	R-MAMMA1001606//ESTs, Weakly similar to finger protein kox1 [H.sapiens]//1.9e-97:488:96//Hs.143263:AI057616
5	R-MAMMA1001620//Homo sapiens mRNA, clone:RES4-16//5.4e-43:408:76//Hs.121493:D25272
	R-MAMMA1001627//Homo sapiens mRNA for KIAA0772 protein, complete cds//2.0e-49:472:76//Hs.15519:AB018315
	R-MAMMA1001630//ESTs, Weakly similar to putative p150 [H.sapiens]//6.8e-15:168:73//Hs.115216:AA291074
	R-MAMMA1001633//EST//5.1e-14:228:68//Hs.141456:N36377
10	R-MAMMA1001635//ESTs//3.4e-37:368:75//Hs.164033:AA769606
	R-MAMMA1001649
	R-MAMMA1001663//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//1.7e-54:272:81//Hs.129735:AF010144
	R-MAMMA1001670//Small inducible cytokine A5 (RANTES)//5.7e-50:304:89//Hs.155464:AF088219
15	R-MAMMA1001671//EST//1.9e-14:312:65//Hs.137153:R46248
	R-MAMMA1001679//H.sapiens mRNA for rho GDP-dissociation Inhibitor 1//0.066:196:62//Hs.159161:X69550
	R-MAMMA1001683//ESTs//4.9e-94:447:98//Hs.134464:AI151081
	R-MAMMA1001686//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//1.0e-17:246:73//Hs.67619:AB007957
20	R-MAMMA1001692//Human mRNA for KIAA0063 gene, complete cds//2.1e-47:294:89//Hs.3094:D31884
	R-MAMMA1001711//ESTs//2.4e-86:439:96//Hs.18498:N52088
	R-MAMMA1001715//ESTs//1.2e-73:399:931Hs.124620:AI082338
	R-MAMMA1001730//ESTs//1.1e-85:403:99//Hs.125464:AI084596
	R-MAMMA1001735//ESTs, Highly similar to TUBULIN BETA-5 CHAIN [Gallus gallus]//3.7e-110:552:96//Hs.6923:AI161158
25	R-MAMMA1001740//ESTs//4.6e-45:342:82//Hs.37573:H59651
	R-MAMMA1001743//EST//2.7e-58:412:85//Hs.149742:AI285666
	R-MAMMA1001744
	R-MAMMA1001745//EST//5.6e-54:374:84//Hs.137041:AA877817
30	R-MAMMA1001751//EST//3.5e-36:375:73//Hs.139715:N25041
	R-MAMMA1001754//EST//0.18:144:66//Hs.71957:AA151413
	R-MAMMA1001757//ESTs//1.0e-9.8:488:96//Hs.45184:C14904
	R-MAMMA1001760//ESTs//8.7e-29:206:86//Hs.143310:AI142276
	R-MAMMA1001764//ESTs//0.00012:434:58//Hs.120051:AA707847
35	R-MAMMA1001768//Human mRNA for KIAA0327 protein, complete cds//2.3e-41:299:85//Hs.149323:AB002325
	R-MAMMA1001769//EST//1.7e-15:139:81//Hs.162399:AA572825
	R-MAMMA1001771//ESTS, Moderately similar to semaphorin B [M.musculus]//7.6e-43:257:91//Hs.7634:AA481246
	R-MAMMA1001783//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//5.6e-42:272:86//Hs.73614:U83460
40	R-MAMMA1001785//ESTs//1.5e-87:431:98//Hs.131065:AA972238
	R-MAMMA1001788//EST//0.95:108:62//Hs.145881:AI274644
	R-MAMMA1001790//ESTs//4.0e-41:340:80//Hs.158045:AA425744
	R-MAMMA1001806//EST//1.4e-40:297:84//Hs.141240:H60313
	R-MAMMA1001812//ESTs//2.4e-93:446:98//Hs.129034:AA776892
45	R-MAMMA1001815//EST//0.00053:371:59//Hs.133255:AI052659
	R-MAMMA1001817//Human mRNA for KIAA0226 gene, complete cds//2.1e-46:325:87//Hs.44106:D86979
	R-MAMMA1001818
	R-MAMMA1001820//EST//1.9e-49:303:89//Hs.149580:AI281881
50	R-MAMMA1001824//Homo sapiens 4F5S mRNA, complete cds//4.3e-48:438:75//Hs.32567:AF073519
	R-MAMMA1001836//ESTs//3.8e-06:128:71//Hs.143611:M78140
	R-MAMMA1001837//Homo sapiens KIAA0395 mRNA, partial cds//3.8e-47:339:83//Hs.43681:AL022394
	R-MAMMA1001848//ESTs//2.1e-16:125:85//Hs.161662:AA836811
	R-MAMMA1001851//ESTs//4.5e-48:344:84//Hs.138856:H47461
55	R-MAMMA1001854//Small inducible cytokine A5 (RANTES)//2.6e-38:280:83//Hs.155464:AF088219
	R-MAMMA1001858//ESTs//1.1e-44:331:83//Hs.44702:AI148840
	R-MAMMA1001864//Homo sapiens mRNA for KIAA0475 protein, complete cds//7.8e-31:262:77//Hs.5737:AB007944
	R-nnnnnnnnnnnn//Homo sapiens antigen NY-CO-16 mRNA, complete cds//9.2e-06:450:58//Hs.132206:

AF039694

R-MAMMA1001874//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//4.9e-46:332:83//Hs.73614:U83460

R-MAMMA1001878//Cytochrome P450, 51 (lanosterol 14-alpha-demethylase)//1.2e-46:429:78//Hs.2379:U23942

5 R-MAMMA1001880//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//7.6e-26:230:79//Hs.106008:AA147606

R-MAMMA1001890//ESTs//1.1e-39:338:79//Hs.146811:AA410788

R-MAMMA1001907//Kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monoclonal and antibody IA4))//6.7e-47:283:89//Hs.103458:X53795

10 R-nnnnnnnnnnnn//ESTs//0.043:134:65//Hs.145333:AI251374

R-MAMMA1001931//ESTs//1.8e-75:361:99//Hs.148125:AA693801

R-MAMMA1001956//Homo sapiens mRNA for KIAA0706 protein, complete cds//1.4e-18:174:77//Hs.139648:AB014606

R-MAMMA1001963//ESTs//6.7e-28:206:84//Hs.163254:AA828790

15 R-MAMMA1001969//ESTs, Weakly similar to hypothetical protein [H.sapiens]//6.7e-24:331:71//Hs.140506:AA308018

R-MAMMA1001970//ESTs//8.9e-61:286:84//Hs.141575:AA211734

R-MAMMA1001992//ESTs//4.4e-43:339:82//Hs.155498:W27084

R-MAMMA1002009//Small inducible cytokine A5 (RANTES)//4.6e-24:330:70//Hs.155464:AF088219

20 R-MAMMA1002011//ESTs//9.5e-72:360:97//Hs.13525:R39054

R-MAMMA1002032//Human melanoma antigen recognized by T-cells (MART-1) mRNA//3.7e-45:370:80//Hs.154069:U06452

R-MAMMA1002033//EST//4.6e-23:264:74//Hs.161917:AA483223

R-MAMMA1002041//ESTs//3.8e-100:465:100//Hs.141361:AI206412

25 R-MAMMA1002042//Homo sapiens 4F5S mRNA, complete cds//1.1e-43:407:76//Hs.32567:AF073519

R-MAMMA1002047//Homo sapiens mRNA for chemokine LEC precursor, complete cds//1.9e-37:316:74//Hs.10458:AF088219

R-MAMMA1002056//EST//1.3e-51:310:90//Hs.149580:AI281881

R-MAMMA1002058//ESTs//5.9e-16:135:84//Hs.95807:AA146979

30 R-MAMMA1002068//ESTs, Weakly similar to HYPOTHETICAL 43.3 KD PROTEIN IN QOXD-VPR INTERGENIC REGION [Bacillus subtilis]//4.0e-45:404:7811Hs.138596:N38806

R-MAMMA1002078//EST//2.2e-15:207:71//Hs.132635:AI032875

R-MAMMA1002082//Homo sapiens mRNA for TSC403 protein, complete cds//1.7e-42:314:83//Hs.10887:AB013924

35 R-MAMMA1002084//Human mRNA for KIAA0392 gene, partial cds//3.7e-46:308:87//Hs.40100:AB002390

R-MAMMA1002093//EST//0.89:213:60//Hs.151201:AI125907

R-MAMMA1002108//ESTs//1.0e-95:515:93//Hs.29002:H11347

R-MAMMA1002118

R-MAMMA1002125//Thromboxane A2 receptor//7.2e-43:335:83//Hs.89887:D38081

40 R-MAMMA1002132//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//1.4e-58:396:78//Hs.129735:AF010144

R-MAMMA1002140//Homo sapiens nephrin (NPHS1) mRNA, complete cds//1.4e-37:422:75//Hs.128834:AF035835

R-MAMMA1002143//ESTs//0.050:123:69//Hs.8231:AA152276

45 R-MAMMA1002145//Homo sapiens KIAA0426 mRNA, complete cds//5.0e-21:371:69//Hs.97476:AB007886

R-MAMMA1002153//ESTs//2.0e-31:159:77//Hs.130815:AA936548

R-MAMMA1002155//Human Line-1 repeat mRNA with 2 open reading frames//8.7e-39:506:69//Hs.23094:M19503

R-MAMMA1002156//Homo sapiens mRNA for putative lipoic acid synthetase, partial//2.9e-44:336:82//Hs.53531:AJ224162

50 R-MAMMA1002158//ESTs//3.0e-40:313:83//Hs.118273:AA626040

R-MAMMA1002170//Homo sapiens mRNA for TRAF5, complete cds//7.7e-37:370:77//Hs.29736:AB000509

R-MAMMA1002174//ESTs//2.5e-16:186:75//Hs.141203:H52638

R-MAMMA1002198//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//6.2e-51:318:82//Hs.92381:AB007956

55 R-MAMMA1002209//ESTs//9.2e-34:111:88//Hs.141575:AA211734

R-MAMMA1002215//ESTs//3.6e-101:530:94//Hs.26780:N50038

R-MAMMA1002219//Homo sapiens mRNA for KIAA0640 protein, partial cds//5.2e-45:283:88//Hs.153026:AB014540

R-MAMMA1002230//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIP5K) mRNA, complete cds//9.1e-50:330:77//Hs.108966:U48696  
R-MAMMA1002236  
R-MAMMA1002243  
5 R-MAMMA1002250//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.2e-44:299:87//Hs.113283:AF018080  
R-MAMMA1002267//Homo sapiens mRNA, chromosome 1 specific transcript  
KIAA0487//1.6e-54:207:81//Hs.92381:AB007956  
R-MAMMA1002268//ESTs//2.9e-94:439:100//Hs.68061:AI042283  
R-MAMMA1002269//ESTs//7.4e-05:170:65//Hs.140466:AA766772  
10 R-MAMMA1002282//ESTs//7.8e-09:69:78//Hs.159502:AA225141  
R-MAMMA1002292//ESTs//5.3e-64:334:94//Hs.113606:AI138751  
R-MAMMA1002293//ESTs, Moderately similar to plakophilin 2b [H.sapiens]//1.7e-39:203:81//Hs.154257:  
AI275982  
R-MAMMA1002294//EST//8.1e-43:326:82//Hs.149580:AI281881  
15 R-MAMMA1002297//ESTs//6.5e-45:323:83//Hs.155475:AA761454  
R-MAMMA1002298//ESTs//1.7e-68:355:96//Hs.52683:H87153  
R-MAMMA1002299//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//  
2.3e-58:346:91//Hs.140385:AA773359  
R-MAMMA1002308  
20 R-MAMMA1002310//Human melanoma antigen recognized by T-cells (MART-1) mRNA//2.2e-44:280:87//Hs.  
154069:U06452  
R-MAMMA1002311//Human Line-1 repeat mRNA with 2 open reading frames//2.3e-70:503:81//Hs.23094:M19503  
R-MAMMA1002312//EST//1.7e-31:144:80//Hs.135936:N36094  
R-MAMMA1002317//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//4.3e-49:457:76//Hs.144563:  
25 AF057280  
R-MAMMA1002319//ESTs//3.9e-38:297:70//Hs.140326:AA827183  
R-MAMMA1002322//ESTs//1.1e-46:301:86//Hs.155498:W27084  
R-MAMMA1002329//EST//2.6e-09:146:72//Hs.132366:AI026658  
R-MAMMA1002332//Homo sapiens clone 23892 mRNA sequence//2.6e-45:387:70//Hs.91916:AF035317  
30 R-MAMMA1002333//EST//1.8e-09:139:74//Hs.137800:AA886897  
R-MAMMA1002339//ESTs//4.2e-47:310:76//Hs.138865:W57618  
R-MAMMA1002347//ESTs//1.5e-44:326:83//Hs.111723:H57439  
R-MAMMA1002351//ESTs//3.0e-112:545:97//Hs.26209:AI143127  
R-MAMMA1002352//Homo sapiens mRNA for leukemia associated gene 2//1.5e-58:259:92//Hs.43628:Y15228  
35 R-MAMMA1002353//Human mRNA for KIAA0392 gene, partial cds//4.5e-40:360:77//Hs.40100:AB002390  
R-MAMMA1002355//ESTs//1.4e-29:307:75//Hs.3769:AI085367  
R-MAMMA1002356//Clathrin, light polypeptide (Lcb)/4.9e-31:217:88//Hs.73919:X81637  
R-MAMMA1002359//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.1e-70:483:84//Hs.113283:AF018080  
R-MAMMA1002360//ESTs//3.5e-19:301:69//Hs.124701:AA701475  
40 R-MAMMA1002361//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//  
2.6e-30:244:81//Hs.129727:AF035587  
R-MAMMA1002362//ESTs//2.3e-43:241:88//Hs.150727:AI292236  
R-MAMMA1002380//ESTs//5.1e-36:322:79//Hs.136994:AA843542  
R-MAMMA1002384//Small inducible cytokine A5 (RANTES)//1.8e-42:298:84//Hs.155464:AF088219  
45 R-MAMMA1002385//ESTs//0.57:203:63//Hs.146303:AA579061  
R-MAMMA1002392//Human mRNA for platelet-activating factor acetylhydrolase 2, complete cds//5.8e-41:305:  
83//Hs.86188:D87845  
R-MAMMA1002411//ESTs//4.4e-68:385:92//Hs.53478:N92294  
R-MAMMA1002413//Homo sapiens mRNA for small GTP-binding protein, complete cds//3.3e-14:138:75//Hs.  
50 115325:D84488  
R-MAMMA1002417//ESTs//1.6e-98:475:98//Hs.96345:N22588  
R-MAMMA1002427//ESTs//3.1e-39:274:79//Hs.141130:H28477  
R-MAMMA1002428//ESTs//8.4e-11:215:66//Hs.141022:H06475  
R-MAMMA1002434//ESTs, Moderately similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!! [H.sapiens]//  
55 2.5e-106:521:98//Hs.112152:AA487348  
R-MAMMA1002446//ESTs, Weakly similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//4.7e-  
37:374:68//Hs.157142:U85996  
R-MAMMA1002454//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0485//2.0e-60:323:81//Hs.

89121:AB007954  
R-MAMMA1002461//ESTs//4.7e-111:548:97//Hs.104281:AA147076  
R-MAMMA1002470//ESTs, Highly similar to HYPOTHETICAL 80.7 KD PROTEIN IN ERG7-NMD2 INTERGENIC REGION [Saccharomyces cerevisiae]//8.5e-104:544:93//Hs.94570:AI192106  
5 R-MAMMA1002475//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.4e-31:263:79//Hs.38687:AA744496  
R-MAMMA10024807//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.0e-34:159:79//Hs.133526:N21103  
R-MAMMA1002485//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds//8.9e-116:560:97//Hs.155223:  
10 AF055460  
R-MAMMA1002494//ESTs//3.2e-47:303:88//Hs.155243:N70293  
R-MAMMA1002498//Human novel homeobox mRNA for a DNA binding protein//0.0043:331:58//Hs.37035:U07664  
R-MAMMA1002524//ESTs//0.0039:354:61//Hs.125797:AA806277  
15 R-MAMMA1002530//Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 gamma) mRNA, complete cds//3.9e-103:529:95//Hs.18858:AF065214  
R-MAMMA1002545//Homo sapiens mRNA for KIAA0575 protein, complete cds//9.5e-50:317:88//Hs.153468:AB011147  
R-MAMMA1002554//ESTs//2.3e-85:445:95//Hs.139140:AA218851  
20 R-MAMMA1002556//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.0e-12:280:65//Hs.12725:T65058  
R-MAMMA1002566//ESTs//2.3e-88:421:99//Hs.17602:AA705681  
R-MAMMA1002571//ESTs//5.1e-97:456:99//Hs.152834:AA595693  
R-MAMMA1002573//ESTs//3.1e-38:258:87//Hs.163989:R74433  
25 R-MAMMA1002585//ESTs//7.8e-96:533:91//Hs.26009:H49371  
R-MAMMA1002590//ESTs//0.61:202:62//Hs.161190:AI419258  
R-MAMMA1002597//Cytochrome P450, subfamily IIB (phenobarbital-inducible), polypeptide 6//2.9e-21:177:75//  
Hs.1360:M29874  
R-MAMMA1002598//ESTs//3.4e-113:544:97//Hs.20263:AA573737  
30 R-MAMMA1002603//Thiopurine S-methyltransferase//7.6e-35:225:80//Hs.51124:AF019369  
R-MAMMA1002612//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//4.2e-46:424:  
75//Hs.1361:M55053  
R-MAMMA1002617//ESTs//1.1e-38:229:92//Hs.96987:W27389  
R-MAMMA1002618//Landsteiner-Wiener blood group glycoprotein//1.3e-27:185:73//Hs.108287:L27670  
35 R-MAMMA1002619//ESTs//1.7e-95:480:96//Hs.54873:AA526306  
R-MAMMA1002622//Thromboxane A2 receptor//3.2e-46:298:87//Hs.89887:D38081  
R-MAMMA1002623//EST//4.3e-49:336:85//Hs.149580:AI281881  
R-MAMMA1002625//ESTs, Moderately similar to ovarian-specific protein [R.norvegicus]//2.3e-35:308:79//Hs.  
93332:AA811920  
40 R-MAMMA1002629//Homo sapiens mRNA for small GTP-binding protein, complete cds//9.7e-57:283:86//Hs.  
115325:D84488  
R-MAMMA1002636//Human mRNA for KIAA0392 gene, partial cds//1.2e-49:303:89//Hs.40100:AB002390  
R-MAMMA1002637//ESTs//1.3e-55:391:85//Hs.95074:AI144421  
R-MAMMA1002646//ESTs//7.4e-36:182:80//Hs.163937:N69915  
45 R-MAMMA1002650//ESTs//1.6e-102:547:94//Hs.57841:W63776  
R-MAMMA1002655  
R-MAMMA1002662//Homo sapiens KIAA0426 mRNA, complete cds//2.2e-46:462:75//Hs.97476:AB007886  
R-MAMMA1002665//Human mRNA for KIAA0118 gene, partial cds//9.1e-51:376:82//Hs.154326:D42087  
R-MAMMA1002671//ESTs, Weakly similar to coded for by C. elegans cDNA yk52e10.5 [C.elegans]//5.3e-108:544:  
50 96//Hs.16464:W19606  
R-MAMMA1002673//EST//3.3e-35:169:79//Hs.140046:AA668213  
R-MAMMA1002684//Homo sapiens mRNA for KIAA0214 protein, complete cds//4.6e-109:544:96//Hs.3363:  
D86987  
R-MAMMA1002685//EST//1.9e-31:223:86//Hs.112540:AA601385  
55 R-MAMMA1002698//ESTs//5.9e-43:292:85//Hs.144660:AA652675  
R-MAMMA1002699//ESTs//3.2e-25:134:100//Hs.126049:F22510  
R-MAMMA1002701//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//6.9e-70:  
353:96//Hs.138404:R70986

R-MAMMA1002708//ESTs//2.1e-76:413:94//Hs.57932:W69234  
 R-MAMMA1002711//ESTs//1.9e-44:236:96//Hs.138575:H67858  
 R-MAMMA1002721//Homo sapiens DEC-205 mRNA, complete cds//2.7e-43:273:89//Hs.153563:AF011333  
 R-MAMMA1002727//ESTs//2.9e-84:395:10011Hs.162826:AA679571  
 5 R-MAMMA1002728//Small inducible cytokine A5 (RANTES)//3.4e-42:266:88//Hs.155464:AF088219  
 R-MAMMA1002744//ESTs//4.2e-18:473:63//Hs.42826:AA846757  
 R-MAMMA1002746//ESTs//1.8e-100:473:99//Hs.117558:AA779907  
 R-MAMMA1002748//Human melanoma antigen recognized by T-cells (MART-1) mRNA//5.8e-40:330:80//Hs.  
 154069:U06452  
 10 R-MAMMA1002754//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//4.5e-40:  
 369:77//Hs.105292:AA504776  
 R-MAMMA1002758  
 R-MAMMA1002764//ESTs//4.2e-103:486:99//Hs.159909:AI393281  
 R-MAMMA1002765//ESTs//1.6e-37:338:76//Hs.37573:H59651  
 15 R-MAMMA1002769//ESTs//0.72:409:57//Hs.141376:AI301272  
 R-MAMMA1002780//ESTs//1.6e-52:292:92//Hs.135985:AA342750  
 R-MAMMA1002782//ESTs//1.0e-31:157:80//Hs.159510:AA297145  
 R-MAMMA1002796//ESTs//3.8e-49:284:92//Hs.156479:AA513812  
 R-MAMMA1002807//Archain//1.4e-39:315:80//Hs.33642:X81198  
 20 R-MAMMA1002820//ESTs//5.0e-14:192:74//Hs.134635:AA226260  
 R-MAMMA1002830//EST//4.0e-50:255:97//Hs.160674:AI248319  
 R-MAMMA1002833//EST//1.2e-48:306:88//Hs.149580:AI281881  
 R-MAMMA1002835  
 R-MAMMA1002838//EST//2.7e-12:161:76//Hs.163252:AA828723  
 25 R-MAMMA1002842//ESTs//1.7e-41:366:78//Hs.141899:N22395  
 R-MAMMA1002843//Von Hippel-Lindau syndrome//8.8e-38:258:79//Hs.78160:AF010238  
 R-MAMMA1002844//ESTs//3.5e-51:250:99//Hs.151445:AA351081  
 R-MAMMA1002858//H.sapiens ERF-1 mRNA 3' end//9.0e-101:361:91//Hs.85155:X79067  
 R-MAMMA1002868//ESTs//2.1e-38:301:80//Hs.132717:AA171941  
 30 R-MAMMA1002871//EST//6.0e-88:413:99//Hs.149057:AI243592  
 R-MAMMA1002880//ESTs//6.5e-100:506:96//Hs.163533:N52194  
 R-MAMMA1002881//EST//1.1e-40:335:80//Hs.160895:AI365871  
 R-MAMMA1002886//Small inducible cytokine A5 (RANTES)//3.4e-36:228:88//Hs.155464:AF088219  
 R-MAMMA1002887//ESTs//4.7e-87:409:99//Hs.152155:AA424811  
 35 R-MAMMA1002890//ESTs, Weakly similar to coded for by C. elegans cDNA CEESB82F [C.elegans]//4.2e-92:438:  
 99//Hs.155871:AA533783  
 R-MAMMA1002892//Homo sapiens EVI5 homolog mRNA, complete cds//4.9e-62:322:80//Hs.26929:AF008915  
 R-MAMMA1002895//ESTs//2.7e-32:330:76//Hs.139132:AA211087  
 R-MAMMA1002908//Calcium modulating ligand//4.6e-48:313:86//Hs.13572:AF068179  
 40 R-MAMMA1002909//Human mRNA for KIAA0180 gene, partial cds//3.4e-09:132:76//Hs.90981:D80002  
 R-MAMMA1002930//EST//4.9e-44:260:91//Hs.149580:AI281881  
 R-MAMMA1002938  
 R-MAMMA1002941//Human Line-1 repeat mRNA with 2 open reading frames//1.1e-83:556:85//Hs.23094:M19503  
 R-MAMMA1002947//ESTs//7.0e-22:222:80//Hs.103395:T79243  
 45 R-MAMMA1002964//Human mRNA for KIAA0355 gene, complete cds//1.6e-44:427:77//Hs.153014:AB002353  
 R-MAMMA1002970//Thromboxane A2 receptor//7.9e-48:300:84//Hs.89887:D38081  
 R-MAMMA1002972//ESTs, Weakly similar to KIAA0371 [H.sapiens]//9.6e-104:525:95//Hs.94396:AA399630  
 R-MAMMA1002973//ESTs//4.4e-40:257:87//Hs.163580:H15835  
 R-MAMMA1002982//ESTs//2.5e-28:115:87//Hs.141694:W15279  
 50 R-MAMMA1002987//Homo sapiens DNA fragmentation factor 40 kDa subunit (DFF40) mRNA, complete cds//  
 2.1e-41:402:67//Hs.133089:AF064019  
 R-MAMMA1003003//Calcium modulating ligand//1.9e-45:380:79//Hs.13572:AF068179  
 R-MAMMA1003004//ESTs//3.0e-07:378:60//Hs.61885:AI127857  
 R-MAMMA1003007//ESTs//2.0e-47:404:80//Hs.146314:R99617  
 55 R-MAMMA1003011//ESTs, Highly similar to HISTONE MACRO-H2A.1 [Rattus norvegicus]//1.4e-53:320:90//Hs.  
 92023:AI022248  
 R-MAMMA1003015//ESTs//1.5e-42:363:79//Hs.155184:AA573189  
 R-MAMMA1003019//ESTs//4.8e-10:232:66//Hs.111341:AA251268

R-MAMMA1003026//ESTs//2.3e-83:394:99//Hs.24668:AA897315  
R-MAMMA1003031//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.5e-  
27:257:77//Hs.96337:AA225358  
5 R-MAMMA1003035//ESTs//1.3e-94:481:94//Hs.92411:AA603321  
R-MAMMA1003039//EST//0.56:210:61//Hs.162248:AA552160  
R-MAMMA1003040//ESTs//2.1e-17:261:70//Hs.46980:W55940  
R-MAMMA1003044//EST//2.4e-18:124:91//Hs.130321:AI002941  
R-MAMMA1003047//ESTs//1.0e-20:209:78//Hs.15916:H12862  
R-MAMMA1003049//14-3-3 PROTEIN SIGMA//0.94:184:60//Hs.2510:X57348  
10 R-MAMMA1003055//EST//1.0e-49:281:92//Hs.149580:AI281881  
R-MAMMA1003056//ESTs//0.99:107:66//Hs.30348:AI038559  
R-MAMMA1003057//ESTs, Highly similar to hypothetical protein MD6 [M.musculus]//1.1e-102:545:93//Hs.13755:  
AA878911  
R-MAMMA1003066//H.sapiens mRNA for urea transporter//8.1e-45:322:83//Hs.66710:X96969  
15 R-MAMMA1003089//ESTS, Weakly similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//1.4e-  
34:421:70//Hs.161959:AA493652  
R-MAMMA1003099//ESTs//1.1e-43:379:79//Hs.37573:H59651  
R-MAMMA1003104//ESTs//2.1e-97:498:96//Hs.9299:T51283  
R-MAMMA1003113//EST//3.7e-29:457:70//Hs.123616:AA815366  
20 R-MAMMA1003127//ESTs//2.6e-41:283:86//Hs.146811:AA410788  
R-MAMMA1003135//ESTs//7.2e-101:504:97//Hs.87729:AA863125  
R-MAMMA1003140//ESTs//4.3e-44:200:89//Hs.152093:AI149537  
R-MAMMA1003146//Wingless-type MMTV integration site 5A, human homolog//0.020:413:61//Hs.152213:  
L20861  
25 R-nnnnnnnnnnnnn  
R-MAMMA1003166//ESTs, Moderately similar to PEANUT PROTEIN [Drosophila melanogaster]//2.0e-87:524:89//  
Hs.6884:W30736  
R-NT2RM2002580//Homo sapiens clone 24781 mRNA sequence//1.6e-111:587:94//Hs.108112:AF070640  
R-NT2RM4000024//ESTs//2.9e-98:523:94//Hs.26641:R59312  
30 R-NT2RM4000027  
R-NT2RM4000030//ESTs//1.6e-96:482:96//Hs.90625:T03663  
R-NT2RM4000046//ESTs//1.6e-91:461:97//Hs.151237:AI86169  
R-NT2RM4000061//ESTs//4.3e-31:167:97//Hs.110821:Z78379  
R-NT2RM4000085//Homo sapiens clone 24700 unknown mRNA, partial cds//4.0e-113:549:97//Hs.95665:  
35 AF070639  
R-NT2RM4000086//EST//2.7e-17:212:76//Hs.137041:AA877817  
R-NT2RM4000104//ESTs//3.0e-85:452:94//Hs.101750:H19708  
R-NT2RM4000139//EST//3.3e-05:156:66//Hs.133228:AI052312  
R-NT2RM4000155//ESTs, Moderately similar to THREONYL-TRNA SYNTHETASE, CYTOPLASMIC [H.sapiens]  
40 //1.9e-99:536:92//Hs.127810:AI246301  
R-NT2RM4000156//EST//0.89:169:62//Hs.162967:AA676397  
R-nnnnnnnnnnnnn//ESTs//1.0:214:61//Hs.119370:W52962  
R-NT2RM4000169//ESTs//5.4e-82:440:93//Hs.159379:AI382160  
R-NT2RM4000191//ESTs, Weakly similar to P68 PROTEIN [H.sapiens]//4.1e-99:542:93//Hs.6366:AA614113  
45 R-NT2RM4000197//ESTs//5.4e-113:567:96//Hs.22975:AA156723  
R-NT2RM400019911ESTs10.020:95:6511Hs.146203:AI254528  
R-NT2RM4000200//ESTs//1.4e-100:488:97//Hs.1265338:AA931876  
R-NT2RM4000202//Small inducible cytokine A5 (RANTES)//4.3e-37:330:77//Hs.155464:AF088219  
R-NT2RM4000210//Homo sapiens mRNA for KIAA0712 protein, complete cds//1.7e-103:546:94//Hs.111138:  
50 AB018255  
R-NT2RM4000215  
R-nnnnnnnnnnnnn//ESTs//7.1e-92:457:97//Hs.162074:AA477760  
R-NT2RM4000233//Fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor  
receptor)//0.00020:174:66//Hs.235:X51602  
55 R-NT2RM4000244//ESTs//6.6e-61:320:95//Hs.108646:AA613031  
R-NT2RM4000251//Homo sapiens mRNA for TRIP6 (thyroid receptor interacting protein)//0.63:219:62//Hs.  
119498:AF000974  
R-NT2RM4000265//ESTs//8.8e-105:489:99//Hs.131001:AI378742

R-NT2RM4000290//ESTs//4.0e-87:435:96//Hs.162592:AA594128  
 R-NT2RM4000324//ESTs//2.2e-80:413:96//Hs.12313:R43673  
 R-NT2RM4000327//Small inducible cytokine A5 (RANTES)//3.2e-45:286:87//Hs.155464:AF088219  
 R-NT2RM4000344//Clathrin, light polypeptide (Lcb)//8.6e-60:452:84//Hs.73919:X81637  
 5 R-NT2RM4000349//ESTs, Weakly similar to KIAA005 [H.sapiens]//2.5e-. 117:579:96//Hs.5216:AA534881  
 R-NT2RM4000354//ESTs//2.1e-85:406:99//Hs.126774:AI224479  
 R-NT2RM4000356//ESTs//7.9e-109:548:96//Hs.44278:AA418063  
 R-NT2RM4000366//Homo sapiens mRNA for KIAA0642 protein, partial cds//2.8e-113:577:95//Hs.8152:AB014542  
 R-NT2RM4000368//ESTs//2.2e-61:310:97//Hs.143611:M78140  
 10 R-NT2RM4000386//ESTs, Weakly similar to tenascin-like protein [D.melanogaster]//1.0e-93:521:92//Hs.41793:  
 AA775879  
 R-NT2RM4000395//ESTs, Highly similar to HYPOTHETICAL 52.9 KD PROTEIN IN SAP155-YMR31 INTERGENIC REGION [Saccharomyces cerevisiae]//1.9e-99:524:94//Hs.5249:U55977  
 R-NT2RM4000414//EST//2.7e-06:196:64//Hs.136648:AA688285  
 15 R-NT2RM4000421//ESTs, Weakly similar to No definition line found [C.elegans]//5.4e-75:470:90//Hs.69235:  
 AA192359  
 R-NT2RM4000425//H.sapiens mRNA for MACH-alpha-2 protein//0.17:112:69//Hs.19949:X98173  
 R-NT2RM4000433//ESTs//2.7e-100:479:98//Hs.24553:AI150687  
 R-NT2RM4000457//ESTs//5.1e-107:535:95//Hs.7579:AA775865  
 20 R-NT2RM4000471//ESTs, Highly similar to NIFS-LIKE 54.5 KD PROTEIN [Saccharomyces cerevisiae]//6.0e-99:  
 492:96//Hs.21090:AA418587  
 R-NT2RM4000486//ESTs, Moderately similar to unnamed protein product [H.sapiens]//2.2e-102:493:97//Hs.  
 111279:W84558  
 R-NT2RM4000496  
 25 R-NT2RM4000511//EST//5.1e-43:326:81//Hs.157658:AI358465  
 R-NT2RM4000514//ESTs//1.7e-112:552:96//Hs.6686:AA205496  
 R-nnnnnnnnnnnnn//ESTs, Weakly similar to HYPOTHETICAL 85.0 KD PROTEIN IN CPA2-ATP2 INTERGENIC REGION [Saccharomyces cerevisiae]//1.4e-60:343:93//Hs.16014:AA074879  
 R-NT2RM4000520//ESTs//2.7e-55:266:100//Hs.99838:AA204731  
 30 R-NT2RM4000531//ESTs//2.0e-88:502:91//Hs.13110:T67461  
 R-NT2RM4000532//ESTs//0.47:290:58//Hs.148753:T91777  
 R-NT2RM4000534//EST//0.00025:303:60//Hs.162809:AA632198  
 R-NT2RM4000585//EST//0.28:63:77//Hs.150024:AI291981  
 R-NT2RM4000590//ESTs//5.8e-65:320:98//Hs.116017:AA613437  
 35 R-NT2RM4000595//Homo sapiens KIAA0431 mRNA, partial cds//0.99:189:64//Hs.16349:AB007891  
 R-NT2RM4000603//ESTs//4.6e-68:356:96//Hs.48855:AA134589  
 R-nnnnnnnnnnnnn//ESTs//1.5e-89:431:97//Hs.26117:W16697  
 R-NT2RM4000616//ESTs, Highly similar to ACETYL-COENZYME A SYNTHETASE [Escherichia coli]//1.4e-102:  
 519:96//Hs.14779:N64822  
 40 R-NT2RM4000674//ESTs//5.1e-78:398:97//Hs.8268:N70144  
 R-NT2RM4000689//ESTs, Weakly similar to T01G9.4 [C.elegans]//2.9e-115:550:98//Hs.11820:AA205531  
 R-NT2RM4000698//ESTs//2.0e-17:130:87//Hs.86420:AA927510  
 R-nnnnnnnnnnnnn  
 R-NT2RM4000712//EST//0.99:103:65//Hs.114039:AA701128  
 45 R-NT2RM4000717//ESTs, Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus]//2.2e-103:519:95//Hs.6823:W18181  
 R-NT2RM4000733//ESTs//8.7e-88:429:98//Hs.72185:AA465311  
 R-NT2RM4000734//Homo sapiens mRNA for KIAA0760 protein, partial cds//3.6e-105:536:95//Hs.137168:  
 AB018303  
 50 R-NT2RM40007.41//ESTs//0.99:266:58//Hs.142718:AA034046  
 R-NT2RM4000751//ESTs//1.6e-20:351:66//Hs.43145:AA776988  
 R-NT2RM4000764  
 R-NT2RM4000778//EST//0.066:254:61//Hs.148232:AA904174  
 R-NT2RM4000779//Homo sapiens mRNA for KIAA0451 protein, complete cds//9.3e-106:546:94//Hs.18586:  
 55 AB007920  
 R-NT2RM4000787//Human melanoma antigen recognized by T-cells (MART-1) mRNA//6.5e-40:424:73//Hs.  
 154069:U06452  
 R-NT2RM4000790//EST//9.0e-48:259:94//Hs.159694:AI417008

R-NT2RM4000795//Human mRNA for KIAA0067 gene, complete cds//1.0:203:63//Hs.20991:D31891  
R-NT2RM4000796//ESTs//7.0e-106:506:98//Hs.43559:AI003520  
R-NT2RM4000798//Human polymorphic epithelial mucin core protein mRNA, 3' end//2.5e-28:158:96//Hs.118249:  
M21868  
5 R-NT2RM4000813  
R-NT2RM4000820//ESTs, Weakly similar to hypothetical protein [H.sapiens]//1.3e-109:539:97//Hs.99636:  
AI219667  
R-NT2RM4000833//ESTs, Moderately similar to ZK863.3 [C.elegans]//4.0e-112:448:99//Hs.20223:AA482031  
R-NT2RM4000848//ESTs//8.1e-97:476:97//Hs.16036:AA883864  
10 R-NT2RM4000852//ESTs//6.4e-94:467:97//Hs.11556:AI309597  
R-NT2RM4000855//ESTs//2.9e-95:544:90//Hs.106525:AI283343  
R-nnnnnnnnnnnnn  
R-NT2RM4000895//ESTs, Moderately similar to !!! ALU SUBFAMILY SQ WARNING ENTRY !!! [H.sapiens]//9.3e-  
96:450:99//Hs.142076:AA604514  
15 R-NT2RM4000950//ESTs//2.6e-91:438:98//Hs.43827:AA455262  
R-NT2RM4000971//EST//2.9e-96:461:99//Hs.139709:AA227887  
R-NT2RM4000979//EST//1.6e-67:329:98//Hs.96927:AA349647  
R-NT2RM4000996//ESTs, Weakly similar to ZINC FINGER PROTEIN 91 [H.sapiens]//1.7e-82:414:96//Hs.115342:  
AA650126  
20 R-NT2RM4001002//Homo sapiens mRNA for KIAA0729 protein, partial cds//3.8e-114:545:97//Hs.19542:  
AB018272  
R-NT2RM4001016//Homo sapiens mRNA for KIAA0639 protein, partial cds//2.5e-114:556:97//Hs.15711:  
AB014539  
R-NT2RM4001032//ESTs//7.8e-17:132:84//Hs.138720:N53352  
25 R-NT2RM4001047//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds//0.42:133:67//Hs.  
32170:AB015132  
R-NT2RM4001054//ESTs//1.7e-84:404:99//Hs.116407:AA815300  
R-nnnnnnnnnnn//ESTs//3.4e-91:439:99//Hs.103177:W72798  
R-NT2RM4001092//ESTs//1.4e-86:517:8911Hs.132969:Z78324  
30 R-NT2RM4001116//EST//5.2e-57:275:100//Hs.131115:AI016962  
R-NT2RM4001140//ESTs//5.5e-96:461:98//Hs.86965:AA252276  
R-NT2RM4001151//ESTs//0.40:263:58//Hs.113189:R08311  
R-NT2RM4001155//ESTs//8.3e-105:544:94//Hs.29647:W60848  
R-NT2RM4001160//EST//7.6e-25:380:68//Hs.147405:AI209085  
35 R-NT2RM4001187//ESTs, Moderately similar to !!! ALU SUBFAMILY SC WARNING ENTRY !!! [H.sapiens]//9.2e-  
43:273:91//Hs.109005:N31174  
R-NT2RM4001191//Cytochrome P450, 51 (lanosterol 14-alpha-demethylase)//3.1e-32:274:70//Hs.2379:U23942  
R-NT2RM4001200//ESTs//4.5e-102:494:97//Hs.31844:N32849  
R-NT2RM4001203  
40 R-NT2RM4001204//ESTs//9.8e-88:468:93//Hs.4990:T65307  
R-NT2RM4001217//ESTs//1.2e-75:396:94//Hs.25042:R72410  
R-NT2RM4001256//ESTs//1.0:157:62//Hs.65377:AA994677  
R-NT2RM4001258//ESTs//9.6e-41:260:88//Hs.27633:N76184  
R-NT2RM4001309  
45 R-NT2RM4001313//EST//0.0022:150:66//Hs.161573:W84857  
R-NT2RM4001316//ESTs//3.5e-26:139:99//Hs.23100:AI128899  
R-NT2RM4001320//ESTs//1.6e-97:308:99//Hs.112024:AI042352  
R-NT2RM4001340//ESTs, Highly similar to UTR4 PROTEIN [Saccharomyces cerevisiae]//1.9e-105:522:97//Hs.  
18442:AI129307  
50 R-NT2RM4001344//EST//1.1e-90:436:99//Hs.95900:AA160339  
R-NT2RM4001347//EST//0.17:186:61//Hs.16751:T90476  
R-NT2RM4001371//EST//0.0069:270:62//Hs.99239:AA450211  
R-NT2RM4001382  
R-NT2RM4001384//ESTs//9.6e-91:445:98//Hs.55000:AA805507  
55 R-NT2RM4001410//EST//0.13:50:82//Hs.157675:AI358790  
R-NT2RM4001411//ESTs, Weakly similar to lymphocyte specific adaptor protein Lnk [M.musculus]//4.0e-102:539:  
94//Hs.15744:AI055859  
R-NT2RM4001412

R-NT2RM4001414//ESTs//6.5e-35:226:88//Hs.121727:AA775895  
 R-NT2RM4001437//EST//0.017:169:67//Hs.13207:F10054  
 R-NT2RM4001444//ESTs, Weakly similar to ISOLEUCYL-TRNA SYNTHETASE, MITOCHONDRIAL [S.cerevisiae]//7.4e-108:544:94//Hs.7558:AA526812  
 5 R-NT2RM4001454//ESTs//4.7e-108:517:98//Hs.32295:N32277  
 R-NT2RM4001455//EST//9.6e-81:395:97//Hs.127978:AA969739  
 R-NT2RM4001483//Human mRNA for KIAA0033 gene, partial cds//1.8e-58:324:85//Hs.22271:D26067  
 R-NT2RM4001489//Homo sapiens mRNA for KIAA0685 protein, complete cds//7.0e-104:547:93//Hs.153121:  
 AB014585  
 10 R-NT2RM4001519//Histatin 1//0.53:340:59//Hs.119101:M26664  
 R-NT2RM40015227/Small inducible cytokine A5 (RANTES)//8.4e-55:306:80//Hs.155464:AF088219  
 R-NT2RM40015577//ESTs, Weakly similar to F11A10.4 [C.elegans]//6.1e-21:165:83//Hs.29134:H43072  
 R-NT2RM4001565//ESTs//2.0e-103:483:99//Hs.121273:AA758027  
 R-NT2RM4001566//Human DNA sequence from clone 1409 on chromosome Xp11.1-11.4. Contains a Inter-Alpha-Trypsin Inhibitor Heavy Chain LIKE gene, a alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSs and genomic marker DXS8032//2.7e-43:446:72//Hs.4943:Z98046  
 15 R-NT2RM4001569//ESTs//3.6e-37:186:100//Hs.86959:AA888009  
 R-NT2RM4001582//ESTs//1.2e-96:459:98//Hs.114432:N52946  
 20 R-nnnnnnnnnnnnn  
 R-NT2RM4001594//ESTs//1.6e-83:404:98//Hs.134740:AA282171  
 R-NT2RM4001597//ESTs//6.9e-111:558:96//Hs.11408:AI358871  
 R-NT2RM4001605//Homo sapiens mRNA for KIAA0791 protein, complete cds//2.1e-112:565:95//Hs.23255:  
 AB018334  
 25 R-NT2RM4001611//EST//5.9e-74:353:99//Hs.125318:AA837079  
 R-NT2RM4001629//ESTs//6.1e-95:453:99//Hs.115765:AA485957  
 R-NT2RM4001650  
 R-NT2RM4001662  
 R-NT2RM4001666//Homo sapiens mRNA for KIAA0469 protein, complete cds//3.6e-36:230:70//Hs.7764:  
 30 AB007938  
 R-NT2RM4001682//EST//4.3e-68:393:90//Hs.157362:AI367496  
 R-NT2RM4001710//ESTs//4.3e-48:235:99//Hs.7299:AA203440  
 R-NT2RM4001714//ESTs//0.0014:568:58//Hs.50458:AA868686  
 R-nnnnnnnnnnnn//ESTs//6.5e-104:487:99//Hs.153581:AA630465  
 35 R-NT2RM4001731//ESTs, Weakly similar to No definition line found [C.elegans]//3.1e-108:563:94//Hs.18510:  
 AA522887  
 R-NT2RM4001741//T3 receptor-associating cofactor-1 [human, fetal liver, mRNA, 2930 nt]//0.083:124:68//Hs.  
 120980:S83390  
 R-NT2RM4001746//ESTs//6.1e-90:420:100//Hs.139003:AA948200  
 40 R-NT2RM4001754//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//5.4e-59:504:78//Hs.139107:K00629  
 R-NT2RM4001758//ESTs//8.9e-27:140:100//Hs.149973:AI290740  
 R-NT2RM4001776//Homo sapiens mRNA for KIAA0727 protein, partial cds//6.4e-24:236:80//Hs.39871:AB018270  
 R-NT2RM4001783//ESTs//9.9e-30:156:99//Hs.115260:AA314956  
 R-NT2RM4001810//ESTs//1.3e-65:346:95//Hs.131915:W22567  
 45 R-NT2RM4001813//ESTs//5.7e-102:473:100//Hs.87574:AI089920  
 R-NT2RM4001823//ESTs//3.8e-62:324:95//Hs.124109:AA888839  
 R-NT2RM4001828//ESTs//1.3e-119:563:98//Hs.102397:AA706551  
 R-NT2RM4001836//ESTs//5.5e-16:92:100//Hs.26996:AA551070  
 R-NT2RM4001841//ESTs//1.3e-99:540:94//Hs.42322:AA082619  
 50 R-NT2RM4001842//ESTs, Weakly similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//4.1e-10:  
 274:62//Hs.161959:AA493652  
 R-NT2RM4001856//ESTs, Weakly similar to contains similarity to ATP/GTP-binding site motif [C.elegans]//3.0e-  
 43:292:86//Hs.14202:N46000  
 R-nnnnnnnnnnnn//ESTs//6.2e-104:495:98//Hs.118686:AA682280  
 55 R-NT2RM40018657//Homo sapiens mRNA for atopy related autoantigen CALC//1.6e-120:592:97//Hs.61628:  
 Y17711  
 R-NT2RM4001876//ESTs//2.9e-98:532:92//Hs.100734:AA158252  
 R-NT2RM4001880//ESTs//2.5e-29:224:86//Hs.6193:AA045149

EP 1 074 617 A2

R-NT2RM4001905//ESTs//5.6e-109:565:95//Hs.9536:AA114178  
 R-NT2RM4001922//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.2e-105:  
 535:95//Hs.30991:AA994438  
 R-NT2RM4001930//ESTs//4.1-84:425:96//Hs.80042:N63143  
 5 R-NT2RM4001938//EST//0.00040:241:60//Hs.147235:AI205893  
 R-NT2RM4001940//Homo sapiens timeless homolog mRNA, complete cds//2.0e-110:556:95//Hs.118631:  
 AF098162  
 R-NT2RM4001953//ESTs//5.3e-65:338:96//Hs.33718:AA453268  
 R-NT2RM4001965//ESTs, Weakly similar to T14B4.2 gene product [C.elegans]//5.7e-62:326:95//Hs.3385:N25917  
 10 R-nnnnnnnnnnnnnnnnnnn//ESTs, Weakly similar to IP63 protein [R.norvegicus]//1.9e-21:121:98//Hs.8772:AA521097  
 R-NT2RM4001979//ESTs//1.4e-96:465:98//Hs.157103:W60265  
 R-NT2RM4001984  
 R-NT2RM4001987  
 R-NT2RM4002013//EST//2.2e-14:110:90//Hs.160835:AI345528  
 15 R-NT2RM4002018  
 R-NT2RM4002034//Human mRNA for KIAA0118 gene, partial cds//9.4e-46:293:87//Hs.154326:D42087  
 R-NT2RM4002044//ESTs//2.8e-107:537:96//Hs.24078:W44435  
 R-NT2RM4002054//ESTs//3.7e-88:482:94//Hs.4243:T78226  
 R-NT2RM4002062//ESTs//1.4e-55:377:85//Hs.152592:AA587887  
 20 R-NT2RM4002063//Calcium modulating ligand//1.8e-43:385:78//Hs.13572:AF068179  
 R-nnnnnnnnnnnnnnnnn//Homo sapiens OPA-containing protein mRNA, complete cds//5.5e-42:554:68//Hs.85313:  
 AF071309  
 R-NT2RM4002067//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//2.3e-43:468:73//Hs.139107:K00629  
 R-NT2RM4002073//ESTs, Weakly similar to very-long-chain acyl-CoA synthetase [H.sapiens]//6.8e-57:290:96//  
 25 Hs.109274:AA193416  
 R-NT2RM4002075//ESTs//0.078:267:61//Hs.163563:AA641655  
 R-NT2RM4002093//ESTs//1.2e-64:316:99//Hs.34956:AI052528  
 R-nnnnnnnnnnnnnnnnn//ESTs//1.0:95:69//Hs.25897:W65409  
 R-NT2RM4002128//Homo sapiens mRNA for BCL9 gene//0.51:258:60//Hs.122607:Y13620  
 30 R-NT2RM4002140//ESTs//5.5e-46:187:94//Hs.8737:W22712  
 R-NT2RM4002145//ESTs//4.6e-70:374:94//Hs.141082:H18987  
 R-NT2RM4002146//ESTs//1.9e-93:43 9:99//Hs.119295:AA442090  
 R-NT2RM4002161//Homo sapiens laforin (EPM2A) mRNA, partial cds//1.5e-111:560:96//Hs.22464:AF084535  
 R-NT2RM4002174//Homo sapiens LIM protein mRNA, complete cds//3.2e-46:552:72//Hs.154103:AF061258  
 35 R-NT2RM4002189//ESTs//9.6e-75:352:100//Hs.98350:H15400  
 R-NT2RM4002194//EST//0.22:68:72//Hs.149104:AI244343  
 R-NT2RM4002205//EST//0.00028:103:72//Hs.130032:AA897678  
 R-NT2RM4002213//ESTs//3.3e-15:160:78//Hs.63304:W22079  
 R-NT2RM4002226//ESTs, Highly similar to GTPASE ACTIVATING PROTEIN ROTUND [Drosophila melanogaster]  
 40 //5.1e-112:569:95//Hs.23900:U82984  
 R-NT2RM4002251//ESTs, Weakly similar to similar to alpha-1,3-mannosyl-glycoprotein beta-1, 2-N-acetylglu-  
 cosaminyltransferase [C.elegans]//1.1e-100:544:93//Hs.27567:W72190  
 R-NT2RM4002256//Small inducible cytokine A5 (RANTES)//1.0e-44:341:81//Hs.155464:AF088219  
 R-NT2RM4002266//ESTs//2.6e-100:539:93//Hs.57976:AA535864  
 45 R-NT2RM4002278//ESTs//1.8e-112:569:95//Hs.87281:AA128263  
 R-NT2RM4002281//ESTs//4.9e-20:187:80//Hs.141203:H52638  
 R-NT2RM4002287//ESTs//7.9e-84:388:94//Hs.33977:N52461  
 R-NT2RM4002294  
 R-NT2RM4002301//ESTs//4.5e-111:556:96//Hs.85916:AA194164  
 50 R-NT2RM4002323//ESTs//4.5e-102:498:97//Hs.85782:AA191498  
 R-nnnnnnnnnnnnnnnnn//ESTs//5.0e-59:283:100//Hs.125048:AA682913  
 R-NT2RM4002344//V-akt murine thymoma viral oncogene homolog 2//0.29:153:66//Hs.155129:M77198  
 R-NT2RM4002373//Homo sapiens mRNA for KIAA0649 protein, complete cds//2.8e-122:593:97//Hs.26163:  
 AB014549  
 55 R-NT2RM4002374//ESTs//3.3e-40:505:70//Hs.95115:AA206594  
 R-NT2RM4002383//ESTs//2.7e-93:455:97//Hs.134278:AA648884  
 R-NT2RM4002390//ESTs//3.3e-93:481:95//Hs.48764:AA613328  
 R-NT2RM4002409//ESTs, Weakly similar to coded for by C. elegans cDNA yk52e10.5 [C.elegans]//1.3e-97:473:

98//Hs.16464:W19606  
 R-NT2RM4002438//ESTs//0.74:162:61//Hs.65377:AA994677  
 R-NT2RM4002446  
 R-NT2RM4002452//EST//1.0:164:60//Hs.1166I9:AA668142  
 5 R-NT2RM4002457  
 R-NT2RM4002460//ESTs//3.0e-74:385:96//Hs.6933:R07890  
 R-NT2RM4002479//Homo sapiens RNA helicase-related protein mRNA, complete cds//1.6e-103:507:97//Hs.  
 8765:AF083255  
 R-NT2RM4002482//Homo sapiens mRNA for KIAA0691 protein, complete cds//2.3e-32:172:98//Hs.94781:  
 10 AB014591  
 R-NT2RM4002493//ESTs//6.4e-73:366:97//Hs.157114:T58884  
 R-NT2RM4002499//ESTs//3.5e-61:307:97//Hs.117737:AI088029  
 R-NT2RM4002504//ESTs//2.1e-55:306:94//Hs.10949:AA464464  
 15 R-nnnnnnnnnnnn//ESTs, Weakly similar to peroxisome targeting signal 2 receptor [H.sapiens]//1.4e-73:360:91//  
 Hs.31030:H50467  
 R-NT2RM4002532//ESTs//1.3e-21:191:78//Hs.146811:AA410788  
 R-NT2RM4002534//ESTs//1.8e-99:512:95//Hs.13526:AI417057  
 R-NT2RM4002567//ESTs//7.6e-41:272:87//Hs.7114:R24312  
 R-NT2RM4002571//ESTs, Highly similar to POLYPEPTIDE N-ACETYLGLACTOSAMINYLTRANSFERASE [Bos  
 20 taurus]//2.3e-89:435:97//Hs.15830:AA165698  
 R-NT2RM4002593//ESTs//2.3e-109:552:96//Hs.17424:AA190569  
 R-NT2RM4002623//ESTs, Weakly similar to ASPARTYL-TRNA SYNTHETASE [Thermus aquaticus thermophilus]  
 //9.6e-28:194:87//Hs.59346:AI126802  
 R-NT2RP2000001//ESTs//2.6e-80:386:99//Hs.105061:N45096  
 25 R-NT2RP2000006//Thromboxane A2 receptor//7.2e-37:253:84//Hs.89887:D38081  
 R-NT2RP2000008//Zinc finger protein 37a (KOX 21)//5.2e-25:366:67//Hs.54488:X69115  
 R-NT2RP2000027//ESTs//9.5e-74:377:96//Hs.96557:AA286713  
 R-NT2RP2000040//Homo sapiens mRNA for KIAA0747 protein, partial cds//2.7e-42:223:96//Hs.8309:AB018290  
 R-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds//  
 30 4.3e-64:309:98//Hs.6216:AF061749  
 R-NT2RP2000054//EST//1.2e-71:375:96//Hs.98835:AA435798  
 R-NT2RP2000056//EST//2.8e-28:342:69//Hs.135526:AI094910  
 R-NT2RP2000067//ESTs, Weakly similar to tenascin-like protein [D.melanogaster]//2.3e-35:199:94//Hs.41793:  
 AA775879  
 35 R-NT2RP2000070//ESTs, Weakly similar to proto-cadherin 3 [R.norvegicus]//1.4e-78:383:98//Hs.58254:W72881  
 R-NT2RP2000076//EST//0.0014:227:63//Hs.136761:AA738097  
 R-NT2RP2000077//Homo sapiens growth arrest specific 11 (GAS11) mRNA, complete cds//1.1e-78:379:97//Hs.  
 54877:AF050078  
 R-NT2RP2000079//Homo sapiens RET finger protein-like 1 antisense transcript, partial//2.9e-21:232:75//Hs.  
 40 102576:AJ010230  
 R-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cds//1.8e-75:378:96//Hs.22926:AB018338  
 R-NT2RP2000091//Carcinoembryonic antigen gene family member 6//0.030:236:63//Hs.41:D90064  
 R-NT2RP2000097//ESTs//4.2e-15:92:97//Hs.7432:AA281757  
 R-NT2RP2000098//ESTs//9.0e-53:279:94//Hs.87807:AA813827  
 45 R-NT2RP2000108//EST//1.5e-75:378:96//Hs.162105:AA524419  
 R-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds//5.8e-76:386:95//Hs.17706:AB018356  
 R-NT2RP2000120//ESTs, Weakly similar to HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III  
 [C.elegans]//1.9e-19:153:86//Hs.5268:W22670  
 R-nnnnnnnnnnnn//ESTs//1.0e-55:293:95//Hs.14570:AI422099  
 50 R-nnnnnnnnnnnn//ESTs//0.24:354:59//Hs.157564:AI356513  
 R-NT2RP2000147//ESTs, Highly similar to CLATHRIN COAT ASSEMBLY PROTEIN AP47 [Mus musculus]//3.0e-  
 89:457:95//Hs.3832:AI208601  
 R-NT2RP2000153//EST//0.0039:93:68//Hs.140386:AA773548  
 R-NT2RP2000157//ESTs//1.1e-53:322:91//Hs.6877:AA040820  
 R-NT2RP2000161//EST5//1.6e-99:492:97//Hs.21738:AI188190  
 R-NT2RP2000175//ESTs//1.4e-98:489:96//Hs.4849:AI143741  
 R-NT2RP2000183//ESTs//9.0e-72:358:96//Hs.4856:N51373  
 R-NT2RP2000195//ESTs//3.9e-92:439:98//Hs.145091:AA814510

R-NT2RP2000205//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.4e-80:415:95//Hs.11807:T86897  
R-NT2RP2000224//RNA polymerase II, polypeptide C (33kD)//1.1e-57:306:94//Hs.79402:AC004382  
R-NT2RP2000232  
5 R-NT2RP2000233//ESTs//1.1e-08:63:96//Hs.124861:AI090683  
R-NT2RP2000239//ESTs//5.3e-87:427:96//Hs.86211:AA604379  
R-NT2RP2000248//ESTs, Weakly similar to O-linked GlcNAc transferase [H.sapiens]//1.3e-95:454:99//Hs.102057:AA649005  
10 R-NT2RP2000257//ESTs//5.1e-58:282:99//Hs.122565:AI126840  
R-NT2RP2000258//EST//1.0:67:68//Hs.61812:AA035649  
R-NT2RP2000270//ESTs, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//8.4e-59:298:96//Hs.16085:AI261382  
R-NT2RP2000274//ESTs//7.5e-61:296:98//Hs.86081:AA196635  
15 R-NT2RP2000288//ESTs//1.8e-56:305:93//Hs.7579:AA775865  
R-NT2RP2000289  
R-NT2RP2000297//ESTs, Highly similar to MKR2 PROTEIN [Mus musculus]//9.8e-106:494:99//Hs.102951:AA574249  
R-NT2RP2000298//ESTs//2.1e-62:256:90//Hs.8737:W22712  
R-NT2RP2000310//Human proline dehydrogenase/proline oxidase (PRODH) mRNA, complete cds//2.8e-39:222:  
20 93//Hs.58218:U82381  
R-NT2RP2000327//Homo sapiens DNA sequence from PAC 434014 on chromosome 1q32.3.-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two unknown genes. Contains ESTs and GSSs//2.9e-71:342:98//Hs.87684:AL022398  
25 R-NT2RP2000329//ESTs, Highly similar to GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL [Bos taurus]//3.4e-69:371:94//Hs.43436:N32441  
R-NT2RP2000337//ESTs//5.2e-79:411:95//Hs.101799:AI276062  
R-NT2RP2000346//Homo sapiens apoptosis associated protein (GADD34) mRNA, complete cds//1.1e-47:262:  
94//Hs.76556:U83981  
30 R-NT2RP2000369//ESTs//4.3e-102:531:94//Hs.15855:H98103  
R-NT2RP2000414//Homo sapiens HnRNP F protein mRNA, complete cds//8.4e-09:93:83//Hs.808:L28010  
R-NT2RP2000420//ESTs//8.2e-24:142:94//Hs.144893:AI222324  
R-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds//4.2e-20:140:  
90//Hs.5819:AF102265  
35 R-NT2RP2000438//ESTs, Weakly similar to misato [D.melanogaster]//1.3e-65:362:93//Hs.22197:AI151425  
R-NT2RP2000448//ESTs, Highly similar to HYPOTHETICAL 51.6 KD PROTEIN IN PAP1-MRPL13 INTERGENIC REGION [Saccharomyces cerevisiae]//3.6e-75:435:92//Hs.21938:W81045  
R-NT2RP2000459//ESTs//2.8e-95:527:93//Hs.103422:AI352013  
R-NT2RP2000498//ESTs//2.3e-17:119:79//Hs.161714:AA229078  
40 R-NT2RP2000503//ESTs//5.2e-91:438:98//Hs.152335:AI290215  
R-NT2RP2000510//Homo sapiens KIAA0436 mRNA, partial cds//0.13:455:58//Hs.110:AB007896  
R-nnnnnnnnnn//ESTs//9.9e-63:376:89//Hs.47546:AA181348  
R-NT2RP2000523  
R-NT2RP2000603//Homo sapiens mRNA for KIAA0572 protein, partial cds//3.5e-30:167:97//Hs.14409:AB011144  
45 R-NT2RP2000617//ESTs//9.5e-103:493:98//Hs.9412:W72446  
R-NT2RP2000634//Homo sapiens mRNA for KIAA0614 protein, partial cds//8.1e-66:335:96//Hs.7314:AB014514  
R-NT2RP2000644//ESTs//1.1e-18:372:63//Hs.82419:AA789222  
R-NT2RP2000656//ESTs//1.0e-10:128:80//Hs.23977:AA115275  
50 R-NT2RP2000658//ESTs//0.31:278:59//Hs.15661:W02396  
R-NT2RP2000668//ESTs//8.2e-40:255:88//Hs.113310:R16767  
R-NT2RP2000678//ESTs//2.6e-53:271:9611Hs.23790:N99347  
R-NT2RP2000710//ESTs//0.49:190:63//Hs.145521:AI261368  
R-NT2RP2000715//EST//1.2e-87:418:9911Hs.139425:AA429279  
R-NT2RP2000731//EST//5.3e-65:322:97//Hs.136754:AA713965  
55 R-NT2RP2000758//ESTS//1.0:187:61//Hs.10545:N62642  
R-NT2RP2000764//ESTs//5.8e-84:485:91//Hs.121816:AA775419  
R-NT2RP2000809  
R-NT2RP2000812//ESTs//1.2e-45:231:97//Hs.121028:AA902745

R-nnnnnnnnnnnn//ESTs//6.3e-87:433:97//Hs.145479:AA969404  
R-NT2RP2000816//ESTs//0.45:100:69//Hs.147529:AA458918  
R-NT2RP2000819  
R-NT2RP2000841//ESTs//1.9e-73:351:99//Hs.116385:AI224511  
5 R-NT2RP2000842//TUMOR NECROSIS FACTOR-INDUCIBLE PROTEIN TSG-6  
PRECURSOR//4.6e-10:247:66//Hs.29352:M31165  
R-NT2RP2000845//ESTs//2.8e-91:443:97//Hs.66810:AI206552  
R-NT2RP2000863//ESTs//4.3e-49:310:88//Hs.104336:W07345  
R-NT2RP2000880//Homo sapiens mRNA for KIAA0741 protein, complete cds//2.8e-43:277:89//Hs.3615:  
10 AB018284  
R-NT2RP2000892//ESTs//2.8e-50:25 8:96//Hs.119238:AA476267  
R-NT2RP2000931//MATRIN 3//7.2e-57:290:96//Hs.78825:AB018266  
R-NT2RP2000938//ESTs, Highly similar to HYPOTHETICAL 6.3 KD PROTEIN ZK652.2 IN CHROMOSOME III  
[Caenorhabditis elegans]//3.9e-37:199:95//Hs.112318:AA186477  
15 R-NT2RP2000943//Homo sapiens mRNA for KIAA0755 protein, complete cds//9.8e-98:494:96//Hs.19822:  
AB018298  
R-NT2RP2000965//EST//0.22:223:60//Hs.105703:AA487021  
R-NT2RP2000970//EST//8-7e-06:255:62//Hs.149202:AI246481  
R-NT2RP2000985//ESTs, Weakly similar to HYPOTHETICAL 96.8 KD PROTEIN IN SIS2-MTD1 INTERGENIC  
20 REGION [S.cerevisiae]//7.8e-92:468:95//Hs.12124:AA522537  
R-NT2RP2000987//ESTs//4.5e-78:419:93//Hs.21968:H97521  
R-NT2RP2001036//EST//2.0e-33:148:82//Hs.163196:AA767643  
R-NT2RP2001044//ESTs//5.6e-95:493:95//Hs.21958:AA453660  
R-NT2RP2001065//ESTs//3.6e-28:153:96//Hs.119314:AA432108  
25 R-NT2RP2001070//EST//0.30:94:67//Hs.94289:N73665  
R-NT2RP2001094//EST//0.75:101:69//Hs.161040:H82068  
R-NT2RP2001119  
R-NT2RP2001127//Homa sapiens mRNA for HRIHFB2060, partial cds//1.5e-56:304:94//Hs.146282:AB015348  
R-NT2RP2001137  
30 R-NT2RP2001149//ESTs//5.1e-66:324:9711Hs.27475:AA704512  
R-NT2RP2001168//ESTs//2.0e-98:539:92//Hs.77870:AI188145  
R-NT2RP2001173//Homo sapiens mRNA for KIAA0480 protein, complete cds//1.5e-96:490:96//Hs.26247:  
AB007949  
R-NT2RP2001174//ESTs//2.2e-63:354:93//Hs.24266:R28287  
35 R-NT2RP2001196//ESTs//1.4e-83:463:93//Hs.124304:AA825510  
R-NT2RP2001218//ESTs//1.4e-100:506:96//Hs.93391:AI188402  
R-NT2RP2001226//EST//0.0074:154:63//Hs.128612:AA909358  
R-NT2RP2001233//TESTs, Highly similar to ZINC FINGER PROTEIN ZFP-36 [Homo sapiens]//3.7e-65:538:80//  
Hs.44014:AA632298  
40 R-NT2RP2001245//ESTs//5.2e-90:447:97//Hs.14559:H92996  
R-NT2RP2001268//Homo sapiens mRNA for KIAA0810 protein, partial cds//1.5e-112:544:97//Hs.7531:AB018353  
R-NT2RP2001277//ESTs//2.0e-81:387:99//Hs.13751:AA908229  
R-NT2RP2001290//ESTs//2.4e-91:501:92//Hs.12600:AA044775  
R-NT2RP2001295//ESTs//1.4e-70:337:99//Hs.123854:AA412665  
45 R-NT2RP2001312//ESTs//4.6e-53:276:95//Hs.7961:AA401205  
R-NT2RP2001327//ESTs, Moderately similar to tumor necrosis factor-alpha-induced protein B12 [H.sapiens]//  
2.3e-43:238:93//Hs.106632:N25679  
R-NT2RP2001328//ESTs//5.1e-99:499:96//Hs.34868:AI341138  
R-NT2RP2001347//ESTs//6.7e-05:100:77//Hs.9536:AA114178  
50 R-NT2RP2001378//ESTs//4.2e-83:456:93//Hs.10554:N50028  
R-NT2RP2001381//ESTs//1.1e-26:148:96//Hs.161859:AA444038  
R-NT2RP2001392//ESTs, Weakly similar to MITOCHONDRIAL LON PROTEASE HOMOLOG PRECURSOR [H.  
sapiens]//3.9e-74:411:93//Hs.47305:AA195153  
R-NT2RP2001394//ESTs//9.5e-54:305:93//Hs.70256:R07875  
55 R-NT2RP2001397//ESTs, Highly similar to G2/MITOTIC-SPECIFIC CYCLIN B2 [Mesocricetus auratus]//5.2e-97:  
469:97//Hs.20483:AA522505  
R-NT2RP2001420//ESTs//1.6e-49:228:88//Hs.163602:N32030  
R-NT2RP2001423//ESTs//2.0e-37:190:99//Hs.101565:R35431

R-NT2RP2001427//EST//1.7e-1 1:107:84//Hs.148584:AI201728  
R-NT2RP2001436//ESTs, Weakly similar to F02D8.3 [C.elegans]//2.9e-114:558:97//Hs.7627:AI341556  
R-NT2RP2001440//EST//0.17:192:58//Hs.133442:AI061394  
R-NT2RP2001445//ESTs//1.1e-43:215:100//Hs.145497:AA501453  
5 R-NT2RP2001449//ESTs//4.1e-08:234:61//Hs.134067:AI076765  
R-NT2RP2001450//ESTs//9.5e-65:356:94//Hs.61829:AI079539  
R-NT2RP2001467//Small inducible cytokine A5 (RANTES)//1.2e-34:255:83//Hs.155464:AF088219  
R-NT2RP2001506//ESTs//2.9e-23:170:88//Hs.7147:T23513  
R-NT2RP2001511//ESTs//2.0e-08:59:100//Hs.57660:AA251146  
10 R-NT2RP2001520//Homo sapiens mRNA for mitochondrial carrier protein ARALAR1//6.7e-106:545:95//Hs.4277:Y14494  
R-NT2RP2001526//ESTs//3.7e-23:295:72//Hs.8514:AF039240  
R-NT2RP2001536//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds//1.9e-15:99:95//Hs.99742:AF035586  
15 R-NT2RP2001560//ESTs//2.2e-58:310:94//Hs.87454:AA732816  
R-NT2RP2001569//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//2.0e-76:387:96//Hs.67619:AB007957  
R-NT2RP2001576//Human mRNA for KIAA0105 gene, complete cds//0.17:193:60//Hs.119:D14661  
R-NT2RP2001581//ESTs//5.1e-08:107:78//Hs.157114:T58884  
20 R-NT2RP2001597//EST//5.2e-22:151:88//Hs.158613:AI369995  
R-NT2RP2001601//ESTs//1.5e-78:373:99//Hs.137558:AI393767  
R-NT2RP2001613  
R-NT2RP2001628//EST//0.99:195:60//Hs.144238:W52294  
R-NT2RP2001663//ESTs//4.0e-37:282:84//Hs.12319:W56090  
25 R-NT2RP2001677//ESTs//1.4e-44:232:96//Hs.159387:AI370845  
R-NT2RP2001678//ESTs//0.91:124:60//Hs.10593:AI201336  
R-NT2RP2001699//EST//0.0033:230:61//Hs.146544:AI125323  
R-NT2RP2001720//ESTs//1.8e-52:255:99//Hs.101064:AA290579  
R-NT2RP2001721//ESTs//7.0e-101:479:99//Hs.129750:AA987538  
30 R-NT2RP2001740//ESTs//3.3e-76:379:96//Hs.144704:AI147100  
R-NT2RP2001748//ESTs//1.4e-44:352:81//Hs.142259:AA828840  
R-NT2RP2001762//Homo sapiens exonuclease 1a (EXO1a) mRNA, complete cds//2.1e-105:519:96//Hs.47504:AF091754  
R-NT2RP2001813//ESTs//6.3e-78:406:95//Hs.21902:R44037  
35 R-NT2RP2001861  
R-NT2RP2001869//EST//2.8e-21:173:82//Hs.130321:AI002941  
R-NT2RP2001876//ESTs//6.1e-102:526:95//Hs.4944:AA533088  
R-NT2RP2001883//ESTs, Weakly similar to No definition line found [C.elegans]//6.9e-110:556:95//Hs.23159:AA113849  
40 R-NT2RP2001900//ESTs//6.9e-85:442:95//Hs.154220:AA171724  
R-NT2RP2001907//ESTs//2.1e-82:432:94//Hs.142257:AA188423  
R-NT2RP2001926//EST//2.3e-24:299:71//Hs.135085:AI097268  
R-NT2RP2001936//ESTs//1.1e-45:265:92//Hs.112482:T66087  
R-NT2RP2001943//EST//1.4e-05:246:61//Hs.144096:AI032180  
45 R-NT2RP2001946//ESTs//3.6e-87:410:99//Hs.20242:W72594  
R-NT2RP2001947//ESTs//1.9e-55:338:88//Hs.58582:T72588  
R-NT2RP2001969  
R-NT2RP2001976//ESTs//1.2e-98:499:95//Hs.121028:AA902745  
R-NT2RP2001985//ESTs, Weakly similar to GTPASE-ACTIVATING PROTEIN SPA-1 [M.musculus]//8.3e-15:118:  
50 89//Hs.18760:AA166678  
R-NT2RP2002025//ESTs//2.1e-82:393:98//Hs.159488:AI378233  
R-NT2RP2002032//ESTs//4.4e-98:531:91//Hs.93836:AA813332  
R-NT2RP2002033//ESTs//3.5e-43:229:96//Hs.30563:AA102627  
R-NT2RP2002041  
55 R-NT2RP2002046//ESTs//1.6e-101:476:99//Hs.101107:AA825938  
R-NT2RP2002047//ESTs//9.1e-85:431:95//Hs.116750:AA629895  
R-NT2RP2002058//ESTs//1.3e-31:163:99//Hs.33085:AA258068  
R-NT2RP2002066//ESTS//1.9e-87:459:93//Hs.118871:AA846091

R-NT2RP2002070//ESTs//4.1e-63:332:96//Hs.156446:T92265  
R-NT2RP2002076//Homo sapiens clone 24804 mRNA sequence//1.7e-26:178:87//Hs.11039:AF052183  
R-NT2RP2002079//ESTs//1.2e-79:389:97//Hs.135214:AI350524  
R-NT2RP2002099//Homo sapiens mRNA for E1B-55kDa-associated protein//1.5e-60:376:89//Hs.155218:  
5 AJ007509  
R-NT2RP2002105//ESTs//8.4e-54:313:90//Hs.98702:AI123000  
R-NT2RP2002124//ESTs//6.6e-81:431:93//Hs.127326:AA525134  
R-NT2RP2002137//Deoxycytidine kinase//0.29:183:62//Hs.709:M60527  
R-NT2RP2002154//ESTs//9.6e-97:539:91//Hs.18624:AA523268  
10 R-NT2RP2002172//EST//0.69:53:75//Hs.156238:AI334495  
R-NT2RP2002185//ESTs, Weakly similar to F15C11.2 [C.elegans]//1.4e-54:269:98//Hs.107201:W52859  
R-NT2RP2002192//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.9e-  
15 15:245:71//Hs.87578:AI125363  
R-NT2RP2002193//ESTs//3.5e-79:45 3:90//Hs.76578:AI290672  
R-NT2RP2002208//ESTs//2.0e-72:347:99//Hs.164028:AI003946  
R-NT2RP2002219//EST//0.039:229:63//Hs.149830:AI287499  
R-NT2RP2002231//ESTs//3.3e-64:337:94//Hs.79828:AA642341  
R-nnnnnnnnnnnnn//ESTs, Highly similar to co-repressor protein [M.musculus]//5.4e-48:238:99//Hs.22583:  
20 AA188168  
R-NT2RP2002256//Homo sapiens retinoic acid hydroxylase mRNA, complete cds//1.6e-15:131:83//Hs.150595:  
AF005418  
R-NT2RP2002259//Human L-myc protein gene, complete cds//5.3e-99:548:91//Hs.92137:M19720  
R-NT2RP2002270//ESTs, Weakly similar to AF-9 PROTEIN [H.sapiens]//4.8e-100:550:91//Hs.4029:Z78373  
R-NT2RP2002292//ESTs, Weakly similar to F13B12.1 [C.elegans]//3.2e-92:482:93//Hs.5570:AI377863  
25 R-NT2RP2002312//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds//4.1e-103:527:94//  
Hs.24812:AF069532  
R-NT2RP2002316//ESTs//4.2e-91:425:100//Hs.3350:AI368015  
R-NT2RP2002325//Homo sapiens peroxisomal biogenesis factor (PEX11a) mRNA, complete cds//1.2e-112:567:  
95//Hs.31034:AB015594  
30 R-NT2RP2002333//ESTs//1.9e-86:483:91//Hs.155198:AA767372  
R-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant mRNA, complete cds//1.2e-103:600:  
89//Hs.109051:AF038958  
R-NT2RP2002394//ESTS//0.11:158:65//Hs.28792:AI343467  
R-NT2RP2002408//ESTs//1.5e-51:278:93//Hs.6044:W22815  
35 R-NT2RP2002426//Homo sapiens mRNA for KIAA0563 protein, complete cds//1.7e-33:285:80//Hs.15731:  
AB011135  
R-NT2RP2002439//ESTS//3.2e-12:134:76//Hs.32246:AA464020  
R-NT2RP2002457//ESTs//4.7e-52:282:94//Hs.21968:H97521  
R-NT2RP2002464//ESTs//5.3e-27:148:98//Hs.115660:AI362230  
40 R-NT2RP2002475//ESTs//3.9e-85:439:94//Hs.9873:W27233  
R-nnnnnnnnnnnnn//Homo sapiens mRNA for ABC transporter 7 protein, complete cds//9.9e-115:605:92//Hs.  
125856:AB005289  
R-NT2RP2002498//ESTs//6.3e-37:227:93//Hs.108779:N73180  
R-NT2RP2002503//ESTs//1.9e-54:358:86//Hs.57800:W60838  
45 R-NT2RP2002504//Homo sapiens mRNA for KIAA0791 protein, complete cds//8.5e-107:583:91//Hs.23255:  
AB018334  
R-NT2RP2002520//ESTs//4.2e-99:509:94//Hs.32368:AA205305  
R-NT2RP2002537//ESTs//4.2e-105:552:93//Hs.154363:AA533090  
50 R-NT2RP2002546//Homo sapiens clone TUA8 Cri-du-chat region mRNA//2.6e-109:570:93//Hs.49476:AF009314  
R-NT2RP2002549//DNA polymerase gamma//1.1e-35:189:86//Hs.80961:U60325  
R-NT2RP2002591//ESTs, Weakly similar to ZINC FINGER PROTEIN 84 [H.sapiens]//7.5e-118:564:97//Hs.94549:  
AA149547  
R-NT2RP2002595//EST//1.4e-15:101:95//Hs.129528:AA994783  
R-NT2RP2002606//ESTs//4.5e-99:475:98//Hs.45046:N40170  
55 R-NT2RP2002609//ESTs//1.9e-104:568:92//Hs.9175:AI184220  
R-NT2RP2002618//ESTs//0.014:493:57//Hs.96322:AA541615  
R-NT2RP2002621//EST//4.4e-36:252:84//Hs.149580:AI281881  
R-NT2RP2002643//ESTs//6.9e-32:247:74//Hs.33354:AA179944

R-NT2RP2002672  
R-NT2RP2002701//N-acetylglucosaminidase, alpha- (Sanfilippo disease IIIB//0.99:184:63//Hs.50727:U43572  
R-NT2RP2002706//EST//2.8e-41:148:86//Hs.161917:AA483223  
R-NT2RP2002710//EST//0.34:105:71//Hs.136747:AA749210  
5 R-NT2RP2002727//ESTs//8.7e-68:368:94//Hs.14366:T78626  
R-NT2RP2002736//ESTs//9.7e-98:457:99//Hs.74899:AA993300  
R-NT2RP2002740//Homo sapiens mRNA for KIAA0536 protein, partial cds//0.66:360:59//Hs.119139:AB011108  
R-NT2RP2002741//ESTs//3.1e-102:489:98//Hs.112024:AI042352  
R-NT2RP2002750//EST//3.6e-43:166:86//Hs.162404:AA573131  
10 R-NT2RP2002752//ESTs//5.0e-56:355:89//Hs.95867:M62042  
R-NT2RP2002753//ESTs//1.7e-49:262:96//Hs.49005:W89124  
R-NT2RP2002769//ESTs//1.3e-59:376:88//Hs.4046:H03587  
R-NT2RP2002778//Homo sapiens clone 24606 mRNA sequence//4.0e-65:341:94//Hs.17481:AF070537  
R-NT2RP2002800//ESTs//6.5e-08:79:84//Hs.153262:AA551124  
15 R-NT2RP2002839//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.6e-100:501:97//Hs.136202:AA206578  
R-NT2RP2002857//ESTs//4.3e-94:463:97//Hs.134292:AA603031  
R-NT2RP2002862//ESTs//2.3e-42:302:82//Hs.117969:H94870  
R-NT2RP2002880  
20 R-NT2RP2002891  
R-NT2RP2002925//ESTs//1.3e-103:564:92//Hs.142079:AA182894  
R-NT2RP2002928//ESTs//3.9e-108:502:99//Hs.29105:AA574143  
R-NT2RP2002929//ESTs//4.1e-106:499:99//Hs.44743:AA837096  
R-NT2RP2002954//ESTs//2.6e-88:417:99//Hs.100824:AI308771  
25 R-NT2RP2002959//ESTs//7.5e-101:489:97//Hs.32690:N57480  
R-NT2RP2002979//ESTs//5.4e-06:197:65//Hs.146726:AI147060  
R-NT2RP2002980//ESTs//1.0e-110:562:96//Hs.28444:AA083213  
R-NT2RP2002986//ESTs, Highly similar to RING CANAL PROTEIN [Drosophila melanogaster]//3.1e-119:578:97//Hs.106290:AI125291  
30 R-NT2RP2002987//Human mRNA for KIAA0331 gene, complete cds//1.0:78:74//Hs.146395:AB002329  
R-NT2RP2002993//ESTS, Weakly similar to DNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE [H. sapiens]//2.4e-98:467:98//Hs.86337:AA149311  
R-NT2RP2003000//ESTs//0.0070:400:61//Hs.138506:U85642  
R-NT2RP2003034//ESTs//9.3e-87:408:96//Hs.164042:H12594  
35 R-NT2RP2003073//Human transporter protein (g17) mRNA, complete cds//0.95:259:61//Hs.76460:U49082  
R-NT2RP2003099//Thromboxane A2 receptor//2.6e-42:328:81//Hs.89887:D38081  
R-NT2RP2003108//ESTs//2.3e-82:398:98//Hs.5105:AA115512  
R-NT2RP2003117//Human mRNA for KIAA0347 gene, complete cds//2.4e-49:336:86//Hs.101996:AB002345  
R-NT2RP2003121//ESTs//2.0e-75:380:96//Hs.133127:AA133355  
40 R-NT2RP2003125  
R-NT2RP2003129//EST//0.68:115:69//Hs.122196:AA780986  
R-NT2RP2003137//ESTs//2.1e-37:259:85//Hs.63169:N78506  
R-NT2RP2003161//ESTs//2.5e-88:451:96//Hs.29041:W37379  
R-NT2RP2003164//ESTs//4.3e-113:543:97//Hs.8980:AA629067  
45 R-NT2RP2003165//ESTs//6.9e-83:486:89//Hs.138632:H97952  
R-NT2RP2003177//ESTs//0.47:38:100//Hs.61790:AA421156  
R-NT2RP2003194//ESTs//4.7e-118:582:96//Hs.27266:AA053816  
R-NT2RP2003206//ESTs//0.032:388:58//Hs.122148:AA442074  
R-NT2RP2003230//ESTs//8.8e-103:478:99//Hs.40140:AI079253  
50 R-NT2RP2003237//ESTs//2.7e-76:392:96//Hs.106278:R37661  
R-NT2RP2003243//ESTs//3.6e-53:300:92//Rs.18793:AA192438  
R-NT2RP2003265//ESTs, Highly similar to protein NGD5 [M.musculus]//3.3e-110:557:96//Hs.24994:AA236937  
R-NT2RP2003272//ESTs, Weakly similar to F15C11.2 [C.elegans]//1.2e-34:228:89//Hs.107201:W52859  
R-NT2RP2003277//Homo sapiens mRNA for KIAA0625 protein, partial cds//1.4e-111:565:95//Hs.154919:  
55 AB014525  
R-NT2RP2003280//ESTs//2.6e-101:541:94//Hs.6982:AA622427  
R-NT2RP2003286//ESTs//1.2e-104:497:98//Hs.113052:AI222106  
R-NT2RP2003293//Human mRNA for KIAA0118 gene, partial cds//9.1e-44:458:74//Hs.154326:D42087

R-NT2RP2003295//Protein serine/threonine kinase stk2//0.31:321:57//Hs.1087:L20321  
 R-NT2RP2003297//ESTs//3.0e-15:118:87//Hs.16621:AA098874  
 R-NT2RP2003308//ESTs, Moderately similar to CROOKED NECK PROTEIN [Drosophila melanogaster]//4.8e-109:553:96//Hs.26089:AA195126  
 5 R-NT2RP2003329//ESTs//0.99:208:62//Hs.143607:AI424948  
 R-NT2RP2003339//ESTs//1.3e-85:441:96//Rs.24115:N32618  
 R-NT2RP2003347//ESTs//1.5e-70:365:96//Hs.155773:AI312825  
 R-NT2RP2003367//EST//5.8e-80:376:100//Hs.112500:AA599014  
 R-NT2RP2003391//ESTs//2.8e-98:484:97//Hs.5842:AA534476  
 10 R-NT2RP2003393//ESTs//2.0e-96:510:93//Hs.75844:AA115502  
 R-NT2RP2003394//EST//5.2e-06:264:63//Hs.144234:W52249  
 R-NT2RP2003401//ESTs//6.1e-25:161:90//Hs.155360:AA984683  
 R-NT2RP2003433//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]//1.2e-106:508:98//Hs.131840:AI016073  
 15 R-NT2RP2003445//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//5.6e-21:161:70//Hs.43153:N22360  
 R-NT2RP2003446//ESTs, Weakly similar to C27H6.4 [C.elegans]//6.0e-105:529:96//Hs.8055:W60903  
 R-NT2RP2003456//ESTs//7.5e-96:449:99//Hs.25362:AI277332  
 R-NT2RP2003480//ESTs//1.6e-116:583:96//Hs.59757:AA176121  
 20 R-NT2RP2003499//ESTs, Weakly similar to elastin like protein [D.melanogaster]//7.0e-71:365:95//Hs.101056:R52777  
 R-NT2RP2003506//ESTs, Weakly similar to ORF YPL207w [S.cerevisiae]//2.3e-115:577:96//Hs.16277:N36831  
 R-NT2RP2003511//ESTs//1.6e-22:182:85//Hs.28249:AA203733  
 R-NT2RP2003513//Human mRNA for KIAA0270 gene, partial cds//1.3e-108:566:94//Hs.78482:Y16270  
 25 R-NT2RP2003517//Platelet-derived growth factor beta polypeptide (simian sarcoma viral (v-sis) oncogene homolog)//4.9e-62:518:79//Hs.1976:M12783  
 R-NT2RP2003522//ESTs//2.0e-97:462:99//Hs.24512:D60170  
 R-NT2RP2003533//ESTs//4.4e-45:273:78//Hs.140225:AA704101  
 R-NT2RP2003543//EST//1.0:80:68//Hs.65646:F13684  
 30 R-NT2RP2003559//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.8e-58:316:94//Hs.28891:W72439  
 R-NT2RP2003564//ESTs//3.2e-112:528:99//Hs.53940:N46696  
 R-NT2RP2003581//ESTs//1.3e-88:506:93//Hs.16157:AA203719  
 R-NT2RP2003596//ESTs, Weakly similar to No definition line found [C.elegans]//4.7e-101:495:98//Hs.34627:  
 35 AA126463  
 R-NT2RP2003604//Homo sapiens alpha-catenin related protein (ACRP) mRNA, complete cds//1.7e-103:501:97//Hs.58488:U97067  
 R-NT2RP2003629//EST//0.032:440:59//Hs.135297:AI038981  
 R-NT2RP2003643//ESTs, Weakly similar to HYPOTHETICAL 14.1 KD PROTEIN IN MURZ-RPON INTERGENIC  
 40 REGION [E.coli]//9.1e-62:359:92//Hs.12492:AA203188  
 R-NT2RP2003668//EST//9.4e-110:535:97//Hs.116279:AA628951  
 R-NT2RP2003687//EST//5.9e-05:196:65//Hs.139064:AA135523  
 R-NT2RP2003691//ESTs, Weakly similar to F59C6.9 [C.elegans]//1.0:202:62//Hs.65539:AI148540  
 R-NT2RP2003702//ESTs, Moderately similar to ovarian-specific protein [R.norvegicus]//4.3e-99:492:96//Hs.  
 45 9332:AA811920  
 R-NT2RP2003704//ESTs//1.0:155:63//Hs.104166:AA740246  
 R-NT2RP2003706//Homo sapiens mRNA for KIAA0525 protein, partial cds//8.4e-47:265:93//Hs.78494:AB011097  
 R-NT2RP2003713//EST//0.81:210:59//Hs.14551:T79401  
 R-NT2RP2003714//ESTs//1.7e-99:495:96//Hs.158101:AI365003  
 50 R-nnnnnnnnnnnnnn//Human 19.8 kDa protein mRNA, complete cds//0.84:221:60//Hs.2384:U18914  
 R-NT2RP2003737//ESTs, Highly similar to UBIQUITIN-CONJUGATING ENZYME E2-17 KD [Caenorhabditis el-  
 egans]//2.4e-50:302:90//Hs.19196:W74577  
 R-NT2RP2003751  
 R-NT2RP2003760//ESTs//2.6e-101:548:93//Hs.115987:AA483808  
 55 R-NT2RP2003764//ESTs//8.2e-25:134:98//Hs.64036:AA127709  
 R-NT2RP2003769//ESTs//1.7e-108:545:95//Hs.56847:AA541606  
 R-NT2RP2003770//Homo sapiens sperm acrosomal protein mRNA, complete cds//6.0e-106:531:96//Hs.90436:  
 AF047437

R-NT2RP2003777//ESTs//2.6e-59:323:94//Hs.10101:AI381811  
R-NT2RP2003781//ESTs//2.0e-25:269:75//Hs.144951:N34836  
R-NT2RP2003793//ESTs//8.7e-94:466:97//Hs.93949:AA782955  
R-NT2RP2003840//ESTs//3.4e-97:533:93//Hs.16130:AA195077  
5 R-NT2RP2003857//H.sapiens mRNA for G9a//2.8e-23:351:65//Hs.75196:X69838  
R-NT2RP2003859//ESTs//3.0e-07:96:81//Hs.153262:AA551124  
R-NT2RP2003871//ESTs//1.9e-102:509:97//Hs.25726:AA430167  
R-NT2RP2003885//ESTs//1.0e-102:502:97//Hs.36353:AA702341  
R-NT2RP2003912//EST//1.2e-38:336:76//Hs.134975:AI094611  
10 R-NT2RP2003952//Homo sapiens DNA-binding protein (CROC-1B) mRNA, complete cds//0.90:190:60//Hs.75875:U49278  
R-NT2RP2003968//Homo sapiens hUBP mRNA for ubiquitin specific protease, complete cds//7.6e-116:568:97//Hs.35086:AB014458  
R-NT2RP2003976//Homo sapiens mRNA for KIAA0447 protein, complete cds//3.6e-109:540:97//Hs.7302:AB007916  
15 R-NT2RP2003981//Homo sapiens mRNA for KIAA0804 protein, partial cds//2.5e-115:568:96//Hs.7316:AB018347  
R-NT2RP2003984  
R-NT2RP2003986//ESTs//4.9e-36:272:82//Hs.158268:AA738087  
R-NT2RP2003988//ESTs, Weakly similar to reverse transcriptase [H.sapiens]//3.2e-110:519:99//Hs.36093:  
20 AI149968  
R-NT2RP2004014//ESTs//8.4e-102:483:99//Hs.22867:AI417478  
R-NT2RP2004041  
R-NT2RP2004042//ESTs//1.5e-105:466:97//Hs.7296:N29706  
25 R-nnnnnnnnnnnn//ESTs//1.4e-110:559:96//Hs.71916:AA219699  
R-NT2RP2004081//ESTs//3.7e-105:503:98//Hs.27542:AA977204  
R-NT2RP2004098//EST//7.3e-26:203:87//Hs.21897:R41461  
R-NT2RP2004124//ESTs//1.1e-83:435:95//Hs.43299:N23036  
R-NT2RP2004142//EST//1.3e-06:165:65//Hs.146742:AI147500  
30 R-NT2RP2004152//ESTs//7.0e-98:455:100//Hs.17731:AI342241  
R-NT2RP2004165//ESTs, Highly similar to DYNEIN BETA CHAIN, CILIARY [Anthocidaris crassispina]//1.0e-118:  
583:97//Hs.16520:AI224533  
R-NT2RP2004170//ESTs//6.7e-66:407:88//Hs.157138:AI348544  
R-NT2RP2004172//ESTs//1.5e-109:567:95//Hs.159091:AA033974  
35 R-NT2RP2004187//ESTs//3.6e-92:488:93//Hs.22954:W26589  
R-NT2RP2004194//ESTs//6.2e-114:585:95//Hs.18778:AA203167  
R-NT2RP2004196  
R-NT2RP2004207//ESTs//6.3e-102:488:98//Hs.22678:AA604756  
R-NT2RP2004226//ESTs//8.8e-18:252:71//Hs.11924:W26972  
40 R-NT2RP2004232//ESTs, Highly similar to protein kinase C mu [H.sapiens]//5.2e-105:499:98//Hs.143460:  
AA483305  
R-NT2RP2004239//ESTs//1.2e-16:171:80//Hs.16134:AA203116  
R-NT2RP2004240//Homo sapiens antigen NY-CO-1 (NY-CO-1) mRNA, complete cds//3.4e-103:530:93//Hs.  
54900:AF039687  
45 R-NT2RP2004242//ESTs//1.3e-85:460:93//Hs.104535:AA211483  
R-NT2RP2004245//ESTs//6.4e-117:575:97//Hs.23744:AA035744  
R-NT2RP2004270//ESTs//1.0:95:69//Hs.141371:H92187  
R-NT2RP2004300//ESTs//4.4e-80:379:99//Hs.130874:AA905056  
50 R-NT2RP2004316//Homo sapiens EXT-like protein 2 (EXTL2) mRNA, complete cds//4.7e-110:544:96//Hs.61152:  
AF000416  
R-NT2RP2004321//ESTs//2.1e-18:104:99//Hs.107207:AA044788  
R-NT2RP2004339//EST//1.4e-47:309:86//Hs.161917:AA483223  
R-NT2RP2004347  
55 R-NT2RP2004364//ESTs//1.1e-113:566:96//Hs.25880:AI268173  
R-NT2RP2004365//ESTs//0.022:271:62//Hs.38897:AI129310  
R-NT2RP2004366//ESTs//9.5e-71:335:100//Hs.91867:AI218624  
R-NT2RP2004373//ESTs//4.2e-25:172:87//Hs.83243:N32192  
R-NT2RP2004389//ESTs, Highly similar to HYPOTHETICAL 70.7 KD PROTEIN F09G8.3 IN CHROMOSOME III  
[Caenorhabditis elegans]//1.4e-11:108:82//Hs.30490:AA146916

R-NT2RP2004392//ESTs//3.4e-81:427:94//Hs.5827:AA581646  
 R-NT2RP2004396//EST//5.6e-06:100:77//Hs.138623:H92473  
 R-NT2RP2004399//EST//0.98:337:59//Hs.118446:N67900  
 R-NT2RP2004400//ESTs//2.1e-90:422:100//Hs.152460:AA602921  
 5 R-NT2RP2004412//ESTs//1.4e-105:503:98//Hs.15929:AA403121  
 R-NT2RP2004425//EST//0.00017:225:60//Hs.146935:AI168124  
 R-NT2RP2004476//ESTs//1.4e-88:477:94//Hs.4859:N29695  
 R-NT2RP2004490//Homo sapiens 3-phosphoinositide dependent protein kinase-1 (PDK1) mRNA, complete cds//  
 8.6e-34:143:98//Hs.154729:AF017995  
 10 R-NT2RP2004512//ESTs//2.6e-91:426:100//Hs.94133:AI270700  
 R-NT2RP2004523//ESTs//1.6e-74:377:97//Hs.14217:R61320  
 R-NT2RP2004538//Thromboxane A2 receptor//1.4e-45:279:89//Hs.89887:D38081  
 R-NT2RP2004551//ESTs//0.47:147:66//Hs.131519:AI024347  
 15 R-NT2RP2004568//ESTs//1.3e-107:567:94//Hs.65234:AA195470  
 R-NT2RP2004580//ESTs//5.9e-29:156:98//Hs.147801:AI221661  
 R-NT2RP2004587//ESTs//1.0e-102:495:97//Hs.91662:AA781126  
 R-NT2RP2004594//ESTs//4.1e-56:298:95//Hs.24641:AA954666  
 R-NT2RP2004600//ESTs//4.8e-67:374:93//Hs.49762:N69862  
 R-NT2RP2004602//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//4.5e-07:  
 20 149:76//Hs.12845:N28835  
 R-NT2RP2004614//ESTs//1.0e-111:557:96//Hs.37892:N53497  
 R-NT2RP2004655//Homo sapiens mRNA for leucine rich protein//2.4e-118:587:96//Hs.5198:AJ006291  
 R-NT2RP2004664//Homo sapiens mRNA for KIAA0460 protein, partial cds//5.9e-107:520:96//Hs.29956:  
 AB007929  
 25 R-NT2RP2004675//ESTs//2.7e-82:407:97//Hs.116113:F18930  
 R-NT2RP2004681//NUCLEOLIN//0.34:387:58//Hs.79110:M60858  
 R-NT2RP2004689//Homo sapiens mRNA for KIAA0625 protein, partial cds//5.0e-120:600:96//Hs.154919:  
 AB014525  
 R-NT2RP2004709//ESTs//1.1e-106:511:98//Hs.38034:AI149793  
 30 R-NT2RP2004710//ESTs//9.9e-87:477:93//Hs.6834:AA203433  
 R-NT2RP2004736//Homo sapiens mRNA for KIAA0478 protein, complete cds//1.3e-118:594:96//Hs.4236:  
 AB007947  
 R-NT2RP2004743//ESTs//2.1e-48:327:88//Hs.43635:AA447015  
 R-NT2RP2004767//EST//4.0e-57:328:81//Hs.142796:N51423  
 35 R-NT2RP2004775//ESTs//9.4e-60:326:94//Hs.115339:AA136774  
 R-NT2RP2004791//ESTs//3.2e-82:367:96//Hs.141911:N64013  
 R-NT2RP2004799//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds//  
 8.0e-116:564:96//Hs.40820:AF058953  
 R-NT2RP2004802//ESTs//6.5e-111:586:94//Hs.90375:W74579  
 40 R-NT2RP2004816//Homo sapiens H beta 58 homolog mRNA, complete cds//8.7e-120:584:97//Hs.67052:  
 AF054179  
 R-NT2RP2004841//EST//3.8e-31:323:74//Hs.147714:AI219906  
 R-NT2RP2004861//EST//0.92:147:63//Hs.23064:R20803  
 R-NT2RP2004897//ESTs//1.7e-46:390:80//Hs.139225:H96567  
 45 R-NT2RP2004936//EST//0.97:176:63//Hs.137436:AA280529  
 R-nnnnnnnnnnnn//ESTs//0.059:137:64//Hs.144109:AI345543  
 R-NT2RP2004961//ESTs//1.8e-87:409:100//Hs.138297:AA781941  
 R-NT2RP2004962//ESTs//0.0021:292:59//Hs.145917:AI275458  
 R-NT2RP2004967//Human mRNA for KIAA0118 gene, partial cds//7.4e-51:506:75//Hs.154326:D42087  
 50 R-NT2RP2004978//ESTs//0.95:138:63//Hs.13619:W93496  
 R-NT2RP2004982//ESTs//7.8e-95:468:97//Hs.22545:R43910  
 R-NT2RP2004985  
 R-NT2RP2004999//ESTs//2.9e-94:450:98//Hs.128766:AI419902  
 R-NT2RP2005000  
 55 R-NT2RP2005001//Homo sapiens mRNA for KIAA0615 protein, complete cds//9.6e-113:577:95//Hs.155972:  
 AB014515  
 R-NT2RP2005003//EST//1.3e-75:387:96//Hs.140843:R42235  
 R-nnnnnnnnnnnn//Homo sapiens SEC63 (SEC63) mRNA, complete cds//3.1e-116:568:97//Hs.31575:AF100141

R-NT2RP2005018//ESTs//7.5e-46:280:90//Hs.126857:AA932161  
 R-NT2RP2005020//ESTs//1.6e-105:554:94//Hs.14846:AA148507  
 R-NT2RP2005031//EST//3.1e-79:379:99//Hs.139709:AA227887  
 R-NT2RP2005037//ESTs//5.3e-102:551:93//Hs.26516:AA195220  
 5 R-NT2RP2005038//ESTs//5.8e-101:566:92//Hs.46964:N49757  
 R-NT2RP2005108  
 R-NT2RP2005116//Homo sapiens mRNA for KIAA0664 protein, partial cds//2.7e-105:518:97//Hs.22616:  
 AB014564  
 R-NT2RP2005126//H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein)//4.6e-69:464:85//Hs.  
 10 100555:X98743  
 R-NT2RP2005139//ESTs//1.0e-108:545:95//Hs.21006:AA523383  
 R-NT2RP2005140//ESTs//4.3e-90:422:99//Hs.62180AI341261  
 R-NT2RP2005144//ESTs//0.91:162:62//Hs.52399:AI075744  
 R-NT2RP2005147//ESTs//4.6e-100:502:96//Hs.27931:AA633438  
 15 R-NT2RP2005159//ESTs//7.5e-105:533:95//Hs.109819:AI357582  
 R-NT2RP2005162//ESTs//6.6e-83:419:96//Hs.113998:H50648  
 R-NT2RP2005168//Homo sapiens mRNA for EIB-55kDa-associated protein//2.4e-101:513:95//Hs.155218:  
 AJ007509  
 R-NT2RP2005204//ESTs, Weakly similar to UBIQUITIN-ACTIVATING ENZYME E1 HOMOLOG [H.sapiens]//1.9e-  
 20 115:577:96//Hs.7600:H98166  
 R-NT2RP2005227//Homo sapiens UM protein mRNA, complete cds//1.0e-45:359:82//Hs.154103:AF061258  
 R-NT2RP2005239//ESTs, Highly similar to NIFS-LIKE 54.5 KD PROTEIN [Saccharomyces cerevisiae]//1.0e-47:  
 245:97//Hs.21090:AA418587  
 R-NT2RP2005254//ESTs//3.3e-111:581:94//Hs.22549:AA524503  
 25 R-NT2RP2005270//ESTs, Highly similar to HYPOTHETICAL 67.6 KD PROTEIN ZK637.3 IN CHROMOSOME III  
 [Caenorhabditis elegans]//1.1e-79:412:95//Hs.23047:N66596  
 R-NT2RP2005276//ESTs//4.6e-85:426:96//Hs.24550:AA316272  
 R-NT2RP2005287//ESTs//1.7e-109:565:94//Hs.61976:AI279001  
 R-NT2RP2005288//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds//2.4e-125:594:98//  
 30 Hs.27007:AF060219  
 R-NT2RP2005289//Homo sapiens mRNA for XPR2 protein//4.9e-112:545:96//Hs.44766:AJ007590  
 R-NT2RP2005293//ESTs//5.1e-116:538:99//Hs.62180:AI341261  
 R-NT2RP2005315//ESTs//1.4e-82:415:97//Hs.155829:AA018338  
 R-NT2RP2005325//Human LIM-homeobox domain protein (hLH-2) mRNA, complete cds//2.5e-45:272:91//Hs.  
 35 1569:U11701  
 R-NT2RP2005336//ESTs//1.9e-93:444:99//Hs.110966:AA151699  
 R-NT2RP2005344//Homo sapiens GDP-L-fucose pyrophosphorylase (GFPP) mRNA, complete cds//0.011:463:  
 58//Hs.150926:AF017445  
 R-NT2RP2005354//ESTs//7.2e-22:148:91//Hs.153783:H14544  
 40 R-NT2RP2005360//ESTs//0.048:225:60//Hs.7602:AA099247  
 R-NT2RP2005393//Homo sapiens mRNA for KIAA0761 protein, partial cds//2.9e-41:248:82//Hs.93121:AB018304  
 R-NT2RP2005407//ESTs, Weakly similar to OSH1 PROTEIN [Saccharomyces cerevisiae]//2.5e-75:461:88//Hs.  
 70849:AA121697  
 R-NT2RP2005436//ESTs, Weakly similar to HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II  
 45 [C.elegans]//8.1e-96:491:95//Hs.7194:AI185631  
 R-NT2RP2005441//ESTs//1.1e-110:548:96//Hs.5209:AA780068  
 R-NT2RP2005453//ESTs//0.94:352:58//Hs.25870:H14423  
 R-NT2RP2005457//ESTs//2.1e-46:236:97//Hs.19522:AA975096  
 R-NT2RP2005464//ESTS//1.8e-72:349:99//Hs.44045:N51307  
 50 R-NT2RP2005465//ESTs//0.0058:322:58//Hs.127009:AI378936  
 R-NT2RP2005472//ESTs//0.47:309:60//Hs.144838:AI222019  
 R-NT2RP2005476//ESTS//5.1 e-40:205:9811Hs.101577:AI168526  
 R-NT2RP2005490//ESTs//L3e-70:364:96//Hs.134382:AA083573  
 R-NT2RP2005491//EST//0.012:220:60//Hs.144448:AA812455  
 55 R-NT2RP2005495//ESTs//1.2e-86:501:91//Hs.99445:R93540  
 R-NT2RP2005496//ESTs//3.2e-34:263:81//Hs.70279:AA757426  
 R-NT2RP2005498//ESTS, Highly similar to PROTEIN PHOSPHATASE PP2A, 55 KD REGULATORY SUBUNIT,  
 NEURONAL ISOFORM [Oryctolagus cuniculus]//2.3e-45:284:88//Hs.85752:AI138993

R-NT2RP2005501//ESTs//2.5e-84:404:98//Hs.143812:AI141755  
R-NT2RP2005509//ESTs, Highly similar to HYPOTHETICAL 37.2 KD PROTEIN C12C2.09C IN CHROMOSOME I [Schizosaccharomyces pombe]//8.2e-36:215:92//Hs.5298:AA725071  
R-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds//3.2e-110:  
5 570:9411Hs.119023:AF092563  
R-NT2RP2005525//ESTs, Weakly similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//1.3e-84:  
433:95//Hs.36942:AA524535  
R-NT2RP2005531//EST//0.98:64:70//Hs.146573:AI139856  
R-NT2RP2005539//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//8.8e-108:560:94//Hs.159597:  
10 AJ012449  
R-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds//1.7e-115:583:96//Hs.62515:  
AB007963  
R-NT2RP2005549//EST//0.61:111:62//Hs.147482:AI215572  
R-NT2RP2005555//ESTs//6.6e-108:507:99//Hs.68613:AI357567  
15 R-NT2RP2005557//ESTs//3.1e-105:495:99//Hs.105985:AA885169  
R-NT2RP2005581//ESTs//1.7e-79:445:92//Hs.138152:H03240  
R-NT2RP2005600//ESTs//1.3e-38:192:100//Hs.48329:W92733  
R-NT2RP2005605//ESTs//7.6e-87:409:99//Hs.45005:AA975060  
R-NT2RP2005620//ESTs//2.9e-96:463:97//Hs.7407:AI376788  
20 R-NT2RP2005622//ESTs//1.8e-104:497:98//Hs.22595:AA394229  
R-NT2RP2005637//EST//2.5e-20:163:71//Hs.161164:AI418211  
R-NT2RP2005640//ESTs//5.0e-99:473:98//Hs.23467:AA708740  
R-NT2RP2005645//ESTs//9.5e-23:231:77//Hs.5534:AA195173  
R-NT2RP2005651//ESTS, Highly similar to XFIN PROTEIN [Xenopus laevis]//2.9e-103:525:96//Hs.70589:  
25 AA868470  
R-NT2RP2005654//Insulin-like growth factor binding protein 2//0.94:223:60//Hs.162:X16302  
R-NT2RP2005669//Homo sapiens nitrilase 1 (VIII) mRNA, complete cds//2.7e-14:87:100//Hs.146406:AF069987  
R-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds//5.8e-91:434:98//  
Hs.25664:AF089814  
30 R-NT2RP2005683//ESTs//1.5e-98:494:96//Hs.22595:AA394229  
R-NT2RP2005690//ESTs//4.8e-43:286:86//Hs.150727:AI292236  
R-NT2RP2005694//EST//3.1e-82:386:100//Hs.149391:AI273643  
R-NT2RP2005701//ESTs, Highly similar to BUTYROPHILIN PRECURSOR [Bos taurus]//2.8e-68:376:93//Hs.  
9095:AA532630  
35 R-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds//1.3e-105:503:98//Hs.61638:  
AB018342  
R-NT2RP2005719//ESTs, Weakly similar to GPI-anchored protein p137 precursor [H.sapiens]//5.4e-105:500:98//  
Hs.14298:AI417523  
R-NT2RP2005722//EST//6.5e-76:395:94//Hs.142150:AA223982  
40 R-NT2RP2005723//ESTs//1.5e-84:452:93//Hs.91753:R44455  
R-NT2RP2005726//ESTs//3.5e-64:500:82//Hs.100526:AI223153  
R-NT2RP2005741//ESTs//4.7e-60:333:93//Hs.107242:R40258  
R-NT2RP2005748//ESTs//3.4e-102:498:97//Hs.82660:N78064  
R-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds//4.3e-42:223:96//  
45 Hs.159651:AF068868  
R-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//1.2e-104:494:98//Hs.  
26285:AF082516  
R-NT2RP2005763//ESTs//1.1e-97:456:99//Hs.65412:AI362163  
R-NT2RP2005767//ESTs//8.0e-38:204:96//Hs.18460:AA193463  
50 R-NT2RP2005773//ESTs, Highly similar to PYRROLINE-5-CARBOXYLATE REDUCTASE [Homo sapiens]//5.4e-  
112:559:96//Hs.14214:AI189379  
R-NT2RP2005775//ESTs, Highly similar to NEUROLYSIN PRECURSOR [Sus scrofa]//3.0e-108:544:96//Hs.  
22151:AI214321  
R-NT2RP2005781//ESTs//1.7e-43:217:99//Hs.144391:AA365664  
55 R-NT2RP2005784//EST//0.0071:217:60//Hs.117332:AA699724  
R-NT2RP2005804//ESTs//8.8e-107:512:98//Hs.15496:W44398  
R-NT2RP2005812//ESTs//9.0e-76:359:99//Hs.113937:AI298746  
R-NT2RP2005815//ESTs//5.5e-76:363:99//Hs.136230:AA594981

R-NT2RP2005835//ESTs//1.5e-100:541:94//Hs.86813:N25122  
R-NT2RP2005841//ESTs//2.8e-105:556:92//Hs.69993:AA628403  
R-NT2RP2005853//EST//2.0e-13:219:70//Hs.134016:AI076062  
R-NT2RP2005857//ESTS//1.0e-115:576:96//Hs.30663:AI338462  
5 R-NT2RP2005859//ESTs//7.3e-116:571:97//Hs.85986:AA195105  
R-NT2RP2005868//EST//0.00023:320:61//Hs.149689:AI284133  
R-NT2RP2005890//ESTs//1.0e-96:466:98//Hs.122579:AA766315  
R-NT2RP2005901//ESTs//8.3e-116:548:98//Hs.66296:AI125268  
R-NT2RP2005908//ESTs, Weakly similar to weakly similar to gastrula zinc finger protein [C.elegans]//2.4e-73:397:  
10 94//Hs.16667:T92427  
R-NT2RP2005933//ESTs, Highly similar to nucleoporin p54 [R.norvegicus]//2.8e-114:560:97//Hs.9082:AA873170  
R-NT2RP2005942//ESTs//5.6e-117:582:96//Hs.146123:AI338419  
R-NT2RP2005980//ESTs//6.9e-101:478:98//Hs.43145:AA776988  
R-NT2RP2006023//Homo sapiens PYRIN (MEFV) mRNA, complete cds//8.5e-51:398:80//Hs.113283:AF018080  
15 R-NT2RP2006038//ESTs//0.025:284:59//Hs.97852:AA404347  
R-NT2RP2006043//ESTs, Weakly similar to HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II  
[C.elegans]//1.2e-50:278:94//Hs.7194:AI185631  
R-NT2RP2006052//ESTs//5.0e-52:272:95//Hs.99545:AA461492  
R-NT2RP2006069//ESTs//1.8e-90:495:93//Hs.43654:AA522714  
20 R-NT2RP2006071//ESTs//1.5e-38:218:94//Hs.107882:W72093  
R-NT2RP2006098//ESTs//2.9e-105:540:95//Hs.26860:N56918  
R-NT2RP2006100//Human organic anion transporting polypeptide (OATP) mRNA, complete cds//0.031:254:62//  
Hs.46440:U21943  
R-NT2RP2006103//ESTs//1.5e-86:416:98//Hs.152114:AA401365  
25 R-NT2RP2006141//ESTs//5.3e-88:432:98//Hs.77480:AA100522  
R-NT2RP2006166//Homo sapiens LIM protein mRNA, complete cds//2.8e-17:255:72//Hs.154103:AF061258  
R-NT2RP2006184//ESTs//8.4e-101:487:98//Hs.58009:W69435  
R-NT2RP2006186//Homo sapiens mRNA for KIAA0654 protein, partial cds//6.1e-110:553:95//Hs.109299:  
AB014554  
30 R-NT2RP2006196//Human clone 23960 mRNA sequence//0.0037:48:100//Hs.151293:U79276  
R-NT2RP2006200//ESTs//6.5e-77:398:96//Hs.163953:R01398  
R-NT2RP2006219//H.sapiens mRNA for DGCR6 protein//1.2e-94:532:90//Hs.153910:X96484  
R-NT2RP2006237//ESTs//1.2e-57:305:95//Hs.86149:AI341312  
R-NT2RP2006238//ESTs, Highly similar to rA8 [R.norvegicus]//1.5e-29:183:91//Hs.4048:AA404253  
35 R-NT2RP2006258//ESTs//3.2e-87:462:94//Hs.141556:N49928  
R-NT2RP2006261//ESTs//3.4e-57:3 26:92//Hs.22523:W02999  
R-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds//4.7e-96:481:97//Hs.3404:AF035262  
R-NT2RP2006320//EST//3.4e-21:335:65//Hs.141603:N66015  
40 R-NT2RP2006321//ESTs, Moderately similar to karyopherin beta 3 [H.sapiens]//1.9e-89:460:96//Hs.21889:  
N78664  
R-NT2RP2006323//ESTs//3.5e-91:439:98//Hs.61697:AI081771  
R-NT2RP2006333//ESTs//4.9e-38:301:82//Hs.155999:AA196412  
R-NT2RP2006334//EST//3.1e-45:264:91//Hs.149599:AI282321  
R-NT2RP2006365//ESTs//2.9e-81:417:95//Hs.11814:W44411  
45 R-NT2RP2006393//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//3.9e-48:403:  
77//Hs.1361:M55053  
R-NT2RP2006436//Homo sapiens mRNA for small GTP-binding protein, complete cds//1.4e-27:155:76//Hs.  
115325:D84488  
R-NT2RP2006441//ESTs//6.0e-108:529:97//Hs.101282:N45092  
50 R-NT2RP2006454//ESTs//9.2e-20:110:99//Hs.144687:AI341146  
R-NT2RP2006456//ESTs//7.1e-91:508:92//Hs.12488:W63595  
R-NT2RP2006464//Homo sapiens mRNA for AND-1 protein//2.1e-109:524:97//Hs.72160:AJ006266  
R-NT2RP2006467//EST//0.99:140:61//Hs.146958:AI174478  
R-NT2RP2006472//ESTs//3.3e-92:473:95//Hs.29216:AA916679  
55 R-NT2RP2006534//ESTs//1.2e-83:394:99//Hs.162116:AA524947  
R-NT2RP2006554//ESTs//1.0e-87:460:95//Hs.47095:AA181474  
R-NT2RP2006565//ESTs//3.2e-24:129:100//Hs.13499:AI299886  
R-NT2RP2006571//ESTs//2.6e-56:306:94//Hs.98370:AA316622

R-nnnnnnnnnnnn//ESTs//2.0e-112:533:98//Hs.18685:AI393829  
 R-NT2RP2006598//ESTs, Weakly similar to retinoid X receptor interacting protein [M.musculus]/4.1e-109:542:  
 97//Hs.7889:AI337112  
 R-NT2RP3000002//ESTs//1.3e-08:399:59//Hs.126044:AI301598  
 5 R-NT2RP3000031//Homo sapiens mRNA for histone deacetylase-like protein (JM21)//1.9e-116:560:97//Hs.6764:  
 AJ011972  
 R-NT2RP3000046//Small inducible cytokine A5 (RANTES)//1.9e-57:312:85//Hs.155464:AF088219  
 R-NT2RP3000047//EST//0.91:130:66//Hs.140208:AA702213  
 R-NT2RP3000050//ESTs, Weakly similar to putative p150 [H.sapiens]//3.1e-41:249:90//Hs.156155:AI222202  
 10 R-NT2RP3000055//EST//2.4e-19:146:86//Hs.160497:AI255095  
 R-NT2RP3000072//ESTs//2.2e-82:424:96//Hs.21542:N49574  
 R-NT2RP3000080//ESTs//2.1e-29:186:89//Hs.153372:AA424029  
 R-NT2RP3000085//ESTs//4.5e-101:482:98//Hs.47649:AA838715  
 R-NT2RP3000109//ESTs//9.5e-97:455:99//Hs.17731:AI342241  
 15 R-NT2RP3000134//EST//4.7e-106:497:99//Hs.125531:AA884000  
 R-NT2RP3000142//Homo sapiens mRNA for KIAA0592 protein, partial cds//1.2e-116:578:96//Hs.13273:  
 AB011164  
 R-NT2RP3000149//ESTs//7.7e-62:361:90//Hs.6649:N93418  
 R-NT2RP3000186  
 20 R-NT2RP3000197//ESTs//1.5e-75:436:91//Hs.140931:R51882  
 R-NT2RP3000207//ESTs//1.3e-98:468:98//Hs.126908:AA933091  
 R-NT2RP3000220//ESTs//2.2e-27:144:99//Hs.106861:R61306  
 R-NT2RP3000233//EST//7.8e-77:368:99//Hs.49075:N64817  
 R-NT2RP3000235//ESTs//0.43:82:74//Hs.132828:AI032819  
 25 R-NT2RP3000247//EST//2.2e-97:459:99//Hs.127928:AA969239  
 R-NT2RP3000251  
 R-NT2RP3000252//ESTs, Weakly similar to Lpg15p [S.cerevisiae]//2.0e-108:532:97//Hs.111086:AI379177  
 R-NT2RP3000255//EST//0.67:93:67//Hs.120579:AA743073  
 R-NT2RP3000267//ESTs//8.5e-108:542:95//Hs.24984:AA534446  
 30 R-NT2RP3000299//ESTs, Weakly similar to enhancer of filamentation 1 [H.sapiens]//3.6e-103:516:96//Hs.4894:  
 AI191323  
 R-NT2RP3000312//ESTs//1.3e-100:493:97//Hs.29379:AI094117  
 R-NT2RP3000320//ESTs//3.2e-95:538:91//Hs.118793:AA192438  
 R-NT2RP3000324  
 35 R-NT2RP3000333//ESTs//6.0e-39:194:100//Hs.119238:AA476267  
 R-NT2RP3000341//ESTS//0.51:251:61//Hs.94090:AA777689  
 R-NT2RP3000348//EST//1.8e-80:389:98//Hs.145944:AI276225  
 R-NT2RP3000350//ESTs, Weakly similar to Lpg15p [S.cerevisiae]//3.1e-110:556:96//Hs.111086:AI379177  
 R-NT2RP3000359//EST//4.9e-61:340:92//Hs.126495:AA913741  
 40 R-NT2RP3000361//ESTs, Weakly similar to PRE-MRNA SPLICING FACTOR PRP6 [S.cerevisiae]//4.8e-91:439:  
 97//Hs.31334:AI144423  
 R-NT2RP3000366//EST//0.20:392:57//Hs.149652:AI283303  
 R-NT2RP3000397//EST//8.7e-26:150:94//Hs.124617:AA855106  
 R-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cds//4.2e-111:529:98//Hs.28307:  
 45 AF071185  
 R-NT2RP3000418//EST//3.3e-09:202:67//Hs.117189:AA682947  
 R-NT2RP3000433  
 R-NT2RP3000439//ESTs//3.1e-79:426:92//Hs.26548:W26340  
 R-NT2RP3000441//ESTs//6.3e-84:420:97//Hs.137482:AA421254  
 50 R-NT2RP3000449//ESTs//4.9e-93:435:99//Hs.54617:AI379102  
 R-NT2RP3000451//ESTs//2.3e-89:439:97//Hs.9196:AA748492  
 R-NT2RP3000456//Homo Sapiens (clone B3B3E13) chromosome 4pl6.3 DNA fragment//1.8e-23:347:70//Hs.  
 114963:L34408  
 R-NT2RP3000484//Heparin cofactor II//0.98:166:62//Hs.1478:M58600  
 55 R-NT2RP3000487//ESTs//0.012:384:60//Hs.88684:AA885141  
 R-NT2RP3000512//Homeo box B3//2.0e-69:377:93//Hs.49931:X16667  
 R-NT2RP3000526//ESTS//1.6e-91:432:99//Hs.38042:AA187151  
 R-NT2RP3000527//ESTs//1.2e-100:518:94//Hs.104557:AI078161

R-NT2RP3000531//ESTs, Weakly similar to TH1 protein [D.melanogaster]//0.95:85:71//Hs.5184:AA709151  
R-NT2RP3000542//ESTs//2.6e-53:375:84//Hs.44158:N30180  
R-NT2RP3000561//EST//1.1e-13:170:75//Hs.148421:AI198036  
R-NT2RP3000562//Human mRNA for KIAA0233 gene, complete cds//0.97:141:68//Hs.79077:D87071  
5 R-NT2RP3000578//ESTs//2.6e-68:324:100//Hs.5445:AA779447  
R-NT2RP3000582//ESTS//2.1 e-25:131:80//Hs.152465:AA563785  
R-NT2RP3000584//ESTs//1.8e-97:460:99//Hs.120698:AI241511  
R-NT2RP3000590//ESTs//2.0e-97:453:100//Hs.105355:AA953817  
R-NT2RP3000592//ESTs//2.8e-91:432:99//Hs.144304:AI190916  
10 R-nnnnnnnnnnnn//Human mRNA for KIAA0314 gene, partial cds//1.5e-09:447:58//Hs.155045:AB002312  
R-NT2RP3000599//ESTs//3.8e-93:437:99//Hs.23971:AA829880  
R-NT2RP3000605//ESTs//4.2e-111:554:96//Hs.40780:AA422049  
R-NT2RP3000622//ESTs//2.0e-100:473:99//Hs.11387:AI127394  
15 R-NT2RP3000624//ESTs, Weakly similar to KIAA0256 [H.sapiens]//5.4e-115:545:98//Hs.4857:AI090739  
R-NT2RP3000628//Homo sapiens mRNA for KIAA0772 protein, complete cds//4.3e-49:397:80//Hs.15519:  
AB018315  
R-NT2RP3000632//ESTs, Moderately similar to cyclin-selective ubiquitin carrier protein [H.sapiens]//6.3e-92:434:  
99//Hs.152517:AA719022  
R-NT2RP3000644//ESTs//1.0e-44:306:84//Hs.155498:W27084  
20 R-NT2RP3000661//ESTs//3.1e-95:470:97//Hs.126069:W76185  
R-NT2RP3000665//ESTs//3.3e-95:503:94//Hs.34313:W81185  
R-NT2RP3000685//ESTs//2.7e-99:515:94//Hs.9711:R60873  
R-NT2RP3000690//ESTs//3.3e-88:414:99//Hs.1465 89:AI085578  
R-NT2RP3000736  
25 R-NT2RP3000742//ESTs, Highly similar to 1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODI-  
ESTERASE DELTA 1 [Rattus norvegicus]//1.8e-07:114:75//Hs.136065:W21960  
R-NT2RP3000753//ESTs//3.1e-99:461:100//Hs.150901:AI310447  
R-NT2RP3000759//ESTs//2.0e-74:384:95//Hs.104222:AA207243  
R-NT2RP3000815//ESTs//8.5e-97:455:99//Hs.158897:AI378583  
30 R-NT2RP3000825//EST//0.0089:343:59//Hs.42897:N20810  
R-NT2RP3000826//EST//3.4e-33:342:74//Hs.162236:AA551582  
R-NT2RP3000836//ESTs//6.8e-24:181:84//Hs.134464:AI151081  
R-NT2RP3000841//ESTs//4.5e-93:491:93//Hs.23618:H98082  
R-NT2RP3000845//ESTs//2.4e-88:473:93//Hs.8312:AA813022  
35 R-NT2RP3000847//ESTs//9.3e-89:460:95//Hs.154106:AI051657  
R-NT2RP3000850  
R-NT2RP3000852//Fibrillin 2//0.55:237:63//Hs.79432:U03272  
R-NT2RP3000859//ESTs//1.4e-96:509:94//Hs.7187:AA576895  
R-NT2RP3000865//EST//4.8e-23:461:66//Hs.162088:AA505741  
40 R-NT2RP3000868//ESTs//5.4e-78:430:93//Hs.102796:N70837  
R-NT2RP3000869//ESTs//8.5e-77:397:94//Hs.84484:AI014673  
R-NT2RP3000875//Mevalonate kinase//3.8e-78:531:84//Hs.75138:M88468  
R-NT2RP3000901//ESTs//2.1e-95:466:97//Hs.10647:AA428217  
R-NT2RP3000904//ESTs//1.6e-79:380:99//Hs.100850:AA479385  
45 R-NT2RP3000917//ESTs, Highly similar to mouse Dhml protein [M.musculus]//9.5e-113:566:96//Hs.5900:  
AA035728  
R-NT2RP3000919  
R-NT2RP3000968//40S RIBOSOMAL PROTEIN S15A/1.5e-25:375:71//Hs.2953:X84407  
R-NT2RP3000980//ESTs//3.3e-72:364:96//Hs.9536:AA114178  
50 R-NT2RP3000994//ESTs//3.5e 111:537:97//Hs.21146:AA683542  
R-NT2RP3001004//ESTs//9.6e-91:456:96//Hs.58974:W87405  
R-NT2RP3001007//ESTs//6.7e-99:482:97//Hs.117737:AI088029  
R-NT2RP3001055//ESTs//0.0012:294:60//Hs.66479:AA863044  
R-NT2RP3001057//ESTs, Highly similar to ZINC FINGER PROTEIN HF.12 [Homo sapiens]//5.6e-102:486:99//Hs.  
145956:AA007349  
R-NT2RP3001081//Retinal pigment epithelium-specific protein (65kD)//0.0012:447:58//Hs.2133:U18991  
R-NT2RP3001084//ESTs//4.3e-102:528:96//Hs.25277:W87874  
R-NT2RP3001096//ESTS//1.1e-110:540:96//Hs.42824:AA873182

R-NT2RP3001107//ESTs//7.6e-100:478:98//Hs.99669:AA287832  
R-nnnnnnnnnnnn//DNA polymerase gamma//0.0014:50:100//Hs.80961:U60325  
R-NT2RP3001111//ESTs, Weakly similar to Trf-proximal protein [D.melanogaster]//3.2e-104:543:95//Hs.93796:  
C06063  
5 R-NT2RP3001113//ESTs//3.3e-100:467:99//Hs.97757:AA401575  
R-NT2RP3001115//Oxytocin receptor//7.9e-30:505:67//Hs.2820:X64878  
R-NT2RP3001116//ESTs//4.6e-41:229:96//Hs.58412:W74779  
R-NT2RP3001119//ESTs//6.9e-88:478:92//Hs.19469:AA203180  
R-NT2RP3001120//ESTs//3.1e-82:430:93//Hs.110956:AI190166  
10 R-NT2RP3001126//ESTs//4.4e-52:264:96//Hs.25264:R78188  
R-NT2RP3001133//ESTs//4.7e-105:541:94//Hs.73239:AA573761  
R-NT2RP3001140//Homo sapiens mRNA for KIAA0762 protein, partial cds//2.6e-115:549:97//Hs.5378:AB018305  
R-NT2RP3001147//ESTs, Highly similar to GTPASE ACTIVATING PROTEIN ROTUND [Drosophila melanogaster]  
//9.6e-113:552:97//Hs.23900:U82984  
15 R-NT2RP3001150//ESTs//2.9e-90:444:97//Hs.99601:AA760717  
R-NT2RP3001155//Homo sapiens mRNA for AND-1 protein//9.4e-118:563:98//Hs.72160:AJ006266  
R-NT2RP3001176//ESTs//1.8e-110:534:98//Hs.58650:AI074460  
R-NT2RP3001214//ESTs//1.7e-109:545:96//Hs.24481:AA573139  
R-NT2RP3001216//EST//0.00098:128:66//Hs.160493:AI254963  
20 R-NT2RP3001221//EST//0.010:106:66//Hs.147774:AI221196  
R-NT2RP3001232//ESTs//1.5e-101:518:94//Hs.21630:AA778399  
R-NT2RP3001236//ESTs, Highly similar to KIAA0377 [H.sapiens]//2.8e-89:462:95//Hs.116793:AA779588  
R-NT2RP3001239//ESTs, Moderately similar to NEURAXIN [Rattus norvegicus]//5.2e-82:466:91//Hs.66048:  
AA524416  
25 R-NT2RP3001245//EST//0.53:237:62//Hs.161131:AI417631  
R-NT2RP3001253//ESTs//1.7e-105:535:96//Hs.42315:AI222997  
R-NT2RP3001260//EST//0.16:144:62//Hs.126856:AA932135  
R-NT2RP3001268//Human Aac11(aac11) mRNA, complete cds//0.12:494:59//Hs.151031:U83857  
R-NT2RP3001272//ESTs//1.4e-92:436:99//Hs.149831:AI383965  
30 R-NT2RP3001274//ESTs//3.9e-81:424:95//Hs.1113184:N25651  
R-NT2RP3001281//EST//3.1e-60:298:98//Hs.149230:AI247332  
R-NT2RP3001307//EST//0.42:215:62//Hs.126165:AA868691  
R-NT2RP3001318//ESTs//4.1e-74:363:97//Hs.130832:H92571  
R-NT2RP3001325//ESTs//1.7e-106:534:96//Hs.21214:H98989  
35 R-NT2RP3001338//Human protein tyrosine phosphatase sigma mRNA, complete cds//0.22:199:63//Hs.159534:  
U35234  
R-NT2RP3001339//Homo sapiens mRNA for KIAA0451 protein, complete cds//3.9e-114:566:96//Hs.18586:  
AB007920  
R-NT2RP3001340//ESTs//1.1e-72:411:92//Hs.21135:W81653  
40 R-NT2RP3001355//ESTs//9.0e-103:521:95//Hs.99486:AA776798  
R-NT2RP3001374//ESTs//2.7e-82:395:98//Hs.117102:AA993090  
R-NT2RP3001383//ESTs//3.6e-10:118:78//Hs.111055:AA169778  
R-NT2RP3001384//ESTs, Weakly similar to A-kinase anchor protein 95, AKAP95 [R.norvegicus]//5.7e-92:522:90//  
Hs.96200:AA218942  
45 R-NT2RP3001392//ESTs//5.9e-62:296:100//Hs.125034:AA907375  
R-NT2RP3001396//ESTS//3.7e-111:528:98//Hs.22612:AA152232  
R-NT2RP3001398//ESTs//2.6e-94:449:99//Hs.146332:AI276628  
R-NT2RP3001399//ESTs//2.6e-82:401:97//Hs.7932:AI041186  
R-NT2RP3001407//ESTs//2.2e-101:488:97//Hs.71573:AA496898  
50 R-NT2RP3001420//EST//7.4e-44:394:79//Hs.137041:AA877817  
R-NT2RP3001426//Homo sapiens clone 24616 mRNA sequence//3.6e-106:550:94//Hs.6957:AF052158  
R-NT2RP3001427//ESTs//1.3e-87:374:97//Hs.5457:H05692  
R-nnnnnnnnnnnn//Neurotrophic tyrosine kinase, receptor, type 1//4.7e-96:533:91//Hs.85844:X66397  
R-NT2RP3001432//ESTs//1.9e-102:523:95//Hs.132978:AI041374  
55 R-NT2RP3001447//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//5.1e-  
101:482:98//Hs.124135:AA910560  
R-NT2RP3001449//ESTs//2.2e-99:502:96//Hs.7834:N45994  
R-NT2RP3001453//Small inducible cytokine A5 (RANTES)//8.1e-45:295:85//Hs.155464:AF088219

R-NT2RP3001457//ESTS//1.5e-52:256:99//Hs.117982:AA644658  
R-NT2RP3001459//ESTs//3.4e-62:299:99//Hs.146098:AA167280  
R-NT2RP3001472//ESTs//4.8e-108:540:96//Hs.69594:N37009  
R-NT2RP3001490//ESTs//3.5e-91:549:88//Hs.6606:AA211783  
5 R-NT2RP3001495//Human oxidoreductase (HHCMA56) mRNA, complete cds//1.4e-61:338:93//Hs.519:U13395  
R-NT2RP3001497//Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA, complete cds//  
6.8e-112:549:9711Hs.28285:AF064801  
R-NT2RP3001527//ESTs//4.4e-105:543:95//Hs.158761:AA631047  
R-NT2RP3001529//Homo sapiens tapasin (NGS-17) mRNA, complete cds//7.9e-59:427:83//Hs.5247:AF029750  
10 R-NT2RP3001538//ESTs//1.6e-94:521:92//Hs.6846:AA209463  
R-NT2RP3001554//ESTs, Moderately similar to NEURAXIN [Rattus norvegicus]//2.8e-76:392:95//Hs.66048:  
AA524416  
R-NT2RP3001580//ESTs//3.7e-82:398:98//Hs.23490:N49477  
R-NT2RP3001587//Homa sapiens mRNA for HRIHFB2115, partial cds//1.8e-09:86:88//Hs.4311:AB015337  
15 R-NT2RP3001589//ESTs//0.0029:243:62//Hs.158924:AA605194  
R-NT2RP3001607//EST//0.00096:76:78//Hs.140319:AA748328  
R-NT2RP3001608//ESTs//3.8e-105:525:96//Hs.144655:AI279798  
R-NT2RP3001621//ESTs//3.3e-108:535:97//Hs.47378:AI193598  
R-NT2RP3001629  
20 R-NT2RP3001634//Homo sapiens TRIAD1 type I mRNA, complete cds//2.7e-109:541:96//Hs.9899:AF099149  
R-NT2RP3001642//ESTs//6.0e-105:525:96//Hs.3376:AA915989  
R-NT2RP3001646//ESTs//4.8e-95:523:92//Hs.64036:AA127709  
R-NT2RP3001671//ESTs//0.0013:367:60//Hs.106090:AA457030  
R-NT2RP3001672//ESTs//3.4e-37:191:98//Hs.57475:AI382189  
25 R-NT2RP3001676//ESTs//1.5e-81:408:97//Hs.142547:N67648  
R-NT2RP3001678//ESTs//4.3e-85:405:99//Hs.121915:AI268225  
R-NT2RP3001679//ESTs//3.4e-100:545:93//Hs.5943:AI222558  
R-NT2RP3001688//Human mRNA for KIAA0392 gene, partial cds//8.6e-46:301:87//Hs.40100:AB002390  
R-NT2RP3001690//ESTs//3.3e-111:542:97//Hs.86149:AI341312  
30 R-NT2RP3001708//ESTs//1.4e-96:349:95//Hs.17975:AA868618  
R-NT2RP3001712//ESTs//9.3e-14:102:92//Hs.78041:N29669  
R-NT2RP3001716//ESTs, Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus]  
//4.1e-80:444:91//Hs.6823:W18181  
R-NT2RP3001724//ESTs//1.8e-109:547:96//Hs.14570:AI422099  
35 R-NT2RP3001730//ESTs//4.1e-98:528:92//Hs.155115:AA669923  
R-NT2RP3001739//ESTs//4.4e-87:444:94//Hs.27239:W27810  
R-NT2RP3001752//ESTS//6.1e-93:490:94//Hs.4210:AA740440  
R-NT2RP3001753//ESTs//2.5e-82:395:99//Hs.126435:AA912968  
R-NT2RP3001764//ESTs, Weakly similar to protein-tyrosine phosphatase [H.sapiens]//1.2e-87:450:96//Hs.20281:  
40 N92517  
R-NT2RP3001777//ESTs//1.1e-86:360:97//Hs.100530:H06725  
R-NT2RP3001782//Homo sapiens mRNA for KIAA0459 protein, partial cds//4.2e-113:549:97//Hs.28169:  
AB007928  
R-NT2RP3001792//ESTs, Weakly similar to F35C12.2 [C.elegans]//1.1e-21:119:99//Hs.44268:AA455900  
45 R-NT2RP3001799//OX40L RECEPTOR PRECURSOR//2.8e-45:374:79//Hs.129780:X75962  
R-NT2RP3001819//ESTs//2.6e-87:432:96//Hs.10414:AI291292  
R-NT2RP3001844//ESTs//0.024:128:67//Hs.25131:N50117  
R-NT2RP3001854//ESTs//1.4e-92:490:92//Hs.15165:N52900  
R-NT2RP3001855//ESTs//1.9e-66:361:93//Hs.10043:D81792  
50 R-NT2RP3001896//ESTs//1.4e-96:343:97//Hs.24809:N73642  
R-NT2RP3001898//ESTs//4.1e-90:515:91//Hs.4867:AA521180  
R-NT2RP3001915//ESTs//4.4e-32:175:95//Hs.24641:AA954666  
R-NT2RP3001926//ESTs, Highly similar to NUCLEOLYSIN TIA-1 [Homo sapiens]//1.0e-40:202:100//Hs.24709:  
AI123300  
55 R-NT2RP3001929//ESTs//6.6e-84:449:94//Hs.26962:AA682781  
R-NT2RP3001931//ESTs//1.0e-41:214:99//Hs.32360:AA534737  
R-NT2RP3001938//ESTs, Highly similar to SPORULATION-SPECIFIC PROTEIN 1 [Saccharomyces cerevisiae]  
//1.3e-95:483:96//Hs.5771:W74591

R-NT2RP3001943//ESTs//1.2e-23:169:88//Hs.103930:AA160990  
 R-NT2RP3001944//ESTs//2.0e-90:439:97//Hs.103380:AI291325  
 R-NT2RP3001969//ESTs//0.95:133:65//Hs.131669:AI025889  
 R-NT2RP3001989//ESTS, Weakly similar to C01A2.4 [C.elegans]//8.9e-64:310:99//Hs.11449:AI201540  
 5 R-NT2RP3002002//ESTs//2.1e-95:562:89//Hs.5997:AA897088  
 R-NT2RP3002004//H.sapiens mRNA for FAST kinase//1.6e-42:335:82//Hs.75087:X86779  
 R-NT2RP3002007//ESTs//0.12:184:66//Hs.94030:AA846729  
 R-NT2RP3002014//Small inducible cytokine A5 (RANTES)//6.8e-47:291:89//Hs.155464:AF088219  
 R-NT2RP3002033  
 10 R-NT2RP3002045//ESTs//1.0e-92:555:88//Hs.106411:W29081  
 R-NT2RP3002054//EST//0.45:155:63//Hs.5656:D20426  
 R-NT2RP3002056//ESTs//1.4e.95:504:93//Hs.17428:AI365221  
 R-NT2RP3002057//Human mRNA for KIAA0152 gene, complete cds//0.69:127:66//Hs.90438:D63486  
 R-NT2RP3002062  
 15 R-nnnnnnnnnnnn//ESTs//2.1e-113:552:97//Hs.9591:AA069657  
 R-NT2RP3002081//ESTs//5.5e-43:212:100//Hs.124852:AA969139  
 R-NT2RP3002097//EST//2.3e-10:80:91//Hs.102717:N59148  
 R-NT2RP3002102  
 R-NT2RP3002108  
 20 R-NT2RP3002146//ESTs//5.5e-58:296:97//Hs.65328:AA625385  
 R-NT2RP3002147//EST//2.5e-53:387:81//Hs.147928:M249703  
 R-NT2RP3002151//ESTs, Highly similar to G1 TO S PHASE TRANSITION PROTEIN 1 HOMOLOG [Homo sapiens]//6.2e-107:534:96//Hs.59523:AA602837  
 R-NT2RP3002163//ESTs//2.7e-106:520:97//Hs.21258:AA412293  
 25 R-NT2RP3002165//ESTs//7.4e-93:479:95//Hs.27299:AI074024  
 R-NT2RP3002166//ESTs//1.0:261:59//Hs.132817:AA593713  
 R-NT2RP3002173//ESTs//2.7e-93:512:92//Hs.23648:H07120  
 R-NT2RP3002181//ESTs//1.0e-84:435:96//Hs.47378:AI193598  
 R-NT2RP3002244//ESTs//2.7e-11:97:89//Hs.9412:W72446  
 30 R-NT2RP3002248//ESTs//4.3e-90:459:95//Hs.9848:AA130588  
 R-NT2RP3002255//ESTs//1.3e-45:289:88//Hs.9100:AA431672  
 R-NT2RP3002273//ESTs//2.3e-100:489:97//Hs.8258:AA744743  
 R-NT2RP3002276//ESTs//1.2e-50:306:91//Hs.16160:AA778171  
 R-NT2RP3002303//ESTs//1.1e-67:323:99//Hs.129761:AA836898  
 35 R-NT2RP3002304//ESTs//2.8e-86:405:99//Hs.29643:AA418500  
 R-NT2RP3002330//ESTs, Weakly similar to G1 TO S PHASE TRANSITION PROTEIN 1 HOMOLOG [H.sapiens]//1.8e-19:136:87//Hs.106928:AI041737  
 R-NT2RP3002343//ESTs//1.0e-42:260:93//Hs.7797:W25667  
 R-NT2RP3002351//Homo sapiens 9G8 splicing factor mRNA, complete cds//0.0048:221:64//Hs.556:L41887  
 40 R-NT2RP3002352//Homo sapiens mRNA for protein encoded by cxorf5 (71-7A) gene//5.8e-105:516:94//Hs.6483:Y16355  
 R-NT2RP3002455//Homo sapiens mRNA for KIAA0678 protein, partial cds//1.5e-103:524:95//Hs.12707:AB014578  
 R-NT2RP3002484//Human APRT gene for adenine phosphoribosyltransferase//0.54:108:71//Hs.28914:Y00486  
 45 R-NT2RP3002501//ESTs//2.7e-96:489:95//Hs.27335:N74185  
 R-NT2RP3002512//ESTs, Weakly similar to HYPOTHETICAL 31.0 KD PROTEIN R107.2 IN CHROMOSOME III [C.elegans]//3.2e-90:526:90//Hs.8083:AA521436  
 R-NT2RP3002529//ESTs, Highly similar to PUTATIVE VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN C2G11.03C [Schizosaccharomyces pombe]//3.8e-101:497:96//Hs.6650:AA843246  
 50 R-NT2RP3002545//Homo sapiens mRNA for KIAA0729 protein, partial cds//1.1e-83:438:94//Hs.19542:AB018272  
 R-NT2RP3002549//ESTs//3.8e-98:493:96//Hs.7358:AA191673  
 R-NT2RP3002566//Homo sapiens calcium-activated potassium channel (KCNN3) mRNA, complete cds//0.14:184:63//Hs.89230:AF031815  
 R-NT2RP3002587//Homo sapiens KIAA0420 mRNA, complete cds//2.0e-18:138:78//Hs.129883:AB007880  
 55 R-NT2RP3002590//ESTs//2.9e-51:290:93//Hs.162942:AI243850  
 R-NT2RP3002602//Homo sapiens stannin mRNA, complete cds//5.5e-06:58:100//Hs.76691:AF070673  
 R-NT2RP3002603  
 R-NT2RP3002631//ESTs//4.8e-54:367:85//Hs.13109:AA192514

R-NT2RP3002659//ESTs//5.3e-30:229:85//Hs.152114:AA401365  
 R-NT2RP3002660//ESTs//1.9e-88:452:95//Hs.120146:AA708573  
 R-NT2RP3002663//EST//3.2e-89:469:95//Hs.105767:AA525172  
 R-NT2RP3002671//ESTs, Highly similar to ELONGATION FACTOR 2 [Drosophila melanogaster]//5.9e-109:537:  
 5 97//Hs.19348:AA151678  
 R-NT2RP3002682//ESTs//2.3e-98:541:91//Hs.75844:AA115502  
 R-NT2RP3002687//ESTs//5.5e-103:498:97//Hs.72782:AA910871  
 R-NT2RP3002688//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//5.0e-101:  
 10 524:95//Hs.32580:AI123601  
 R-NT2RP3002701//EST//0.87:131:63//Hs.161916:AA483169  
 R-NT2RP3002713//ESTs//4.7e-106:542:95//Hs.14479:AA160945  
 R-NT2RP3002763//ESTs//1.3e-54:290:94//Hs.142031:AA809159  
 R-NT2RP3002770//ESTs//0.047:275:61//Hs.122984:AA526973  
 R-NT2RP3002785//ESTs//2.4e-52:255:99//Hs.132959:AI376958  
 15 R-NT2RP3002799//EST//8.2e-61:321:94//Hs.140992:R71377  
 R-NT2RP3002810//EST//0.19:116:68//Hs.121810:AA775240  
 R-NT2RP3002818//ESTs//1.3e-109:531:98//Hs.58924:AI348080  
 R-NT2RP3002861//ESTs//2.5e-84:429:95//Hs.23920:AA909678  
 R-NT2RP3002869//EST//0.00011:116:71//Hs.161606:AA019641  
 20 R-NT2RP3002876//ESTs//0.0024:182:63//Hs.117306:AA687262  
 R-NT2RP3002877//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//  
 8.1e-14:146:72//Hs.129727:AF035587  
 R-NT2RP3002909//Homo sapiens mRNA for KIAA0771 protein, partial cds//1.5e-110:570:95//Hs.6162:AB018314  
 R-NT2RP3002911//ESTs//3.6e-92:436:99//Hs.143917:AI206286  
 25 R-NT2RP3002948//EST//1.0:102:65//Hs.144730:AI191975  
 R-NT2RP3002953//ESTs//1.8e-107:513:98//Hs.119693:AI201698  
 R-NT2RP3002955//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0492//0.23:563:56//Hs.127338:  
 AB007961  
 R-NT2RP3002969//ESTs, Weakly similar to LONG-CHAIN-FATTY-ACID-COA LIGASE 1 [Saccharomyces cere-  
 30 visiae]112.0e-56:387:86//Hs.144597:W20143  
 R-NT2RP3002972//ESTs//1.7e-97:502:96//Hs.7274:AA476850  
 R-NT2RP3002978//ESTs//8.6e-104:498:98//Hs.118923:AA252116  
 R-NT2RP3002988//EST//1.2e-59:315:94//Hs.157743:AI360553  
 R-NT2RP3003008//ESTs//1.4e-97:515:94//Hs.6544:AA524423  
 35 R-NT2RP3003032//ESTs, Weakly similar to RETROVIRUS-RELATED POL POLYPROTEIN [Mus musculus]//  
 3.0e-100:528:94//Hs.90353:N98551  
 R-NT2RP3003059//ESTs//1.7e-76:398:95//Hs.102971:W05355  
 R-NT2RP3003061//ESTs//4.9e-82:414:96//Hs.99603:AI141912  
 R-NT2RP3003068//ESTs, Weakly similar to M18.3 [C.elegans]//5.9e-83:392:99//Hs.101364:AA534439  
 40 R-NT2RP3003071//ESTs//6.3e-85:399:99//Hs.109755:AA180809  
 R-NT2RP3003078//ESTs//1.0e-98:471:99//Hs.7995:AI359466  
 R-NT2RP3003101//EST//0.032:235:60//Hs.147920:AI202441  
 R-NT2RP3003121//ESTs//3.0e-47:238:97//Hs.43559:AI003520  
 R-NT2RP3003133//EST//1.5e-77:395:96//Hs.142150:AA223982  
 45 R-NT2RP3003138//ESTs, Highly similar to KINESIN-LIKE PROTEIN KIF4 [Mus musculus]//3.3e-107:535:96//Hs.  
 27437:AA004208  
 R-NT2RP3003139//ESTs//2.5e-106:504:98//Hs.106795:AI271632  
 R-NT2RP3003150//ESTs//1.6e.99:539:91//Hs.46500:AA129774  
 R-NT2RP3003157//ESTs//1.5e-114:563:97//Hs.58608:AA081007  
 50 R-NT2RP3003185//ESTs//3.9e-93:443:98//Hs.9741:AI131226  
 R-NT2RP3003193//ESTs//2.0e-37:428:71//Hs.33354:AA179944  
 R-NT2RP3003197//ESTs//5.8e-56:312:94//Hs.7016:AA215796  
 R-NT2RP3003203//EST//0.0073:212:63//Hs.161355:AI422634  
 R-NT2RP3003204//ESTs//7.4e-52:253:99//Hs.120146:AA708573  
 55 R-NT2RP3003212//ESTs//1.8e-76:401:95//Hs.29067:N26107  
 R-NT2RP3003230//ESTs, Highly similar to CORONIN [Dictyostelium discoideum]//2.0e-40:229:93//Hs.17377:  
 AI078151  
 R-NT2RP3003242//ESTs//8.3e-97:458:99//Hs.23057:AI290343

R-NT2RP3003251//ESTs//1.5e-60:320:95//Hs.36495:AA151628  
 R-NT2RP3003264//ESTs//2.1e-103:521:95//Hs.4094:AA173960  
 R-NT2RP3003278//ESTs//8.2e-109:536:96//Hs.23788:AA524061  
 R-NT2RP3003282//Homo sapiens dynamin (DNM) mRNA, complete cds//2.4e-102:550:93//Hs.11702:L36983  
 5 R-NT2RP3003290//EST//4.3e-27:372:70//Hs.159131:AI384035  
 R-NT2RP3003301//ESTs//4.4e-56:285:97//Hs.95370:AA601055  
 R-NT2RP3003302//EST//7.2e-10:395:63//Hs.162554:AA584818  
 R-NT2RP3003311//ESTs//4.2e-110:538:97//Hs.62180:AI341261  
 R-NT2RP3003313//ESTs//2.1e-106:531:96//Hs.22630:C05931  
 10 R-NT2RP3003327//ESTs//4.3e-102:518:95//Hs.120355:AA625445  
 R-NT2RP3003330//ESTs//8.6e-104:497:97//Hs.72071:AI125289  
 R-NT2RP3003344//ESTs//2.5e-105:494:99//Hs.112188:AA872993  
 R-NT2RP3003346//ESTs//1.0:123:69//Hs.116029:AA813102  
 R-NT2RP3003353//EST//0.0014:162:68//Hs.149191:AI246155  
 15 R-NT2RP3003377//EST//4.5e-15:119:85//Hs.148129:AA885567  
 R-NT2RP3003384//EST//0.0057:86:74//Hs.127735:AA962272  
 R-NT2RP3003385//ESTs//0.64:347:59//Hs.5646:W72721  
 R-NT2RP3003403//ESTs, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [H.sapiens]//2.2e-  
 24:418:67//Hs.139488:AI124095  
 20 R-NT2RP3003409//ESTs//5.3e-98:479:97//Hs.155198:AA767372  
 R-NT2RP3003411//ESTs//4.8e-86:416:97//Hs.129059:AA126041  
 R-NT2RP3003427//ESTs//7.4e-103:510:96//Hs.25303:AA641023  
 R-NT2RP3003433//ESTs//3.5e-85:405:99//Hs.63131:AA664156  
 R-NT2RP3003464//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds//3.6e-97:479:96//Hs.14934:  
 25 AF004828  
 R-NT2RP3003490//Homo sapiens mRNA for KIAA0725 protein, partial cds//4.1e-102:527:93//Hs.26450:  
 AB018268  
 R-NT2RP3003491//ESTs, Weakly similar to No definition line found [C.elegans]//4.0e-106:549:94//Hs.7886:  
 AI057529  
 30 R-NT2RP3003500//Human RP3 mRNA, complete cds//0.66:401:60//Hs.75307:U02556  
 R-NT2RP3003543//Human clone A9A2BRB7 (CAC)n/(GTG)n repeat-containing mRNA//4.1e-33:217:88//Hs.  
 8068:U00952  
 R-NT2RP3003552//ESTs//3.1e-106:546:94//Hs.101754:AI123430  
 R-NT2RP3003555//ESTs//3.4e-106:537:95//Hs.85550:AA187681  
 35 R-NT2RP3003564  
 R-NT2RP3003572//ESTs//1.2e-20:122:88//Hs.8253:N48721  
 R-NT2RP3003576//ESTs//2.7e-71:394:94//Hs.151136:R99944  
 R-NT2RP3003589//EST//0.58:242:59//Hs.130804:AA894759  
 R-NT2RP3003625//ESTs//7.6e-41:349:80//Hs.140608:N53448  
 40 R-NT2RP3003656//Human LIM protein (LPP) rRNA, partial cds//0.26:222:60//Hs.17217:U49957  
 R-NT2RP3003659//ESTs//2.0e-113:547:97//Hs.23389:AA769310  
 R-NT2RP3003665//ESTs//1.6e-80:415:95//Hs.141084:H11714  
 R-NT2RP3003672  
 R-NT2RP3003686//ESTs//6.8e-114:552:97//Hs.43299:N23036  
 45 R-NT2RP3003701//ESTs//2.1e-16:282:66//Hs.115512:AI208768  
 R-NT2RP3003716//ESTs//2.1e-45:195:91//Hs.41296:N71923  
 R-NT2RP3003726//Homo sapiens mRNA for KIAA0757 protein, complete cds//5.6e-103:492:97//Hs.48513:  
 AB018300  
 R-NT2RP3003746//ESTs//1.9e-85:411:98//Hs.54835:AI050863  
 50 R-NT2RP3003795//EST//6.2e-97:459:99//Hs.134769:AI089747  
 R-NT2RP3003799//ESTs//2.8e-62:337:94//Hs.124023:H18913  
 R-NT2RP3003800//PROTO-ONCOGENE TYRO SINE-PROTEIN KINASE SRC//8.9e-108:551:95//Hs.115742:  
 AF077754  
 R-NT2RP3003805//ESTs//2.2e-103:490:99//Hs.9412:W72446  
 55 R-NT2RP3003809//ESTs, Highly similar to SAV PROTEIN [Sulfolobus acidocaldarius]//3.4e-89:456:95//Hs.5555:  
 AI285198  
 R-NT2RP3003819//Interleukin 10//3.3e-43:173:89//Hs.2180:M57627  
 R-NT2RP3003825//ESTs//1.6e-66:485:80//Hs.7405:W27761

**EP 1 074 617 A2**

R-NT2RP3003828//ESTs, Weakly similar to unknown.[H.sapiens]//9.6e-98:511:95//Hs.26955:AI333224  
R-NT2RP3003831//ESTs//2.2e-38:317:79//Hs.142173:AA757743  
R-NT2RP3003833//Homo sapiens clones 24718 and 24825 mRNA sequence//5.2e-110:541:97//Hs.25300:  
AF070611  
5 R-NT2RP3003842//EST//9.9e-44:506:70//Hs.139093:AA166888  
R-NT2RP3003846//ESTs//4.6e-10:66:100//Hs.74924:AI332962  
R-NT2RP3003870//ESTs//3.4e-82:449:92//Hs.122691:AA152298  
R-NT2RP3003876//ESTs//1.9e-89:449:96//Hs.45046:N40170  
R-NT2RP3003914//ESTs//1.3e-99:470:98//Hs.118966:AA926726  
10 R-NT2RP3003918//ESTs//1.3e-79:417:94//Hs.5005:W25933  
R-NT2RP3003932//ESTs//6.0e-83:427:94//Hs.93581:H50221  
R-NT2RP3003989//ESTs//4.8e-76:403:93//Hs.127243:W80409  
R-NT2RP3003992//ESTs//2.4e-88:508:90//Hs.134200:D19593  
15 R-NT2RP3 004013//ESTs//3.7e-111:551:97//Hs.105108:AA781142  
R-NT2RP3004016//ESTs//1.7e-81:394:98//Hs.63368:AA613714  
R-NT2RP3004041  
R-NT2RP3004051//ESTs//3.5e-69:386:93//Hs.51347:T72820  
R-NT2RP3004070//ESTs//5.5e-108:552:9511Hs.23392:AI310139  
R-NT2RP3004078//ESTs//3.3e-82:443:93//Hs.26407:W4537  
20 R-NT2RP3004093//ESTs//4.4e-83:426:94//Hs.140932:AI262104  
R-NT2RP3004095//ESTs//0.00013:93:78//Hs.36567:AA262045  
R-NT2RP3004110//ESTs, Weakly similar to similar to oxysterol-binding proteins: partial CDS [C.elegans]//3.5e-  
76:402:95//Hs.55847:W31092  
R-NT2RP3004125//ESTs//9.3e-74:363:97//Hs.32988:C01696  
25 R-NT2RP3004145//ESTs//2.6e-96:451:99//Hs.59584:AA587334  
R-NT2RP3004148//ESTs//1.3e-10:77:92//Hs.135890:AI183425  
R-NT2RP3004155//ESTS//1.7e-110:558:96//Hs.27003:AI279093  
R-NT2RP3004206//ESTs, Moderately similar to CROOKED NECK PROTEIN [Drosophila melanogaster]//1.8e-40:  
200:100//Hs.26089:AA195126  
30 R-NT2RP3004207//ESTs, Weakly similar to gene SEZ-6 [M.musculus]//1.1e-41:266:89//Hs.6314:AA522619  
R-NT2RP3004209//ESTs, Highly similar to PUTATIVE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE  
C13A11.04C [Schizosaccharomyces pombe]//3.7e-112:547:97//Hs.99819:AI346680  
R-NT2RP3004215//ESTs//1.1e-103:541:95//Hs.124918:N64794  
R-NT2RP3004242//ESTs//4.5e-105:524:96//Hs.29724:N46252  
35 R-NT2RP3004246//EST//1.9e-07:67:91//Hs.125687:AA884827  
R-NT2RP3004253//EST//2.9e-88:454:94//Hs.127713:AA961628  
R-NT2RP3004258//ESTs, Weakly similar to PRE-MRNA SPLICING FACTOR SRP75 [Homo sapiens]//1.6e-89:  
468:95//Hs.5117:AA831530  
R-NT2RP3004262//ESTs//4.1e-86:443:96//Hs.101393:T87623  
40 R-NT2RP3004334//EST//0.00057:206:63//Hs.149388:AI273630  
R-NT2RP3004341//EST//0.00042:151:68//Hs.148498:AI200264  
R-NT2RP3004348//Homo sapiens LIM protein mRNA, complete cds//5.9e-61:299:85//Hs.154103:AF061258  
R-NT2RP3004349//EST//3.6e-42:175:88//Hs.161917:AA483223  
R-NT2RP3004378//ESTs//0.27:294:60//Hs.66479:AA863044  
45 R-NT2RP3004399//ESTs//5.8e-99:479:98//Hs.120234:AA732224  
R-NT2RP3004424//EST, Highly similar to F21G4.6 [C.elegans]//0.30:253:58//Hs.97184:AA385934  
R-NT2RP3004428//ESTs//2.8e-48:279:91//Hs.106826:W25985  
R-NT2RP3004451//ESTs//4.8e-101:509:96//Hs.29725:W74621  
50 R-NT2RP3004454//Homo sapiens mRNA for KIAA0448 protein, complete cds//9.3e-108:526:98//Hs.27349:  
AB007917  
R-NT2RP3004466//ESTs//0.25:51:90//Hs.7778:AA195616  
R-NT2RP3004470//EST//0.032:70:71//Hs.147925:AI249332  
R-NT2RP3004472//ESTs//0.0069:430:59//Hs.116651:AA993406  
R-NT2RP3004475//Homo sapiens mRNA for KIAA0456 protein, partial cds//5.0e-107:521:97//Hs.5003:AB007925  
55 R-NT2RP3004480  
R-NT2RP3004490//ESTs//4.7e-68:354:95//Hs.163721:H42504  
R-NT2RP3004498//ESTs, Moderately similar to ORF2: function unknown [H.sapiens]//3.4e-100:508:95//Hs.  
47393:AA218858

R-NT2RP3004503//ESTs//4.6e-90:478:93//Hs.133998:AA994735  
R-NT2RP3004504//ESTs, Highly similar to cytoplasmic polyadenylation element-binding protein [M.musculus]//  
1.8e-83:465:92//Hs.137064:AA318257  
R-NT2RP3004507//ESTs//1.5e-98:495:96//Hs.128905:AI051971  
5 R-NT2RP3004527//EST//1.6e-109:535:97//Hs.149481:AI279865  
R-nnnnnnnnnnnnn  
R-NT2RP3004544//EST//0.035:226:60//Hs.99195:AA449232  
R-NT2RP3004566//ESTs//4.1e-86:455:95//Hs.13110:T67461  
R-NT2RP3004569//ESTs//2.9e-94:493:94//Hs.24948:AA977674  
10 R-NT2RP3004572//ESTs//1.1e-92:437:99//Hs.24846:AI420493  
R-NT2RP3004578//ESTs//0.98:166:64//Hs.124593:AA854456  
R-NT2RP3004594//EST//5.8e-89:426:98//Hs.134213:AI080213  
R-NT2RP3004617//ESTs//1.4e-40:226:85//Hs.15921:R71157  
R-NT2RP3004618//ESTs//1.8e-38:229:90//Hs.125153:AA453723  
15 R-NT2RP3004670//Homo sapiens GN6ST mRNA for long form of N-acetylglucosamine-6-O-sulfotransferase  
(GlcNAc6ST), complete cds//7.2e-57:291:95//Hs.8786:AB014680  
R-NT2RP4000008//ESTs//8.9e-119:561:98//Hs.25035:AI123335  
R-NT2RP4000023//EST//1.2e-34:271:80//Hs.98300:AA418560  
20 R-NT2RP4000035//Small inducible cytokine A5 (RANTES)//2.1e-68:320:82//Hs.155464:AF088219  
R-NT2RP4000049//Homo sapiens TRAIL receptor 2 mRNA, complete cds//6.7e-60:289:82//Hs.51233:AF016266  
R-NT2RP4000051//ESTs, Weakly similar to protein B [H.sapiens]//8.3e-98:462:99//Hs.10114:AI345945  
R-NT2RP4000078//ESTs//0.00068:367:60//Hs.106090:AA457030  
R-NT2RP4000102//ESTs//9.7e-50:256:97//Hs.24266:R28287  
R-NT2RP4000109//Homo sapiens mRNA for MEGF5, partial cds//1.1e-107:536:96//Hs.57929:AB011538  
25 R-NT2RP4000129//Homo sapiens mRNA for KIAA0483 protein, partial cds//3.5e-112:554:97//Hs.64691:  
AB007952  
R-NT2RP4000147//ESTs//3.9e-11:122:80//Hs.25584:AA632014  
R-NT2RP4000150//EST//4.4e-84:510:88//Hs.144238:W52294  
R-NT2RP4000151//ESTs, Weakly similar to HYPOTHETICAL 31.0 KD PROTEIN R107.2 IN CHROMOSOME III  
30 [C.elegans]//5.7e-93:515:92//Hs.8083:AA521436  
R-NT2RP4000159//ESTs//0.0019:209:65//Hs.161816:AA400295  
R-NT2RP4000167//ESTs//2.1e-113:549:97//Hs.109441:N66569  
R-NT2RP4000185//ESTs//0.65:232:59//Hs.144445:AA807257  
R-NT2RP4000210//Homo sapiens mRNA for KIAA0700 protein, partial cds//1.5e-100:505:96//Hs.13999:  
35 AB014600  
R-NT2RP4000212//ESTs//8.5e-14:169:75//Hs.8520:AA081788  
R-NT2RP4000214//Human mRNA for KIAA0392 gene, partial cds//6.2e-43:272:90//Hs.40100:AB002390  
R-NT2RP4000218//ESTs//6.1e-10:335:64//Hs.105658:AA978185  
R-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP) //2.9e-70:354:96//Hs.155481:  
40 AJ006470  
R-NT2RP4000246//ESTs//7.1e-26:154:94//Hs.14838:AA502757  
R-NT2RP4000259//Homo sapiens clone 683 unknown mRNA, complete sequence//9.3e-79:379:99//Hs.43728:  
AF091092  
R-NT2RP4000263  
45 R-nnnnnnnnnnnn//ESTs, Weakly similar to similar to Achlya ambisexualis antheridiol steroid receptor [C.elegans]  
//4.7e-104:525:96//Hs.152069:AA548972  
R-NT2RP4000312//ESTs//8.2e-66:319:99//Hs.35091:AI271631  
R-NT2RP4000321//Homo sapiens clone 24453 mRNA sequence//1.3e-109:513:99//Hs.13410:AF070524  
R-NT2RP4000323//ESTs//7.7e-109:534:97//Hs.34790:AA192760  
50 R-NT2RP4000355//ESTs//3.1e-44:320:83//Hs.141323:N80390  
R-NT2RP4000360//Homo sapiens mRNA for KIAA0738 protein, complete cds//7.6e-111:520:99//Hs.107479:  
AB018281  
R-NT2RP4000367//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds//2.8e-  
110:527:98//Hs.31323:AF044195  
55 R-NT2RP4000370//ESTs//8.9e-32:166:98//Hs.70488:AI301130  
R-NT2RP4000376//ESTs//6.8e-99:465:99//Hs.27182:AA604498  
R-NT2RP4000381//ESTs//3.0e-50:280:93//Hs.8395:W27376  
R-NT2RP4000415//ESTs, Weakly similar to coded for by C. elegans cDNA yk30b3.5 [C.elegans]//3.9e-87:499:

	91//Hs.26156:AA630975
	R-NT2RP4000417//ESTs, Moderately similar to HYPOTHETICAL 91.2 KD PROTEIN IN RPS7A-SCH9 INTERGENIC REGION [Saccharomyces cerevisiae]//8.9e-95:468:96//Hs.93871:AI191318
5	R-NT2RP4000424//ESTs//3.7e-98:473:98//Hs.24945:AI189011
	R-NT2RP4000448//ESTs//2.6e-79:446:91//Hs.25159:R60955
	R-NT2RP4000449//ESTs//3.6e-98:468:98//Hs.31176:AI037953
10	R-NT2RP4000455//Homo sapiens N-methyl-D-aspartate receptor 2D subunit precursor (NMDAR2D) mRNA, complete cds//0.35:153:63//Hs.113286:U77783
	R-nnnnnnnnnnnn//ESTs//4.5e-89:455:96//Hs.62638:AA127740
15	R-NT2RP4000480//ESTs//4.9e-92:431:99//Hs.121072:AI204167
	R-nnnnnnnnnnnn
	R-NT2RP4000500//ESTs, Weakly similar to HYPOTHETICAL 83.6 KD PROTEIN R05D3.2 IN CHROMOSOME III [C.elegans]//1.2e-40:125:97//Hs.56124:AI424792
20	R-NT2RP4000515//EST//6.7e-30:183:90//Hs.150710:AI122713
	R-NT2RP4000517//Aldehyde dehydrogenase 7//7.5e-28:183:76//Hs.83155:U10868
	R-NT2RP4000518//EST//0.091:178:58//Hs.133031:AI049874
25	R-NT2RP4000519
	R-NT2RP4000524//ESTS, Highly similar to rsec8 [R.norvegicus]//3.4e-93:496:93//Hs.107394:H07126
	R-NT2RP4000528//EST//0.84:130:66//Hs.140208:AA702213
30	R-NT2RP4000541//EST//5.2e-63:337:94//Hs.156337:AI337328
	R-NT2RP4000556//ESTs, Highly similar to 60S RIBOSOMAL PROTEIN L11 [R.norvegicus]//8.2e-92:448:98//Hs.25597:H93026
	R-NT2RP4000588//ESTs//3.8e-94:445:98//Hs.44077:N28840
35	R-NT2RP4000614//ESTs//6.5e-18:159:83//Hs.24549:N57263
	R-NT2RP4000638//ESTs//2.5e-46:296:87//Hs.132722:AA618531
	R-NT2RP4000648//ESTs//2.6e-103:559:93//Hs.23794:W80393
40	R-NT2RP4000657//ESTs//1.0:189:60//Hs.87073:AA972704
	R-NT2RP4000704//ESTs//2.8e-101:509:96//Hs.84824:AA935651
	R-NT2RP4000724//ESTS//1.5e-83:442:94//Hs.142114:AA205615
45	R-NT2RP4000728//ESTs//0.84:61:75//Hs.145334:AI251399
	R-NT2RP4000739//ESTs//8.8e-80:418:94//Hs.42959:N21211
	R-NT2RP4000781//ESTs//1.4e-79:376:99//Hs.135458:AI081312
50	R-NT2RP4000817//Homo sapiens mRNA for KIAA0470 protein, complete cds//3.1e-106:550:94//Hs.25132:AB007939
	R-NT2RP4000833//ESTs//5.8e-46:309:85//Hs.163979:AA828834
	R-NT2RP4000837//ESTs//1.7e-112:539:97//Hs.97718:AI334028
	R-NT2RP4000855//ESTs//1.1e-95:486:95//Hs.5345:AA988104
	R-NT2RP4000865//EST//6.2e-68:412:89//Hs.142196:AA258356
55	R-NT2RP4000878//ESTs//1.9e-80:417:95//Hs.104716:AI023185
	R-NT2RP4000879//ESTs//1.8e-42:211:99//Hs.89991:AI374617
	R-nnnnnnnnnnnn//ESTs//1.2e-89:453:97//Hs.100182:N92594
	R-nnnnnnnnnnnn//EST//9.4e-06:197:63//Hs.145970:AI277106
	R-NT2RP4000925//ESTs, Weakly similar to KIAA0405 [H.sapiens]//5.9e-17:134:85//Hs.14146:W92235
	R-nnnnnnnnnnnn//ESTs//4.3e-14:84:100//Hs.155360:AA984683
60	R-NT2RP4000928//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds//8.2e-108:548:95//Hs.24812:AF069532
	R-NT2RP4000929//ESTs//1.3e-119:567:98//Hs.62717:AA044905
	R-NT2RP4000955//ESTs//3.5e-10:1 19:78//Hs.42946:N21111
65	R-NT2RP4000973//ESTs//2.8e-05:93:69//Hs.155126:AA563986
	R-NT2RP4000975//ESTs//4.4e-58:324:95//Hs.126070:AA045179
	R-NT2RP4000979//ESTs//3.5e-42:468:73//Hs.106210:AI193017
70	R-NT2RP4000984//Homo sapiens clone 23770 mRNA sequence//8.7e-120:570:98//Hs.12457:AF052123
	R-NT2RP4000989//ESTs//1.3e-122:581:98//Hs.10499:AA528018
	R-NT2RP4000996//ESTs//9.2e-113:579:94//Hs.23762:N26620
75	R-NT2RP4000997//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//1.1e-28:439:68//Hs.129735:AF010144
	R-NT2RP4001004//ESTs//3.6e-78:389:98//Hs.156290:AI016769
	R-NT2RP4001006//ESTS, Moderately similar to ORF2: function unknown [H.sapiens]//6.6e-124:574:99//Hs.

47393:AA218858  
R-NT2RP4001010//EST//2.8e-31:194:90//Hs.161186:AI418635  
R-NT2RP4001029//ESTs//4.4e-111:523:99//Hs.28423:AI336292  
R-NT2RP4001041//ESTs, Highly similar to LEUCYL-TRNA SYNTHETASE, CYTOPLASMIC [Saccharomyces cerevisiae]//3.6e-114:569:96//Hs.6762:AA08424  
R-NT2RP4001057//Homo sapiens KIAA0399 mRNA, partial cds//2.0e-51:282:94//Hs.100955:AB007859  
R-NT2RP4001064//ESTs, Weakly similar to protein B [H.sapiens]//2.1e-103:485:99//Hs.10114:AD45945  
R-NT2RP4001078  
R-NT2RP4001079//Homo sapiens mRNA for putative Ca<sup>2+</sup>-transporting ATPase, partial//1.7e-119:569:98//Hs.106778:AJ010953  
R-NT2RP4001080//ESTs//7.6e-10:65:100//Hs.131694:AA927668  
R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0592 protein, partial cds//5.9e-121:548:95//Hs.13273:AB011164  
R-NT2RP4001095//ESTs//1.5e-113:563:96//Hs.118732:AI344055  
R-NT2RP4001100//ESTs//2.0e-46:413:79//Hs.146314:R99617  
R-NT2RP4001117//EST//7.4e-51:294:92//Hs.7260:T23737  
R-NT2RP4001122//ESTs//5.4e-109:509:99//Hs.16390:AI052357  
R-NT2RP4001126//EST//0.97:169:61//Hs.148107:AA693476  
R-NT2RP4001138//ESTs//3.0e-110:543:97//Hs.57655:AI056890  
R-NT2RP4001143//ESTs, Highly similar to HYPOTHETICAL 52.9 KD PROTEIN IN SAP155-YMR31 INTERGENIC REGION [Saccharomyces cerevisiae]//5.4e-113:573:96//Hs.5249:U55977  
R-NT2RP4001148//ESTs//3.1e-103:490:98//Hs.121282:AI091453  
R-NT2RP4001149//EST//1.7e-50:281:93//Hs.101727:H16171  
R-NT2RP4001150//ESTS//1.9e-90:422:100//Hs.125490:AI138884  
R-NT2RP4001159  
R-NT2RP4001174//ESTs//2.5e-110:526:98//Hs.116555:AA639278  
R-nnnnnnnnnnnn//ESTs//1.1 e-25:140:97//Hs.83756:AI002822  
R-NT2RP4001207//ESTs//4.4e-70:432:89//Hs.13109:AA192514  
R-NT2RP4001210//ESTs//1.4e-108:509:99//Hs.27021:AI359495  
R-NT2RP4001213//ESTs, Highly similar to ZINC FINGER PROTEIN 8 [Homo sapiens]//4.4e-123:624:95//Hs.22744:AI379892  
R-NT2RP4001219//ESTs//0.0043:142:65//Hs.6733:AI160750  
R-NT2RP4001228//ESTs//4.9e-101:482:98//Hs.62684:AA806103  
R-NT2RP4001235//ESTs//3.7e-105:571:93//Hs.37706:AA005120  
R-NT2RP4001256//ESTs//1.1e-12:189:74//Hs.20621:W28255  
R-NT2RP4001260//EST//6.9e-05:313:61//Hs.116438:AA648430  
R-NT2RP4001274//EST//0.0020:246:63//Hs.149955:AI289933  
R-nnnnnnnnnnnn//ESTs//2.9e-34:213:91//Hs.43100:AA186588  
R-NT2RP4001313  
R-NT2RP4001315//EST//6.1e-38:217:93//Hs.97832:AA400892  
R-NT2RP4001339//ESTs//3.8e-91:430:99//Hs.34840:AI279612  
R-NT2RP4001345//ESTs//5.3e-89:443:96//Hs.6770:AA972732  
R-NT2RP4001351//ESTs//6.0e-78:394:97//Hs.102796:N70837  
R-NT2RP4001353//ESTs//4.8e-06:90:82//Hs.7778:AA195616  
R-NT2RP4001372  
R-NT2RP4001373//ESTs, Weakly similar to HYPOTHETICAL 48.8 KD PROTEIN IN TRK2-MRS4 INTERGENIC REGION [Saccharomyces cerevisiae]//1.7e-108:546:96//Hs.32271:AA203680  
R-NT2RP4001375//ESTs//2.4e-19:155:87//Hs.62119:AA043299  
R-NT2RP4001379//EST//4.4e-29:288:72//Hs.157848:AI362501  
R-NT2RP4001389//ESTs, Highly similar to HYPOTHETICAL 51.6 KD PROTEIN IN PAP1-MRPL13 INTERGENIC REGION [Saccharomyces cerevisiae]//3.8e-79:438:93//HS.21938:W81045  
R-NT2RP4001407//ESTs//8.3e-112:541:97//Hs.22587:AA743132  
R-NT2RP4001414//ESTs//8.6e-18:117:90//Hs.90789:W27649  
R-NT2RP4001433//ESTs, Moderately similar to PROHIBITIN [H.sapiens]//1.6e-102:498:97//Hs.62386:AA512948  
R-NT2RP4001442//ESTs//8.8e-104:489:99//Hs.101619:AI339433  
R-NT2RP4001447  
R-NT2RP4001474  
R-NT2RP4001483//ESTs//2.1e-100:528:92//Hs.17860:AA706655  
R-NT2RP4001498//ESTs//1.1e-97:470:98//Hs.95744:AI392846

R-NT2RP4001502//ESTs//6.7e-73:382:96//Hs.11874:N93511  
R-NT2RP4001507//ESTs//2.6e-57:302:96//Hs.65328:AA625385  
R-NT2RP4001524//ESTs, Weakly similar to F13B12.1 [C.elegans]//2.9e-107:546:96//Hs.5570:AI377863  
R-NT2RP4001529//ESTs//3.3e-112:524:99//Hs.28423:AI336292  
5 R-NT2RP4001547//ESTs, Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 [Paramecium tetraurelia]//2.8e-120:566:98//Hs.108530:AA523928  
R-nnnnnnnnnnnnn//ESTs, Weakly similar to CELL DIVISION CONTROL PROTEIN 68 [S.cerevisiae]//1.4e-26:184:  
88//Hs.136189:AA133224  
R-NT2RP4001555//ESTs//1.1e-95:445:100//Hs.134403:AA677552  
10 R-NT2RP4001567//ESTs//2.8e-106:506:98//Hs.102708:AA292285  
R-NT2RP4001568//ESTs//6.4e-55:300:94//Hs.57442:N63437  
R-NT2RP4001571//ESTs//1.3e-114:556:97//Hs.30340:AA521251  
R-NT2RP4001574//ESTs//0.0035:120:67//Hs.96339:AA225906  
R-NT2RP4001575  
15 R-NT2RP4001592//ESTs, Weakly similar to ISOLEUCYL-TRNA SYNTHETASE, MITOCHONDRIAL[S.cerevisiae]  
//8.7e-112:557:97//Hs.7558:AA526812  
R-NT2RP4001610//ESTs//6.2e-77:382:96//Hs.21543:AA166776  
R-NT2RP4001614//ESTs//2.8e-117:565:98//Hs.9591:AA069657  
R-NT2RP4001634//ESTs//2.0e-39:213:96//Hs.32360:AA534737  
20 R-NT2RP4001638//Homo sapiens clone 23967 unknown mRNA, partial cds//1.7e-116:559:97//Hs.5332:  
AF007151  
R-NT2RP4001644//ESTs, Moderately similar to MNK1 [H.sapiens]//5.3e-36:192:97//Hs.5662:AA868361  
R-NT2RP4001656//ESTs, Highly similar to HYPOTHETICAL 108.5 KD PROTEIN R06F6.2 IN CHROMOSOME II  
[Caenorhabditis elegans]//1.1e-104:525:96//Hs.20472:W28734  
25 R-NT2RP4001677//ESTs//1.8e-106:522:97//Hs.106390:AA156805  
R-NT2RP4001696//Human chromosome 8 BAC clone CIT987SK-2A8 complete sequence//5.7e-118:583:96//Hs.  
15562:U96629  
R-NT2RP4001725//ESTs//2.0e-11:141:74//Hs.117589:N25941  
R-nnnnnnnnnnnnn//ESTs, Weakly similar to UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRE-  
30 CURSOR [D.melanogaster]//3.4e-73:362:97//Hs.152332:AI141922  
R-NT2RP4001739//ESTs//6.6e-59:340:91//Hs.122293:AA843692  
R-NT2RP4001753//Zinc finger protein 3 (A8-51)//5.6e-113:552:96//Hs.2481:X78926  
R-NT2RP4001760//ESTs//2.5e-94:453:98//Hs.122579:AA766315  
R-NT2RP4001790//ESTs, Weakly similar to ZINC FINGER PROTEIN 84 [H.sapiens]//2.0e-62:326:94//Hs.110839:  
35 W28098  
R-NT2RP4001803  
R-NT2RP4001822//ESTs//4.4e-98:526:92//Hs.96908:AI161133  
R-NT2RP4001823//ESTs//1.7e-72:357:97//Hs.144900:AI218434  
R-NT2RP4001828//ESTs//3.3e-101:536:92//Hs.18851:AA857826  
40 R-NT2RP4001838//ESTs//4.2e-58:344:90//Hs.48723:N66663  
R-NT2RP4001849//EST//0.24:105:71//Hs.136747:AA749210  
R-NT2RP4001889//Human mRNA for KIAA0118 gene, partial cds//3.4e-34:212:88//Hs.154326:D42087  
R-NT2RP4001893//ESTs//3.0e-58:321:95//Hs.158787:W79602  
R-NT2RP4001896//EST//3.8e-15:108:92//Hs.160835:AI345528  
45 R-NT2RP4001901//ESTs//1.2e-110:536:97//Hs.31443:AI018606  
R-NT2RP4001927//ESTs//2.1e-105:546:93//Hs.73291:AI417099  
R-NT2RP4001938//ESTs//2.8e-40:235:78//Hs.163641:R61848  
R-NT2RP4001946//ESTs//1.3e-29:175:93//Hs.43703:AA088436  
R-NT2RP4001950//ESTs//4.6e-95:458:98//Hs.150890:AI341793  
50 R-NT2RP4001953//Clathrin, light polypeptide (Lcb) //2.3e-62:310:82//Hs.73919:X81637  
R-NT2RP4001966//ESTs, Weakly similar to tenascin-like protein [D.melanogaster]//8.3e-87:457:94//Hs.41793:  
AA775879  
R-NT2RP4001975//ESTs//1.9e-52:281:94//Hs.7704:W58252  
R-NT2RP4002018  
55 R-NT2RP4002047//ESTs, Highly similar to GTP-BINDING PROTEIN LEPA [Pseudomonas fluorescens]//4.7e-09:  
90:86//Hs.41127:AA555184  
R-NT2RP4002052//ESTs//0.054:353:60//Hs.117510:AA903738  
R-NT2RP4002058//EST//7.8e-26:151:94//Hs.124617:AA855106

	R-NT2RP4002071//ESTs//6.9e-99:475:98//Hs.29216:AA916679
	R-NT2RP4002075//ESTs//0.67:121:65//Hs.153939:AI284198
	R-NT2RP4002078//ESTs, Highly similar to ZINC FINGER PROTEIN 35 [Homo sapiens]//1.6e-61:464:82//Hs.144228:N99507
5	R-nnnnnnnnnnnn//ESTs, Weakly similar to HYPOTHETICAL 139.1 KD PROTEIN C08B11.3 IN CHROMOSOME II [C.elegans]//2.3e-56:271:100//Hs.6185:AA428565
	R-NT2RP4002083//ESTs//2.0e-108:548:96//Hs.6120:W80407
	R-NT2RP4002408//ESTs//2.6e-77:391:96//Hs.14014:AA745592
10	R-NT2RP4002791//ESTs//7.9e-101:527:93//Hs.22394:N32555
	R-NT2RP4002888//ESTs, Highly similar to ENV POLYPROTEIN [Avian spleen necrosis virus]//1.9e-65:373:92//Hs.31532:H18272
	R-NT2RP4002905//ESTs//1.5e-107:517:98//Hs.40460:N36090
	R-OVARC1000001//Homo sapiens mRNA for KIAA0465 protein, partial cds//2.8e-115:605:94//Hs.108258:AB007934
15	R-OVARC1000004
	R-OVARC1000006//ESTs//1.5e-19:139:89//Hs.143034:AI126929
	R-OVARC1000013//ESTs//5.9e-98:531:93//Hs.16470:AA121635
	R-OVARC1000014//ESTs//0.24:243:60//Hs.19569:AA464273
20	R-OVARC1000017
	R-OVARC1000035//ESTs//0.035:252:63//Hs.134123:AI078286
	R-OVARC1000058//H.sapiens mRNA for translin associated protein X//3.8e-46:331:83//Hs.96247:X95073
	R-OVARC1000060//EST//2.8e-28:348:71//Hs.141728:W73041
	R-OVARC1000068//ESTs//3.0e-83:491:90//Hs.29397:N51367
25	R-OVARC1000071//ESTs//2.5e-60:321:96//Us.25010:R6787
	R-OVARC1000085//Proteasome component C5//8.6e-67:366:92//Hs.75748:AL031259
	R-nnnnnnnnnnnn//ESTs//1.0e-111:526:98//Hs.129020:AI380703
	R-OVARC1000091//ESTS, Weakly similar to HOST CELL FACTOR CI [H.sapiens]//3.9e-112:596:94//Hs.20597:W58370
30	R-OVARC1000092//ESTs//5.1e-18:144:82//Hs.109140:AI289942
	R-OVARC1000106
	R-OVARC1000113//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//8.3e-102:495:97//Hs.3688:AF069250
	R-OVARC1000114//H.sapiens mRNA for phosphoinositide 3-kinase//1.7e-45:489:74//Hs.101238:Y11312
35	R-OVARC1000133//EST//0.00028:284:61//Hs.30547:H05482
	R-OVARC1000145//EST//3.9e-40:201:99//Hs.156148:AI333214
	R-OVARC1000148//EST//0.79:150:62//Hs.100078:T05090
	R-OVARC1000151
	R-OVARC1000168//EST//1.7e-19:142:90//Hs.38441:H66023
40	R-OVARC1000191//EST//0.0072:292:63//Hs.132492:AA922629
	R-OVARC1000198//Homo sapiens LIM protein mRNA, complete cds//6.1e-44:339:81//Hs.154103:AF061258
	R-OVARC1000209//ESTs, Moderately similar to ZINC FINGER PROTEIN 93 [H.sapiens]//1.1e-32:196:92//Hs.64322:AA142864
	R-OVARC1000212//EST//0.20:178:61//Hs.133031:AI049874
45	R-OVARC1000240//ESTs//9.0e-64:314:98//Hs.42300:AA204958
	R-OVARC1000241//EST//0.00018:115:68//Hs.150728:AI123130
	R-OVARC1000288//ESTs, Highly similar to HYPOTHETICAL 54.2 KD PROTEIN IN CDC12-ORC6 INTERGENIC REGION [Saccharomyces cerevisiae]//3.3e-74:403:93//Hs.108117:AI097079
	R-OVARC1000302//EST//4.0e-14:102:90//Hs.136617:AA630476
50	R-OVARC1000304//ESTs, Highly similar to PUTATIVE GTP-BINDING PROTEIN MOV10 [Mus musculus]//2.9e-37:191:98//Hs.20725:AI027777
	R-OVARC1000309//ESTs//3.6e-66:348:94//Hs.9547:AA532449
	R-OVARC1000321//ESTs//3.6e-87:454:95//Hs.110445:AA044743
	R-OVARC1000326//ESTs, Moderately similar to lamina associated polypeptide 1C [R.norvegicus]//1.3e-98:488:96//Hs.125749:AI377682
55	R-OVARC1000335//ESTs//3.0e-115:565:97//Hs.54835:AI050863
	R-OVARC1000347//EST//0.0018:145:65//Hs.136945:AA765672
	R-OVARC1000384//ESTs//2.8e-38:253:89//Hs.15093:AA203423
	R-OVARC1000408//ESTs//2.6e-98:515:94//Hs.119808:C05928

R-OVARC1000411//ESTs//3.2e-82:395:98//Hs.104747:AA406219  
 R-OVARC1000414//Landsteiner-Wiener blood group glycoprotein//1.5e-27:211:79//Hs.108287:L27670  
 R-OVARC1000420//EST//2.8e-38:255:74//Hs.138525:R99237  
 R-OVARC1000427//EST//2.6e-58:302:96//Hs.122914:AA767034  
 5 R-OVARC1000431//ESTs//4.9e-108:551:96//Hs.11668:AI123426  
 R-OVARC1000437  
 R-OVARC1000440//ESTs//2.9e-91:456:96//Hs.93701:AI018671  
 R-OVARC1000442//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//4.3e-45:320:84//  
 Hs.73614:U83460  
 10 R-OVARC1000443//Homo sapiens mRNA for KIAA0683 protein, complete cds//3.6e-79:418:94//Hs.12334:  
 AB014583  
 R-OVARC1000461//ESTs//3.1e-62:342:93//Hs.23241:R46582  
 R-OVARC1000465//ESTs//1.7e-67:349:95//Hs.127238:AA477576  
 15 R-OVARC1000466//ESTs//1.9e-66:337:95//Hs.5212:AI421211  
 R-OVARC1000473//ESTs//5.4e-89:320:99//Hs.29173:AA134926  
 R-OVARC1000479//ESTs, Highly similar to TIP120 [R.norvegicus]//1.1e-102:514:96//Hs.11833:AI299947  
 R-OVARC1000486//ESTs//3.9e-78:405:95//Hs.98312:AA424983  
 R-OVARC1000496  
 R-OVARC1000520//ESTs//1.2e-20:145:88//Hs.87456:AA434484  
 20 R-OVARC1000526//Small inducible cytokine A5 (RANTES)//8.9e-47:217:87//Hs.155464:AF088219  
 R-OVARC1000533//ESTs, Moderately similar to integrase [H.sapiens]//8.5e-48:264:92//Hs.49860:AA702248  
 R-OVARC1000543//ESTs//5.7e-74:410:94//Hs.62817:AA047021  
 R-OVARC1000556//H.sapiens mRNA for ribosomal S6 kinase//9.5e-27:202:85//Hs.90859:X85106  
 R-OVARC1000557//EST//2.8e-18:169:79//Hs.149101:AI244285  
 25 R-OVARC1000564//EST//2.3e-34:199:92//Hs.146637:AI141587  
 R-OVARC1000573//Interleukin 10//4.7e-42:300:83//Hs.2180:M57627  
 R-OVARC1000578//Small inducible cytokine A5 (RANTES)//5.2e-58:392:84//Hs.155464:AF088219  
 R-OVARC1000588//EST//1.8e-41:174:85//Hs.163333:AA879053  
 R-OVARC1000605  
 30 R-OVARC1000622//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//6.4e-47:417:77//Hs.  
 159897:AB007970  
 R-OVARC1000640//H.sapiens mRNA for translin associated protein X//1.9e-28:366:72//Hs.96247:X95073  
 R-OVARC1000661//Homo sapiens mRNA for KIAA0590 protein, complete cds//5.1e-31:162:100//Hs.111862:  
 AB011162  
 35 R-OVARC1000678//EST//0.92:199:60//Hs.122025:AA778480  
 R-nnnnnnnnnnnn//ESTs//0.94:416:59//Hs.130754:AA279522  
 R-OVARC1000681//EST//9.2e-21:179:80//Hs.132635:AI032875  
 R-OVARC1000689//Homo sapiens ataxin-7 (SCA7) mRNA, complete cds//0.053:160:64//Hs.108447:AJ000517  
 R-OVARC1000700//Homo sapiens KIAA0441 mRNA, complete cds//7.1e-09:141:73//Hs.32511:AB007901  
 40 R-OVARC1000703//ESTs//1.7e-46:298:87//Hs.138856:H47461  
 R-OVARC1000730//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]//1.7e-17:137:86//Hs.7049:  
 AI141736  
 R-OVARC1000746//ESTs//0.16:366:60//Hs.136969:AA830918  
 R-OVARC1000769//ESTs, Weakly similar to eukaryotic initiation factor eIF-2 alpha kinase [D.melanogaster]//4.6e-  
 45 28:430:69//Hs.42457:AA523306  
 R-OVARC1000771//ESTs//1.3e-87:461:94//Hs.22399:AA531016  
 R-OVARC1000781//ESTs//8.3e-119:572:97//Hs.41972:AA626793  
 R-OVARC1000787//ESTs//7.4e-18:115:93//Hs.164036:AA845659  
 R-OVARC1000800//MITOCHONDRIAL STRESS-70 PROTEIN PRECURSOR//4.9e-19:119:95//Hs.3069:L11066  
 50 R-OVARC1000802//ESTs//2.2e-41:383:78//Hs.161228:AI419764  
 R-OVARC1000834//Homo sapiens mRNA for atopy related autoantigen CALC//1.2e-106:536:95//Hs.61628:  
 Y17711  
 R-OVARC1000846//Clathrin, light polypeptide (Lcb)//1.6e-66:282:87//Hs.73919:X81637  
 R-OVARC1000850//Homo sapiens PB39 mRNA, complete cds//1.2e-115:579:96//Hs.18910:AF045584  
 55 R-OVARC1000862//EST//4.3e-14:129:81//Hs.150663:AA923096  
 R-OVARC1000876//ESTs//1.0e-115:573:96//Hs.87287:AI150674  
 R-OVARC1000883//ESTs//3.5e-109:523:98//Hs.28423:AI336292  
 R-OVARC1000885//ESTs, Highly similar to HYPOTHETICAL OXIDOREDUCTASE IN ROCC-PTA INTERGENIC

REGION [Bacillus subtilis]//7.9e-98:525:93//Hs.10366:W21953  
 R-OVARC1000886//ESTs//8.2e-79:417:94//Hs.7729:AA830777  
 R-OVARC1000891//ESTs//6.8e-75:401:94//Hs.5833:H15401  
 R-OVARC1000897//ESTs//3.5e-91:440:98//Hs.125264:AA873350  
 5 R-OVARC1000912  
 R-OVARC1000915//ESTs//1.0e-45:328:82//Hs.163980:AA715814  
 R-OVARC1000924//ESTs//1.0e-100:501:96//Hs.30204:AA497127  
 R-OVARC1000936//EST//3.0e-74:367:98//Hs.145098:AA421696  
 R-OVARC1000937//EST//1.1e-53:290:95//Hs.162846:AA631215  
 10 R-OVARC1000945//ESTs//4.9e-51:301:89//Hs.20100:W25794  
 R-OVARC1000948//ESTs//3.7e-67:332:98//Hs.112570:AA621971  
 R-OVARC1000959//Small inducible cytokine A5 (RANTES)//7.2e-44:283:86//Hs.155464:AF088219  
 R-OVARC1000960//Homo sapiens KIAA0395 mRNA, partial cds//1.1e-41:348:80//Hs.43681:AL022394  
 R-OVARC1000971//EST//6.2e-05:126:70//Hs.160491:AI254909  
 15 R-OVARC1000984//ESTS, Weakly similar to No definition line found [C.elegans]//3.5e-68:346:96//Hs.25544:  
 AA532784  
 R-OVARC1000996//EST//0.12:92:71//Hs.117141:AA678811  
 R-OVARC1000999//Homo sapiens KIAA0414 mRNA, partial cds//1.5e-44:513:73//Hs.127649:AB007874  
 R-OVARC1001000//ESTs//1.8e-22:198:80//Hs.140608:N53448  
 20 R-OVARC1001004//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//1.7e-28:181:77//Hs.139107:K00629  
 R-OVARC1001010//EST//2.1e-09:92:85//Hs.147893:AI223270  
 R-OVARC1001011//EST//2.4e-14:200:75//Hs.149290:AI248117  
 R-OVARC1001032//EST//2.7e-29:304:73//Hs.141733:W80630  
 R-OVARC1001034//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//2.1e-09:  
 25 137:74//Hs.77579:AF013263  
 R-OVARC1001038//Homo sapiens TRIAD1 type I mRNA, complete cds//4.1e-101:501:96//Hs.9899:AF099149  
 R-OVARC1001040//ESTs//2.9e-87:415:99//Hs.132812:AI032046  
 R-OVARC1001044//ESTs//1.1e-83:432:96//Hs.55043:N94384  
 R-OVARC1001051//60S RIBOSOMAL PROTEIN L41//1.2e-16:124:88//Hs.108124:Z12962  
 30 R-OVARC1001055//ESTs//2.4e-23:238:76//Hs.141421:H99231  
 R-OVARC1001062//ESTs//3.4e-92:469:96//Hs.34658:N98652  
 R-OVARC1001068//Homo sapiens Era GTPase A protein (HERA-A) mRNA, partial cds//7.3e-97:463:98//Hs.3426:  
 AF082657  
 R-OVARC1001072//ESTs//1.3e-34:227:89//Hs.126704:W95844  
 35 R-OVARC1001074  
 R-OVARC1001085//Human T-cell leukemia virus enhancer factor//1.0:94:69//Hs.103126:U57029  
 R-OVARC1001092//Homo sapiens mRNA for JM5 protein, complete CDS (clone IMAGE 53337,  
 LLNLc110F1857Q7 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin))//1.4e-96:325:98//Hs.21753:AJ005897  
 R-OVARC1001113//Homo sapiens diaphanous 1 (HDIA1) mRNA, complete cds//3.3e-75:386:95//Hs.26584:  
 40 AF051782  
 R-OVARC1001117//Human G protein-coupled receptor (STRL22) mRNA, complete cds//3.9e-37:283:84//Hs.  
 46468:U45984  
 R-OVARC1001118//ESTs//5.3e-99:485:97//Hs.130815:AA936548  
 R-OVARC1001129//ESTs//9.8e-66:351:95//Hs.18616:T99312  
 45 R-OVARC1001161//ESTs, Moderately similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H.sapiens]//2.2e-  
 66:346:95//Hs.53263:AA173226  
 R-OVARC1001162//EST//1.5e-44:376:80//Hs.161917:AA483223  
 R-OVARC1001167//ESTs//4.7e-110:548:96//Hs.35254:AI133727  
 R-OVARC1001169//ESTs//0.22:152:68//Hs.149424:AI274200  
 50 R-OVARC1001170//Small inducible cytokine A5 (RANTES)//1.8e-42:305:84//Hs.155464:AF088219  
 R-OVARC1001173//EST//2.5e-35:182:84//Hs.161917:AA483223  
 R-OVARC1001180//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//6.6e-64:247:  
 80//Hs.97203:U83171  
 R-OVARC1001188//ESTs//4.1e-18:296:69//Hs.139197:AA228343  
 55 R-OVARC1001200//ESTs//2.0e-28:207:85//Hs.35121:AA877826  
 R-OVARC1001232//ESTs//3.2e-61:358:91//Hs.6449:W95025  
 R-OVARC1001240//ESTs//6.7e-45:316:85//Hs.121675:AA629668  
 R-OVARC1001243//ESTs//2.3e-86:409:99//Hs.163091:AA742361

R-OVARC1001261//ESTs//0.63:125:64//Hs.155743:AI344166  
R-OVARC1001268//ESTs//8.1e-20:113:98//Hs.109477:AA477929  
R-OVARC1001270//ESTs//1.5e-107:530:97//Hs.62905:AA460708  
R-OVARC1001271//ESTs//4.5e-36:401:72//Hs.20190:AA525532  
5 R-OVARC1001282//EST//4.0e-91:428:99//Hs.145599:AI263113  
R-OVARC1001296//ESTs//2.6e-63:301:100//Hs.125753:AA740885  
R-nnnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0518 protein, partial cds//3.8e-70:334:100//Hs.23763:  
AB011090  
R-OVARC1001329//Clathrin, light polypeptide (Lcb)//1.3e-68:304:83//Hs.73919:X81637  
10 R-OVARC1001330//Proline arginine-rich end leucine-rich repeat protein//1.0:147:63//Hs.76494:U41344  
R-OVARC1001339//Small inducible cytokine A5 (RANTES)//5.0e-48:452:76//Hs.155464:AF088219  
R-OVARC1001341//ESTs, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//6.9e-  
85:464:93//Hs.23651:AA650356  
R-OVARC1001342//40S RIBOSOMAL PROTEIN S8//4.9e-110:568:95//Hs.118690:X67247  
15 R-OVARC1001344//EST//3.6e-44:341:81//Hs.162197:AA535216  
R-OVARC1001357//TUMOR-ASSOCIATED ANTIGEN L6//9.8e-44:250:93//Hs.3337:M90657  
R-OVARC1001360//ESTs//5.2e-110:534:98//Hs.24743:AA843844  
R-OVARC1001369//ESTs//1.7e-98:478:97//Hs.7729:AA830777  
R-OVARC1001372//ESTs//2.6e-97:456:99//Hs.153648:AI341415  
20 R-OVARC1001376//Homo sapiens mRNA for KIAA0575 protein, complete cds//1.1e-53:344:72//Hs.153468:  
AB011147  
R-OVARC1001381//ESTs//5.1e-19:200:66//Hs.114031:AA700958  
R-OVARC1001391  
R-nnnnnnnnnnnn//ESTs//0.003 9:48:95//Hs.117964:N20913  
25 R-OVARC1001417//Homo sapiens EXLM1 mRNA, complete cds//3.2e-111:561:95//Hs.21586:AB006651  
R-OVARC1001419  
R-OVARC1001425//EST//5.7e-20:395:66//Hs.159707:AI393136  
R-OVARC1001436//ESTs//9.6e-90:427:99//Hs.6982:AA622427  
R-OVARC1001442//ESTs//1.1e-66:317:100//Hs.18437:AI206345  
30 R-OVARC1001453//ESTs//2.0e-20:163:84//Hs.133503:AA628592  
R-OVARC1001476//EST//0.23:125:66//Hs.71444:AA131700  
R-OVARC1001480//ESTs//3.1e-56:181:97//Hs.40109:AA928694  
R-OVARC1001489//ESTs//1.0:297:58//Hs.86723:AA393089  
R-OVARC1001496//Homo sapiens C-terminal binding protein 2 mRNA, complete cds//3.0e-117:585:96//Hs.6534:  
35 AF016507  
R-OVARC1001506//Small inducible cytokine A5 (RANTES)//1.8e-48:283:90//Hs.155464:AF088219  
R-OVARC1001525//EST//0.80:170:60//Hs.157398:AI364539  
R-OVARC1001542//Homo sapiens hJTB mRNA, complete cds//1.6e-111:566:95//Hs.6396:AB016492  
R-OVARC1001547//ESTs//5.7e-105:564:93//Hs.68835:AA088388  
40 R-OVARC1001577//Homo sapiens SRp46 splicing factor retropseudogene mRNA7//4.4e-20:150:89//Hs.155160:  
AF031166  
R-OVARC1001600//Human mRNA for KIAA0118 gene, partial cds//8.6e-21:282:72//Hs.154326:D42087  
R-OVARC1001610//ESTs//4.6e-108:555:95//Hs.44295:N32019  
R-OVARC1001611//ESTs//0.0021:117:71//Hs.135568:AA972965  
45 R-OVARC1001615//Homo sapiens KIAA0409 mRNA, partial cds//9.2e-19:114:78//Hs.5158:AB007869  
R-OVARC1001668//ESTs//1.0:127:69//Hs.153290:AI022659  
R-OVARC1001702//ESTs//4.8e-44:225:97//Hs.96855:AA346854  
R-OVARC1001703//ESTs//2.3e-89:426:99//Hs.27099:W60080  
R-OVARC1001711//ESTs//1.9e-57:251:99//Hs.9732:AA527784  
50 R-OVARC1001726//ESTs, Highly similar to APICAL PROTEIN [Xenopus laevis]//1.2e-27:236:81//Hs.15485:  
AA046954  
R-OVARC1001731//Tropomyosin4(fibroblast)//7.9e-74:422:90//Hs.102824:X05276  
R-OVARC1001745//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//1.7e-62:300:83//Hs.144563:  
AF057280  
55 R-nnnnnnnnnnnnnn//ESTs, Weakly similar to N-TERMINAL ACETYLTRANSFERASE 1 [S.cerevisiae]//6.8e-100:  
540:92//Hs.117741:AA903456  
R-OVARC1001766//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds//  
1.1e-109:567:94//Hs.155377:U97670

R-nnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0675 protein, complete cds//2.0e-109:529:97//Hs.15869:  
AB014575  
R-OVARC1001768//ESTs//3.5e-59:327:94//Hs.107923:H66127  
R-OVARC1001791//ESTs//1.3e-111:565:96//Hs.6107:AA160604  
5 R-OVARC1001795//ESTs//2.8e-97:526:93//Hs.72158:AA156978  
R-OVARC1001802//Homo sapiens DEC-205 mRNA, complete cds//4.8e-36:276:81//Hs.153563:AF011333  
R-OVARC1001805//ESTs//4.1e-78:375:98//Hs.126902:AI374688  
R-OVARC1001812//EST//4.8e-45:349:80//Hs.162677:AA604831  
R-OVARC1001813//Homo sapiens mRNA for KIAA0538 protein, partial cds//2.1e-15:519:63//Hs.25639:AB011110  
10 R-OVARC1001820//ESTs//9.5e-50:314:80//Hs.140491:W52705  
R-OVARC1001828//ESTs//0.11:186:63//Hs.29055:AI374621  
R-OVARC1001846//ESTs//0.34:134:66//Hs.152992:AI242160  
R-OVARC1001861//ESTs//2.3e-19:120:92//Hs.42225:N31809  
15 R-OVARC1001873//Homo sapiens clones 24718 and 24825 mRNA sequence//1.9e-105:571:91//Hs.25300:  
AF070611  
R-OVARC1001879//EST//1.3e-24:185:85//Hs.136617:AA630476  
R-OVARC1001880//Homo sapiens mRNA for KIAA0575 protein, complete cds//2.2e-49:302:90//Hs.153468:  
AB011147  
R-OVARC1001883//ESTs//1.0e-51:295:93//Hs.164059:AA447310  
20 R-OVARC1001900//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds//  
1.6e-87:346:90//Hs.6216:AF061749  
R-OVARC1001901//ESTs//6.8e-24:132:98//Hs.130797:AA904435  
R-OVARC1001911//ESTs//1.1e-88:491:92//Hs.32343:W73855  
R-OVARC1001916//ESTs//7.9e-97:491:95//Hs.24989:H97842  
25 R-OVARC1001928  
R-OVARC1001942//ESTs, Weakly similar to N-TERMINAL ACETYLTRANSFERASE 1 [S.cerevisiae]//2.5e-39:  
253:88//Hs.117741:AA903456  
R-OVARC1001943//ESTs//9.3e-13:78:100//Hs.143680:W38637  
R-OVARC1001949//ESTs, Highly similar to ZINC FINGER PROTEIN 8 [Homo sapiens]//8.3e-96:498:94//Hs.  
30 22744:AI379892  
R-OVARC1001950//EST//1.3e-35:236:81//Hs.132635:AI032875  
R-OVARC1001987//ESTs//5.6e-94:514:92//Hs.21148:AI183729  
R-OVARC1001989//ESTs//9.7e-46:228:99//Hs.127046:AA935887  
R-OVARC1002044//ESTS//3.4e-45:303:85//Hs.132722:AA618531  
35 R-OVARC1002050//Homo sapiens mRNA for KIAA0465 protein, partial cds//4.4e-109:542:96//Hs.108258:  
AB007934  
R-OVARC1002066//ESTs//8.5e-97:455:99//Hs.135477:AI088556  
R-OVARC1002082//Homo sapiens mRNA for KIAA0772 protein, complete cds//8.1e-47:340:82//Hs.15519:  
AB018315  
40 R-OVARC1002107//ESTs//5.9e-103:498:98//Hs.157207:AA629860  
R-OVARC1002127//ESTs//3.0e-87:419:98//Hs.127833:AI347130  
R-OVARC1002138//ESTs, Weakly similar to HYPOTHETICAL 54.7 KD PROTEIN C07A9.1 IN CHROMOSOME  
III [Caenorhabditis elegans]//1.7e-102:485:98//Hs.137516:AA805691  
R-OVARC1002143//ESTs//1.3e-79:428:92//Hs.158126:W26825  
45 R-OVARC1002156//ESTs//1.6e-38:198:98//Hs.22957:AA478923  
R-OVARC1002158//ESTs//7.3e-81:412:96//Hs.12211:AA908631  
R-OVARC1002165//ESTs//1.8e-09:154:72//Hs.49354:AA424160  
R-OVARC1002182//ESTs//4.3e-80:465:91//Hs.77067:AA040478  
R-PLACE1000004//ESTs, Weakly similar to TEICOIC ACID BIOSYNTHESIS PROTEIN A [Bacillus subtilis]//  
50 7.5e-32:164:99//Hs.144194:AA706337  
R-PLACE1000005//EST//0.37:212:60//Hs.127020:AA934920  
R-PLACE1000007//Homo sapiens clone 24422 mRNA sequence//3.8e-16:100:97//Hs.109268:AF070557  
R-PLACE1000014//EST//9.6e-44:344:77//Hs.161917:AA483223  
R-PLACE1000031//ESTs//2.2e-32:374:70//Hs.117969:H94870  
55 R-PLACE1000040//ESTs//0.00017:316:59//Hs.23342:AI310440  
R-PLACE1000048//Human Line-1 repeat mRNA with 2 open reading frames//4.8e-79:519:86//Hs.23094:M19503  
R-PLACE100005011ESTs//9.7e-90:453:96//Hs.27410:N25612  
R-PLACE1000061//Ribosomal protein L37a//5.5e-22:126:97//Hs.1946:L06499

R-PLACE1000066//ESTs, Weakly similar to coded for by *C. elegans* cDNA yk10c10.3 [*C.elegans*]//1.4e-61:331:  
94//Hs.30026:AI356771

R-PLACE1000078//ESTs//2.6e-30:212:85//Hs.89312:AA167659

R-PLACE1000081  
5 R-PLACE1000094

R-PLACE1000133//ESTs//4.4e-87:448:94//Hs.93748:AA884505

R-PLACE1000142//ESTs, Weakly similar to enoyl-CoA hydratase [*H.sapiens*]//5.5e-103:538:94//Hs.9670:  
AA632135

R-PLACE1000184//*Homo sapiens* estrogen-related receptor gamma mRNA, complete cds//4.1e-114:594:94//Hs.  
10 151017:AF058291

R-PLACE1000185//ESTs, Weakly similar to No definition line found [*C.elegans*]//2.0e-19:114:95//Hs.7036:  
W22072

R-PLACE1000213//ESTs//9.4e-99:494:96//Hs.24398:AI262946

R-PLACE1000214//ESTs//5.3e-98:466:98//Hs.28661:AA805916  
15 R-PLACE1000236//Human BENE mRNA, partial cds//1.7e-19:162:84//Hs.85889:U17077

R-PLACE1000246//EST//0.026:134:66//Hs.135611:Z21545

R-PLACE1000292//ESTs//2.5e-80:418:96//Hs.138233:N57912

R-PLACE1000332//EST//1.7e-82:422:96//Hs.118637:T61940  
20 R-PLACE1000347//ESTs//8.5e-36:180:100//Hs.6377:AA632424

R-PLACE1000374//ESTs//2.8e-90:434:98//Hs.161785:AI423126

R-PLACE1000380//ESTs//1.0e-81:399:97//Hs.47105:AI334994

R-PLACE1000383//ESTs//3.7e-75:405:94//Hs.23200:AA203708

R-PLACE1000401//ESTs//1.4e-16:212:72//Hs.151665:AA020959  
25 R-PLACE1000406//ESTs//2.1e-51:259:97//Hs.129651:N53089

R-PLACE1000420//ESTs//7.7e-92:471:95//Hs.144407:AA737799

R-PLACE1000421//ESTs//2.9e-14:282:67//Hs.142068:AA176125

R-PLACE1000424//EST//2.9e-35:453:70//Hs.162404:AA573131

R-PLACE1000435//*Homo sapiens* protein phosphatase with EF-hands-2 long form (PPEF-2) mRNA, complete  
30 cds//1.6e-47:472:77//Hs.113259:AF023456

R-PLACE1000444//ESTs, Moderately similar to platelet glycoprotein IIb precursor [*H.sapiens*]//2.0e-58:410:81//  
Hs.97579:AA398118

R-PLACE1000453//ESTs//2.3e-85:442:95//Hs.9725:AA039793

R-PLACE1000481//ESTS, Weakly similar to Ndr protein kinase [*H.sapiens*]//3.2e-109:549:95//Hs.19074:U69566  
35 R-PLACE1000492//ESTs, Highly similar to vacuolar protein sorting homolog r-vps33b [*R.norvegicus*]//3.5e-83:  
435:94//Hs.26510:AA700425

R-PLACE1000540//ESTs//3.2e-58:281:99//Hs.118270:AA844729

R-PLACE1000547//*Homo sapiens* mRNA for KIAA0640 protein, partial cds//2.2e-32:208:88//Hs.153026:  
AB014540

R-PLACE1000562//ESTs, Weakly similar to HYPOTHETICAL 23.0 KD PROTEIN IN IXR1-TFA1 INTERGENIC  
40 REGION [*Saccharomyces cerevisiae*]//1.9e-26:220:81//Hs.163791:W25348

R-PLACE1000564//ESTs//1.1e-54:302:92//Hs.158520:AI380485

R-PLACE1000583//Human mRNA for KIAA0355 gene, complete cds//5.5e-43:404:75//Hs.153014:AB002353

R-nnnnnnnnnnnnnnnnnnn//Guanylate binding protein 1, interferon-inducible, 67kD//6.1e-79:542:82//Hs.62661:M55542  
45 R-PLACE1000596//ESTs//0.0028:364:59//Hs.106090:AA457030

R-PLACE1000599//Human mRNA for KIAA0118 gene, partial cds//4.3e-49:295:90//Hs.154326:D42087

R-PLACE1000610//ESTs//0.0010:104:74//Hs.17413:N45301

R-PLACE1000636//ESTs//1.8e-64:340:95//Hs.100895:AA479308

R-PLACE1000653//*Homo sapiens* N-acetylglucosamine-phosphate mutase mRNA, complete cds//5.3e-101:506:  
96//Hs.5819:AF102265  
50 R-PLACE1000656//*Homo sapiens* mRNA for JM4 protein, complete CDS (clone IMAGE 546750 and  
LLNLc110F1857Q7 (RZPD Berlin))//1.4e-102:559:92//Hs.29595:AJ005896

R-PLACE1000706//*Homo sapiens* transcription intermediary factor 1 (TIF1) mRNA, complete cds//2.8e-10:281:  
64//Hs.128763:AF009353

R-PLACE1000712//ESTs//7.8e-60:317:95//Hs.8245:AA115485  
55 R-PLACE1000716

R-PLACE1000748//ESTs//8.9e-87:466:93//Hs.25245:AA176701

R-PLACE1000749//EST//0.019:186:61//Hs.135443:AI077396

R-PLACE1000755//ESTs, Weakly similar to HYPOTHETICAL HELICASE K12H4.8 IN CHROMOSOME III [*C.el-*

egans]]//3.9e-40:224:94//Hs.87889:AA262008  
R-PLACE1000769//Homo sapiens clone 24566 mRNA sequence//6.5e-27:531:66//Hs.133342:AF070536  
R-PLACE1000785//Homo sapiens mRNA for KIAA0648 protein, partial cds//8.5e-103:513:96//Hs.31921:  
AB014548  
5 R-PLACE1000786//ESTs//5.2e-93:449:97//Hs.58389:W74482  
R-nnnnnnnnnnnn//H.sapiens mRNA for chemokine HCC-1//0.88:201:60//Hs.20144:AF088219  
R-PLACE1000798//ESTs//1.1e-97:508:94//Hs.139119:N32189  
R-PLACE1000841//ESTs, Highly similar to guanine nucleotide regulatory protein [H.sapiens]//7.7e-31:220:86//Hs.  
117576:R33135  
10 R-nnnnnnnnnnnn//ESTs//1.8e-87:459:94//Hs.43100:AA186588  
R-PLACE1000856//ESTs//0.0084:224:59//Hs.145906:AI275039  
R-PLACE1000863//ESTs, Highly similar to PUTATIVE 40S RIBOSOMAL PROTEIN YHR148W [Saccharomyces  
cerevisiae]//2.2e-92:467:95//Hs.6118.-AI141558  
R-PLACE1000909//ESTs//4.7e-89:435:97//Hs.95744:AI392846  
15 R-PLACE1000931//EST//1.9e-28:261:73//Hs.135545:AI097091  
R-PLACE1000948//ESTs//0.034:329:58//Hs.114851:AA608697  
R-PLACE1000972//EST//3.3e-24:264:74//Hs.130321:AI002941  
R-PLACE1000977//EST//0.085:153:65//Hs.131646:AI025689  
R-PLACE1000979  
20 R-PLACE1001000//ESTs//4.7e-56:284:96//Hs.117978:AA810725  
R-PLACE1001007//ESTs, Moderately similar to MNK1 [H.sapiens]//5.2e-63:343:93//Hs.5662:AA868361  
R-PLACE1001010//EST//0.96:53:71//Hs.96973:AA351146  
R-PLACE1001015//Oxytocin receptor//2.8e-25:308:71//Hs.2820:X64878  
R-PLACE1001024//ESTs//5.0e-12:79:96//Hs.97910:AA404736  
25 R-PLACE1001036//ESTs//4.0e-15:301:65//Hs.137947:AI025762  
R-PLACE1001062//ESTs//5.2e-15:199:73//Hs.138982:AA056120  
R-PLACE1001076//ESTs//3.9e-84:406:98//Hs.115455:AA678124  
R-PLACE1001088//ESTs//3.0e-106:518:97//Hs.158964:AA639580  
R-PLACE1001092//Homo sapiens SEC63 (SEC63) mRNA, complete cds//0.035:259:59//Hs.31575:AF100141  
30 R-PLACE1001104//ESTs//6.1e-115:582:95//Hs.10972:AA164268  
R-PLACE1001118//ESTs//6.9e-81:440:93//Hs.5383:AA913610  
R-PLACE1001136//ESTs//7.4e-41:168:83//Hs.95115:AA206594  
R-PLACE1001168//ESTs//3.9e-21:116:99//Hs.5897:AA148834  
R-PLACE1001171//ESTs, Highly similar to CYTOCHROME B-245 LIGHT CHAIN [H.sapiens]//0.91:77:71//Hs.  
35 115211:AA287527  
R-PLACE1001185//ESTs//1.5e-65:330:96//Hs.26368:AA789297  
R-PLACE1001238//ESTs, Moderately similar to RNA polymerase I associated factor [M.musculus]//1.9e-99:512:  
94//Hs.24884:AA176812  
R-PLACE1001241//ESTs//1.1e-81:446:93//Hs.42278:AI073464  
40 R-PLACE1001257//EST//6.4e-46:298:87//Hs.162404:AA573131  
R-PLACE1001272//ESTs//0.31:158:61//Hs.42960:N95371  
R-PLACE1001279//ESTs//1.8e-77:376:97//Hs.29276:AA427780  
R-PLACE1001280//ESTs//1.1e-30:134:89//Hs.163492:AI334460  
R-PLACE1001294//ESTs, Moderately similar to GAMETOGENESIS EXPRESSED PROTEIN GEG-154 [M.mus-  
45 culus]//2.7e-22:181:84//Hs.48320:AA149548  
R-PLACE1001304//ESTs, Weakly similar to ZINC FINGER PROTEIN 135 [H.sapiens]//4.2e-34:195:92//Hs.86276:  
W27601  
R-PLACE1001311//ESTs//9.1e-91:438:97//Hs.41055:AI339056  
R-PLACE1001323//Human transmembrane 4 superfamily protein (SAS) mRNA, complete cds//5.5e-44:215:86//  
50 Hs.50984:U01160  
R-PLACE1001351//ESTs//2.4e-101:494:97//Hs.23944:AI097077  
R-PLACE1001366//Small inducible cytokine A5 (RANTES)//8.7e-43:284:85//Hs.155464:AF088219  
R-PLACE1001377//Homo sapiens ADAM10 (ADAM10) mRNA, complete cds//2.3e-81:431:93//Hs.152005:  
AF009615  
55 R-PLACE1001383//Homo sapiens clone 24538 mRNA sequence//1.0e-36:192:97//Hs.12342:AF055030  
R-PLACE1001384//Homo sapiens multi PDZ domain protein MUPP1 (MUPP1) mRNA, complete cds//1.0e-86:  
456:94//Hs.21301:AF093419  
R-PLACE1001387//ESTs//6.0e-74:383:94//Hs.55016:AI298280

R-PLACE1001395//ESTs//2.3e-94:473:95//Hs.22394:N32555  
R-PLACE1001399//ESTs//2.6e-41:204:100//Hs.24462:N36348  
R-PLACE1001412//Homo sapiens clone 643 unknown mRNA, complete sequence//2.6e-45:242:95//Hs.110404:  
AF091087  
5 R-PLACE1001414//ESTs//0.0013:77:75//Hs.144614:AA291800  
R-PLACE1001440  
R-PLACE1001456//EST//0.76:120:62//Hs.34011:H48115.  
R-PLACE1001468//ESTs//4.0e-80:403:96//Hs.131832:AI017547  
R-PLACE1001484//ESTs//3.0e-16:201:72//Hs.153413:AI248625  
10 R-PLACE1001502//ESTs//8.1e-31:161:99//Hs.126264:AA455617  
R-PLACE1001503//ESTs//2.4e-37:176:81//Hs.141581:AA315361  
R-PLACE1001517//Homo sapiens hGAAI mRNA, complete cds//2.1e-57:339:90//Hs.4742:AB006969  
R-PLACE1001534//ESTs//3.6e-61:304:97//Hs.45207:AI042153  
15 R-PLACE1001545/TESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.6e-22:  
170:85//Hs.155456:AA707265  
R-PLACE1001551//ESTs//1.5e-39:202:98//Hs.139269:AA894431  
R-PLACE1001570//EST//1.1e-70:495:82//Hs.144234:W52249  
R-PLACE1001602//EST//0.33:297:57//Hs.149839:AI287601  
R-PLACE1001603//ESTs//2.0e-17:181:76//Hs.155334:AA827904  
20 R-PLACE1001610//EST//1.1e-86:442:95//Hs.112580:AA608683  
R-PLACE1001611//Homo sapiens histone macroH2A1.2 mRNA, complete cds//1.1e-42:217:97//Hs.75258:  
AF054174  
R-PLACE1001632//ESTs, Highly similar to ZINC FINGER PROTEIN 91 [Homo sapiens]//1.5e-78:458:91//Hs.  
114547:AA167095  
25 R-PLACE1001634//ESTs//0.0035:40:97//Hs.101577:AI168526  
R-PLACE1001640//ESTs//0.0028:377:57//Hs.131044:D61640  
R-PLACE10016727//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//0.98:  
141:62//Hs.153060:AA195804  
R-PLACE1001691//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//4.7e-  
30 113:545:97//Hs.3688:AF069250  
R-PLACE1001692//EST//3.0e-43:430:75//Hs.162975:AA679124  
R-PLACE1001705//ESTs//3.0e-81:418:94//Hs.22646:AI374903  
R-PLACE1001716//EST//0.76:150:62//Hs.128906:AA983667  
R-PLACE1001720//ESTs//2.4e-64:385:90//Hs.60455:AA010993  
35 R-PLACE1001729//ESTs//2.9e-84:418:96//Hs.134740:AA282171  
R-PLACE1001739//ESTs, Weakly similar to P68 PROTEIN [H.sapiens]//9.1e-32:206:89//Hs.6366:AA614113  
R-PLACE1001740//EST//6.5e-05:113:68//Hs.139949:AA644266  
R-PLACE1001745//ESTs//3.3e-92:473:95//Hs.104270:AA236479  
R-PLACE1001746//ESTs//8.8e-93:443:98//Hs.112198:AI423937  
40 R-PLACE1001748//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds//4.1e-93:540:89//Hs.4812:  
AF061243  
R-PLACE1001756//ESTs//0.17:157:66//Hs.141565:N64662  
R-PLACE1001761  
R-PLACE1001771//ESTs//0.92:165:62//Hs.473 87:N51980  
45 R-PLACE1001781//ESTs//5.7e-84:437:95//Hs.23363:AA081236  
R-PLACE1001799//EST//0.00039:126:65//Hs.123267:AA807352  
R-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA; partial cds//  
1.3e-93:463:95//Hs.40820:AF058953  
R-PLACE1001821//Small inducible cytokine A5 (RANTES)//2.7e-35:328:75//Hs.155464:AF088219  
50 R-PLACE1001845  
R-PLACE1001869//EST//1.0:207:62//Hs.137298:W32868  
R-PLACE1001897//ESTs//2.4e-23:219:80//Hs.7503:H50009  
R-PLACE1001912//ESTs//1.5e-32:162:78//Hs.136810:AA789098  
R-PLACE1001920//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cds//3.9e-74:363:97//Hs.17839:  
AF099936  
55 R-PLACE1001928//Homo sapiens mRNA for KIAA0623 protein, complete cds//0.85:130:66//Hs.151406:  
AB014523  
R-PLACE1001983//ESTs//2.8e-66:334:96//Hs.110155:AA007313

R-PLACE1001989//ESTs//1.3e-88:453:95//Hs.132717:AA171941  
R-PLACE1002046  
R-PLACE1002052//ESTs//1.7e-79:428:94//Hs.6737:N32595  
R-PLACE1002066//ESTs//2.8e-82:427:94//Hs.132972:AA543094  
5 R-PLACE1002072//ESTs//0.27:108:66//Hs.123163:AA809619  
R-PLACE1002073//EST//5.5e-70:369:95//Hs.132339:AI028552  
R-PLACE1002090//ESTs//6.3e-73:361:96//Hs.134469:AA731632  
R-PLACE1002115//ESTs//4.6e-34:233:88//Hs.163443:R23311  
R-PLACE1002119//ESTs//1.2e-88:444:96//Hs.15725:AA521293  
10 R-PLACE1002140//ESTs//6.6e-22:118:100//Hs.22793:W91937  
R-PLACE1002150//ESTs//4.0e-96:465:98//Hs.7312:AI167614  
R-PLACE1002157//EST, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG[H.sapiens]//3.6e-39:400:76//Hs.162172:AA534189  
R-PLACE1002163//ESTs//3.2e-83:428:95//Hs.137011:AI185965  
15 R-PLACE1002171//ESTs//5.3e-68:392:90//Hs.62273:AA143745  
R-PLACE1002205//ESTS//1.5e-39:211:95//Hs.28338:N48793  
R-PLACE1002213//ESTs//5.1e-38:290:83//Hs.146811:AA410788  
R-PLACE1002227//EST//1.3e-14:214:72//Hs.46979:N49892  
R-PLACE1002256//ESTs//2.4e-100:484:98//Hs.9343:AI004257  
20 R-PLACE1002259//Human Line-1 repeat mRNA with 2 open reading frames//5.8e-67:501:81//Hs.23094:M19503  
R-PLACE1002319//ESTs//1.4e-28:17 8:92//Hs.7353:AA209308  
R-PLACE1002342//Homo sapiens mRNA for KIAA0728 protein, partial cds//1.6e-95:501:93//Hs.18277:AB018271  
R-PLACE1002395//ESTs//3.6e-25:248:77//Hs.3853:AA034291  
R-PLACE1002399//ESTs//1.5e-27:238:78//Hs.13014:W26381  
25 R-PLACE1002433//ESTs//4.3e-108:511:98//Hs.98324:AA621959  
R-PLACE1002437//EST//1.2e-06:158:61//Hs.159833:T24110  
R-PLACE1002438//Sjogren syndrome antigen B (autoantigen La)//0.93:176:60//Hs.83715:X69804  
R-PLACE1002450//ESTs//1.5e-89:432:98//Hs.47371:AA136333  
R-PLACE1002465//ESTS//1.6e-92:488:93//Hs.78110:AA741320  
30 R-PLACE1002474//Human matrilin-2 precursor mRNA, partial cds//4.9e-23:166:85//Hs.19368:U69263  
R-PLACE1002477//ESTs//2.5e-62:305:98//Hs.88605:AA421132  
R-PLACE1002493//Homo sapiens signal transducing adaptor molecule 2A (STAM2) mRNA, complete cds//3.6e-55:307:91//Hs.17200:AF042273  
R-PLACE1002499//ESTs//7.4e-72:373:96//Hs.128221:AA972429  
35 R-PLACE1002500//Homo sapiens KIAA0409 mRNA, partial cds//1.2e-40:296:83//Hs.5158:AB007869  
R-PLACE1002514//ESTs, Weakly similar to !!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!! [H.sapiens]//6.4e-14:217:69//Hs.152230:AI140609  
R-PLACE1002529//Homo sapiens mRNA for KIAA0713 protein, partial cds//5.1e-88:582:85//Hs.88756:AB018256  
40 R-PLACE1002532//Homo sapiens BAC clone RG300E22 from 7q21-q31.1//2.7e-19:116:93//Hs.99348:AC004774  
R-PLACE1002537//ESTs//4.8e-93:440:99//Hs.164005:AA766491  
R-PLACE1002571//ESTs, Highly similar to ACTIN-LIKE PROTEIN 13E [Drosophila melanogaster]//1.3e-108:555:  
95//Hs.23259:AA532437  
R-PLACE1002578//EST//1.9e-40:337:81//Hs.162404:AA573131  
R-PLACE1002583//EST//1.2e-07:264:65//Hs.156414:AI339738  
45 R-PLACE1002591//ESTs//2.3e-67:372:94//Hs.143046:N73778  
R-PLACE1002598//ESTs, Highly similar to PROTEIN HI1715 [Haemophilus influenzae]//1.2e-44:228:97//Hs.  
7527:AA843208  
R-PLACE1002604//ESTs//3.3e-106:532:96//Hs.86828:AA632147  
R-PLACE1002625//EST//3.8e-13:173:74//Hs.138597:H77749  
50 R-PLACE1002665//Small inducible cytokine A4 (homologous to mouse Mip-1b)//1.0:189:58//Hs.75703:J04130  
R-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds//3.8e-79:  
390:97//Hs.124903:AF068180  
R-PLACE1002714//ESTs//8.2e-63:340:93//Hs.7973:H19830  
R-PLACE1002722//ESTs, Weakly similar to putative G-protein-coupled receptor [H.sapiens]//6.8e-75:445:90//Hs.  
55 29202:R71586  
R-PLACE1002768//ESTs//1.2e-70:359:95//Hs.132600:H12865  
R-PLACE1002772//ESTs//8.1e-49:362:82//Hs.141254:AI334099  
R-PLACE1002782//ESTs//2.4e-58:284:98//Hs.143545:AI149014

R-PLACE1002794//ESTs//5.4e-21:114:100//Hs.77365:W93593  
R-PLACE1002811//ESTs//6.7e-68:329:98//Hs.78026:AA456955  
R-PLACE1002815//ESTs//6.8e-103:537:93//Hs.5459:AI304392  
R-PLACE1002816//ESTs//3.9e-05:118:68//Hs.98641:AA429916  
5 R-PLACE1002834//ESTs, Highly similar to ZINC FINGER PROTEIN 91 [Homo sapiens]//2.1e-42:233:94//Hs.  
61518:AA167094  
R-PLACE1002839//ESTs//1.7e-10:292:64//Hs.93012:R96142  
R-PLACE1002851//ESTs//1.7e-73:381:95//Hs.135021:AI096756  
R-PLACE1002853//ESTs//1.2e-89:453:96//Hs.23630:N57539  
10 R-PLACE1002881//ESTs//1.1e-71:360:96//Hs.34392:AI066762  
R-PLACE1002908//EST//2.7e-31:177:94//Hs.147925:AI249332  
R-PLACE1002941//ESTs//4.0e-96:519:92//Hs.125139:AA523995  
R-PLACE1002962  
R-PLACE1002968//ESTs//4.7e-31:420:69//Hs.116518:AA653202  
15 R-PLACE1002991//ESTs//9.0e-81:418:95//Hs.132717:AA171941  
R-PLACE10029937//ESTs, Weakly similar to !!! ALU SUBFAMILY SB WARNING ENTRY !!!! [H.sapiens]//1.3e-86:  
502:89//Hs.32232:AA604268  
R-PLACE1002996//ESTs//1.9e-44:218:100//Hs.63657:AI144268  
R-PLACE1003025//ESTs//8.4e-104:517:96//Hs.10711:AI151499  
20 R-PLACE1003027//Human mRNA for KIAA0238 gene, partial cds//0.97:156r60//Hs.82042:D87075  
R-PLACE1003044//Human onconeural ventral antigen-1 (Nova-1) mRNA, complete cds//1.0:200:63//Hs.214:  
U04840  
R-PLACE1003092//ESTs//0.0046:267:60//Hs.133095:AA927777  
R-PLACE1003100//ESTs, Highly similar to NODULATION PROTEIN G [Rhizobium meliloti]//9.5e-94:491:93//Hs.  
25 6318:AI131178  
R-PLACE1003108//ESTs//0.00065:184:66//Hs.154366:AA527359  
R-PLACE1003136//Signal recognition particle 54 kD protein//0.057:317:59//Hs.49346:U51920  
R-PLACE1003145//ESTs//1.9e-98:534:92//Hs.61929:AA044757  
R-PLACE1003153//ESTs//5.8e-76:367:98//Hs.105196:AA483467  
30 R-PLACE1003174//ESTs//1.7e-44:226:98//Hs.59688:AA453924  
R-PLACE1003176  
R-PLACE1003190//ESTs//1.6e-74:356:99//Hs.121282:AI091453  
R-PLACE1003200//ESTs//4.6e-93:461:96//Hs.24321:AA971017  
R-PLACE1003205//ESTs//0.037:171:61//Hs.157077:H44802  
35 R-PLACE100323 8//ESTs, Weakly similar to KIAA0001 [H.sapiens]//2.5e-82:436:94//Hs.58561:W79123  
R-PLACE1003249//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//7.9e-44:313:84//  
Hs.73614:U83460  
R-PLACE1003256//EST//9.6e-46:284:88//Hs.162404:AA573131  
R-PLACE1003258//ESTs, Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//8.3e-102:  
40 551:92//Hs.52431:AA625326  
R-PLACE1003296//ESTs//1.9e-88:451:96//Hs.57749:W92986  
R-PLACE1003302//ESTs, Highly similar to ZINC FINGER PROTEIN 43 [Homo sapiens]//8.2e-93:458:96//Hs.  
29147:AA883993  
R-PLACE1003334//ESTs, Weakly similar to !!! ALU CLASS B WARNING ENTRY !!!! [H.sapiens]//3.3e-94:463:  
45 97//Hs.155050:AA908765  
R-PLACE1003342//ESTs//6.0e-88:447:96//Hs.107527:R66438  
R-PLACE1003343//EST//0.0087:412:58/Hs.159963:AA977701  
R-PLACE1003353//Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3) mRNA, complete  
cds//1.1e-99:469:98//Hs.6564:U92715  
50 R-PLACE1003361//ESTs//3.5e-64:332:95//Hs.163861:AI199636  
R-PLACE1003366//ESTs//1.0e-87:492:92//Hs.72222:AA158234  
R-PLACE1003369//ESTs, Weakly similar to ZK1058.4 [C.elegans]//3.5e-18:109:95//Hs.27670:AI051591  
R-PLACE1003373//Homo sapiens mRNA for KIAA0472 protein, partial cds//2.6e-54:279:80//Hs.6874:AB007941  
R-PLACE1003375//ESTs//1.7e-88:431:97//Hs.41327:AI039909  
55 R-PLACE1003383//ESTs//0.00084:177:64//Hs.120695:AI377755  
R-PLACE1003401//ESTs//1.1e-16:147:80//Hs.132187:AI039020  
R-PLACE1003420//ESTs//1.4e-93:481:94//Hs.122565:AI126840  
R-PLACE1003454//ESTs//4.0e-57:310:93//Hs.121688:AA743697

R-PLACE1003478//EST//1.0:162:63//Hs.147003:AI184671  
R-PLACE1003493//ESTs//1.2e-73:383:95//Hs.28852:R64270  
R-PLACE1003516//ESTs//3.2e-23:206:80//Hs.138632:H97952  
R-PLACE1003519//H.sapiens hnRNP-E1 mRNA//1.7e-22:236:79//Hs.2853:Z29505  
5 R-PLACE1003521//ESTs//5.8e-74:371:96//Hs.30818:AA194980  
R-PLACE1003528//ESTs//1.1e-40:219:82//Hs.138856:H47461  
R-PLACE1003537//ESTs, Weakly similar to multispanning membrane protein [H.sapiens]//7.4e-69:338:98//Hs.  
110439:N93209  
R-PLACE1003553//ESTs//2.2e-87:438:97//Hs.132022:AI040321  
10 R-PLACE1003566//ESTs//1.2e-62:298:92//Hs.30799:AI052591  
R-PLACE1003575//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//2.4e-22:145:80//Hs.  
92381:AB007956  
R-PLACE1003583//ESTs, Weakly similar to hypothetical L1 protein [H.sapiens]//1.5e-14:264:65//Hs.158253:  
R86178  
15 R-PLACE1003584  
R-PLACE1003592//ESTs//1.3e-15:213:69//Hs.139507:T77542  
R-PLACE1003593//ESTs, Highly similar to FRG1 gene product [H.sapiens]//5.8e-75:459:89//Hs.23884:AD77106  
R-PLACE1003596//ESTs//0.011:273:61//Hs.71719:AA142875  
R-PLACE1003602//Homo sapiens mRNA expressed in placenta//7.8e-97:576:88//Hs.56851:D83200  
20 R-PLACE1003605//ESTs//3.7e-86:407:99//Hs.136057:AA988299  
R-nnnnnnnnnnnnnnnnn//ESTs//1.0:78:71//Hs.101248:T26446  
R-PLACE1003618//ESTs//6.8e-30:281:79//Hs.114455:AA411943  
R-PLACE1003625//ESTs//7.2e-78:377:98//Hs.102708:AA292285  
R-PLACE1003638//ESTs//6.7e-38:274:82//Hs.138852:AA284247  
25 R-PLACE1003669//ESTs//9.7e-83:418:95//Hs.4842:AI342607  
R-PLACE1003704//ESTs//3.0e-13:99:89//Hs.81648:W26521  
R-PLACE1003709//ESTs//0.019:178:60//Hs.32100:N59866  
R-PLACE1003711//ESTs//0.99:126:63//Hs.47005:N98639  
R-PLACE1003723//ESTS//1.7e-89:448:96//Hs.157222:AA766987  
30 R-PLACE1003738//ESTs//2.5e-36:182:100//Hs.122162:AI057087  
R-PLACE1003760//Human globin gene//L9e-98:538:91//Hs.100090:M69023  
R-PLACE1003762//EST//2.9e-15:125:85//Hs.162083:AA487512  
R-PLACE1003768//Human P042 gene, complete cds//3.1e-18:300:69//Hs.158302:U88965  
R-PLACE1003771//ESTs//1.2e-09:64:100//Hs.23799:AI003798  
35 R-PLACE1003783//ESTs, Weakly similar to D2085.5 [C.elegans]//3.8e-38:199:97//Hs.115197:AA215757  
R-PLACE1003784//ESTs//3.7e-87:428:97//Hs.157985:AI366909  
R-PLACE1003795//Homo sapiens mRNA for KIAA0575 protein, complete cds//3.2e-36:236:88//Hs.153468:  
AB011147  
R-PLACE1003833//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//8.5e-  
40 62:313:96//Hs.121020:AA526092  
R-PLACE1003850//ESTs//4.0e-67:351:96//Hs.159303:T91059  
R-PLACE1003858//ESTs//0.96:87:66//Hs.107112:AA679058  
R-nnnnnnnnnnnnn  
R-PLACE1003870//EST//2.9e-34:281:79//Hs.160895:AI365871  
45 R-nnnnnnnnnnnnn  
R-PLACE1003886//ESTs//6.7e-85:410:97//Hs.25129:W93595  
R-PLACE1003888//ESTs//0.0085:165:64//Hs.96739:AA441915  
R-PLACE1003900//EST//2.4e-05:129:69//Hs.127931:AA969259  
R-PLACE1003903//ESTs, Highly similar to CTP SYNTHASE [Homo sapiens]//1.5e-54:282:96//Hs.58553:  
50 AA100804  
R-PLACE1003915//EST//0.87:55:76//Hs.145930:AI275760  
R-PLACE1003923//ESTs//1.7e-89:456:95//Hs.14125:AA156236  
R-PLACE1003932//ESTs//3.0e-50:340:84//Hs.151208:AI126110  
R-PLACE1003936//EST//1.8e-08:208:65//Hs.162656:AA603567  
55 R-PLACE1003968//ESTs//7.4e-49:301:90//Hs.93850:AA115330  
R-PLACE1004104//ESTs//1.9e-46:254:94//Hs.96802:AA443231  
R-PLACE1004114//ESTs//1.2e-64:322:97//Hs.28928:AI052052  
R-PLACE1004118//ESTs//1.0e-83:404:98//Hs.112764:AA609770

R-PLACE1004128//ESTs//5.3e-80:415:95//Hs.11835:AA040244  
R-PLACE1004149//ESTs//7.2e-25:331:72//Hs.141084:H11714  
R-PLACE1004156//Homo sapiens PYRIN (MEFV) mRNA, complete cds//2.0e-56:491:76//Hs.113283:AF018080  
R-PLACE1004161//ESTs//2.0e-59:355:88//Hs.13830:AA918601  
5 R-PLACE1004183//Homo sapiens cytochrome c oxidase assembly protein COX11(COX11) mRNA, complete cds//  
4.7e-78:434:91//Hs.153504:AF044321  
R-PLACE1004197  
R-PLACE1004203//Homo sapiens GPI-anchored membrane protein CDw108 precursor, mRNA, complete cds//  
1.5e-105:501:98//Hs.24640:AF069493  
10 R-PLACE1004242//ESTs//1.0e-71:364:87//Hs.138632:H97952  
R-PLACE1004256//EST//0.0011:347:61//Hs.131385:AI022630  
R-PLACE1004257//EST//0.027:99:71//Hs.97587:AA398209  
R-PLACE1004258//KERATIN, TYPE I CYTOSKELETAL 14//0.72:180:63//Hs.117729:100124  
R-PLACE1004270//ESTS//0.011:264:59//Hs.110044:AA181800  
15 R-PLACE1004274//Human retinoic acid receptor-beta associated open reading frame, complete sequence//0.28:  
121:66//Hs.1938:S82362  
R-PLACE1004277//Homo sapiens two pore domain K<sup>+</sup> channel (TASK-2) mRNA, complete cds//1.4e-107:581:  
91//Hs.127007:AF084830  
R-PLACE1004284//ESTs//5.0e-22:187:82//Hs.23141:W92114  
20 R-PLACE1004289//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.9e-28:  
279:77//Hs.38687:AA744496  
R-PLACE1004302//ESTs, Weakly similar to SOF1 PROTEIN [Saccharomyces cerevisiae]//8.2e-61:313:95//Hs.  
71435:AI253099  
R-PLACE1004316//H.sapiens mRNA for apoptosis specific protein//6.0e-115:590:94//Hs.11171:Y11588  
25 R-PLACE1004336//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//6.7e-69:572:  
77//Hs.1361:M55053  
R-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1 mRNA, complete cds//7.7e-72:  
379:93//Hs.16232:AF100153  
R-PLACE1004376//ESTs//0.49:362:59//Hs.138086:AI056309  
30 R-PLACE1004384//EST//1.0:47:76//Hs.128546:AA905556  
R-PLACE1004388//ESTs, Weakly similar to contains similarity to ATP/GTP-binding site motif [C.elegans]//1.3e-  
98:572:90//Hs.14202:N46000  
R-PLACE1004405//ESTs//3.4e-99:507:95//Hs.28792:AI343467  
R-PLACE1004425//ESTs//2.7e-85:442:95//Hs.12544:N53665  
35 R-PLACE1004428//ESTs//1.0e-07:114:78//Hs.140225:AA704101  
R-PLACE1004437//Human NAD<sup>+</sup>-specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene  
encoding mitochondrial protein, complete cds//9.4e-90:516:88//Hs.155410:U49283  
R-PLACE1004451  
R-PLACE1004460//ESTs//5.4e-14:338:64//Hs.97464:AA662980  
40 R-PLACE1004467//ESTs//3.3e-85:467:92//Hs.9527:W52721  
R-PLACE1004471//ESTs//3.0e-73:389:94//Hs.23240:R46578  
R-PLACE1004473//ESTs, Weakly similar to F20D1.2 [C.elegans]//3.8e-101:510:95//Hs.16986:W89194  
R-PLACE1004491//Human mitochondrial 1,25-dihydroxyvitamin D3 24-hydroxylase mRNA, complete cds//0.23:  
278:61//Hs.89663:L13286  
45 R-PLACE1004506//ESTs//2.5e-98:559:90//Hs.19447:AI057117  
R-PLACE1004510//ESTs//1.5e-91:436:98//Hs.24846:AI420493  
R-PLACE1004516//EST//1.7e-66:344:96//Hs.99303:AA453164  
R-PLACE1004518//ESTs//5.2e-79:410:94//Hs.27091:AA436553  
R-PLACE1004548//Homo sapiens mRNA for small GTP-binding protein, complete cds//1.8e-40:332:72//Hs.  
50 115325:084488  
R-PLACE1004550  
R-PLACE1004564//ESTs//5.5e-76:367:98//Hs.49683:AA564742  
R-PLACE1004629//ESTs, Weakly similar to OS-9 precurosor [H.sapiens]//8.1e-40:272:87//Hs.7100:W07181  
R-PLACE1004645//ESTs//6.3e-14:83:100//Hs.17270:AA701903  
55 R-PLACE1004646//ESTs//3.7e-22:231:76//Hs.141250:N29734  
R-PLACE1004658//ESTs//2.0e-12:109:84//Hs.23508:AA101113  
R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0714 protein, partial cds//7.8e-23:129:99//Hs.123129:AB018257  
R-PLACE1004672//ESTs//2.0e-50:256:98//Hs.136367:AI144254

R-PLACE1004674//Homo sapiens calcium binding protein (ALG-2) mRNA, complete cds//L8e-90:510:91//Hs.  
80019:AF035606

R-PLACE1004681//EST//2.1e-08:283:62//Hs.99543:AA461482

R-PLACE1004686  
5 R-PLACE1004691//EST//7.3e-42:305:82//Hs.141833:AA021552

R-PLACE1004693//ESTs//0.014:135:64//Hs.145333:AI251374

R-PLACE1004716//ESTs, Weakly similar to No definition line found [C.elegans]//3.4e-80:413:94//Hs.23528:  
AI279571

R-PLACE1004722//EST//0.14:165:63//Hs.18213:T97997  
10 R-PLACE1004736//ESTs//1.0e-72:385:94//Hs.10657:N6391

R-PLACE1004740//ESTs//1.0:267:58//Hs.101661:AA416619

R-nnnnnnnnnnnn//EST//0.45:94:69//Hs.147174:AI192195

R-PLACE1004751//EST//9.8e-32:174:83//Hs.147901:AI223374

R-PLACE1004773//Homo sapiens inversin protein mRNA, complete cds//2.7e-89:437:96//Hs.104715:AF084367  
15 R-PLACE1004777//ESTs//7.4e-68:351:94//Hs.23395:AA398548

R-PLACE1004793//ESTs//1.3e-53:290:78//Hs.142375:AA398619

R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0606 protein, partial cds//1.9e-99:580:88//Hs.38176:AB011178

R-PLACE1004813//ESTs//7.6e-86:433:96//Hs.85640:AA535856  
20 R-PLACE1004814//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//1.1e-  
108:358:99//Hs.3688:AF069250

R-PLACE1004815//EST//4.7e-50:333:84//Hs.142196:AA258356

R-PLACE1004824//Protein kinase, interferon-inducible double stranded RNA dependent//4.8e-46:450:76//Hs.  
73821:M35663

R-PLACE1004827//ESTs//2.3e-48:250:96//Hs.138766:AA342185  
25 R-PLACE1004836//ESTs//2.7e-39:222:94//Hs.78661:AA195299

R-PLACE1004838//EST//0.056:198:60//Hs.129589:AA995901

R-PLACE1004840//ESTs, Highly similar to TRANSCRIPTIONAL ACTIVATOR GCN5 [Saccharomyces cerevisiae]  
//6.5e-71:381:93//Hs.8383:AA013272

R-PLACE1004868//ESTs//4.9e-70:367:94//Hs.100895:AA479308  
30 R-PLACE1004885//Homo sapiens protein phosphatase with EF-hands-2 long form (PPEF-2) mRNA, complete  
cds//1.8e-37:330:78//Hs.113259:AF023456

R-PLACE1004900//EST//1.2e-46:306:86//Hs.149580:AI211881

R-PLACE1004902//Sucrase-isomaltase//0.87:254:61//Hs.2996:X63597  
35 R-nnnnnnnnnnnn//ESTs//4.5e-75:375:96//Hs.91115:AI221563

R-PLACE1004918//ESTs//2.6e-103:519:95//Hs.143607:AI424948

R-PLACE1004930//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cds//6.6e-102:532:93//Hs.  
17839:AF099936

R-PLACE1004934//EST//0.035:156:67//Hs.162071:AA478980  
40 R-PLACE1004937//ESTs, Weakly similar to F55B12.3 [C.elegans]//6.4e-80:409:95//Hs.31945:AA702I66

R-PLACE1004969//ESTs//9.8e-18:101:99//Hs.112837:N78013

R-PLACE1004972//ESTs//1.3e-65:337:95//Hs.75798:H29106

R-PLACE1004979//EST//1.2e-96:475:96//Hs.120158:AA708789  
45 R-PLACE1004982//ESTs//1.0e-98:471:98//Hs.106496:AI291776

R-PLACE1004985//ESTs//2.1e-88:456:93//Hs.135050:AI420335

R-PLACE1005026  
50 R-PLACE1005027//ESTs, Weakly similar to N-methyl-D-aspartate receptor glutamate-binding chain [R.norvegi-  
cus]//0.72:145:66//Hs.11215:N56719

R-PLACE1005046//Homo sapiens mRNA for KIAA0575 protein, complete cds//5.3e-66:297:88//Hs.153468:  
AB011147

R-PLACE1005052//ESTs, Weakly similar to weak similarity to rat cytosolic acyl coenzyme A thioester hydrolase  
[C.elegans]//1.2e-106:543:95//Hs.18625:AI074605  
55 R-PLACE1005066//ESTs//3.9e-92:459:96//Hs.62684:AA806103

R-PLACE1005077//Human triadin mRNA, complete cds//1.8e-05:121:69//Hs.68731:U18985

R-PLACE1005085//Homo sapiens PYRIN (MEFV) mRNA, complete cds//6.6e-49:314:74//Hs.113283:AF018080

R-PLACE1005086//ESTs//1.2e-73:379:94//Hs.110128:AA584364

R-PLACE1005101//Homo sapiens (clone zap128) mRNA, 3' end of cds//8.0e-99:531:92//Hs.75437:L40401  
R-PLACE1005102//ESTs//7.2e-68:493:84//Hs.10593:AI201336

R-PLACE1005108//Human DNA fragmentation factor-45 mRNA, complete cds//9.2e-40:232:82//Hs.155344:

U91985

R-PLACE1005111//EST//8.1e-10:189:68//Hs.136356:AA493225  
 R-PLACE1005128//ESTs//1.4e-78:501:87//Hs.15093:AA203423  
 R-PLACE1005146//ESTs//4.8e-93:460:97//Hs.37896:AA777349  
 5 R-PLACE1005162//ESTs//7.5e-51:277:95//Hs.28838:AI089013  
 R-nnnnnnnnnnnnn//ESTs//5.4e-75:366:97//Hs.48119:AA454227  
 R-PLACE1005181//EST//0.012:172:66//Hs.147107:AI190589  
 R-PLACE1005187//ESTs//5.6e-72:363:95//Hs.16577:AI022830  
 R-PLACE1005206//ESTs//5.3e-48:203:88//Hs.31792:H45211  
 10 R-PLACE1005232//ESTs//5.1e-41:287:84//Hs.138552:R99532  
 R-PLACE1005243//ESTs//1.1e-48:348:83//Hs.113310:R16767  
 R-PLACE1005261//ESTs//0.19:175:62//Hs.124337:AA829524  
 R-PLACE1005266//ESTs//1.9e-22:388:66//Hs.124146:AA699633  
 R-PLACE1005277//ESTs//1.5e-29:314:72//Hs.163710:AA024516  
 15 R-PLACE1005287//ESTs//3.6e-95:456:98//Hs.49282:AA970322  
 R-PLACE1005305//ESTs//9.9e-71:428:88//Hs.144855:AI197937  
 R-PLACE1005308//ESTs//3.8e-32:173:96//Hs.58239:AA215797  
 R-PLACE1005313//ESTs//5.2e-74:409:93//Hs.33368:AA206614  
 R-PLACE1005327//Chromosome 1 specific transcript KIAA0491//1.7e-104:537:94//Hs.136309:AB007960  
 20 R-PLACE1005331//ESTs//2.1e-91:487:93//Hs.9291:AI189343  
 R-PLACE1005335//ESTs, Weakly similar to F23B2.4 [C.elegans]//3.8e-90:442:97//Hs.70202:AA732975  
 R-PLACE1005373//ESTs//8.0e-93:526:91//Hs.98541:N38901  
 R-PLACE1005374//Homo sapiens KIAA0395 mRNA, partial cds//3.3e-44:344:80//Hs.43681:AL022394  
 R-PLACE1005409//EST//0.43:174:59//Hs.162077:AA479978  
 25 R-PLACE1005453//EST//7.9e-57:330:90//Hs.162306:AA555304  
 R-PLACE1005467//ESTs//2.2e-42:294:84//Hs.142257:AA188423  
 R-PLACE1005471//Human Line-1 repeat mRNA with 2 open reading frames//2.3e-88:561:86//Hs.23094:M19503  
 R-PLACE1005477//Human methionine aminopeptidase mRNA, complete cds//6.9e-80:549:83//Hs.78935:U29607  
 R-PLACE1005480//EST//0.99:39:82//Hs.157275:AI364046  
 30 R-PLACE1005481//EST//1.5e-31:281:79//Hs.132635:AI032875  
 R-PLACE1005494//Homo sapiens mRNA for semaphorin E, complete cds//0.036:319:59//Hs.62705:AB000220  
 R-PLACE1005502//Homo sapiens formin binding protein 21 mRNA, complete cds//5.4e-57:277:98//Hs.28307:  
 AF071185  
 R-PLACE1005526//ESTs//2.5e-30:233:83//Hs.119304:AA443325  
 35 R-PLACE1005528//Homo sapiens mRNA for cartilage-associated protein (CASP)//8.9e-20:321:69//Hs.155481:  
 AJ006470  
 R-PLACE1005530//ESTs//3.7e-81:438:92//Hs.103380:AI291325  
 R-PLACE1005550//ESTs, Highly similar to HYPOTHETICAL 40.2 KD PROTEIN K12H4.3 IN CHROMOSOME III  
 [Caenorhabditis elegans]//5.2e-95:458:98//Hs.38114:N62927  
 40 R-PLACE1005544//ESTs//8.8e-36:267:86//Hs.98288:AA203555  
 R-PLACE1005557//ESTs, Highly similar to MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L2 PRECURSOR  
 [Saccharomyces cerevisiae]//2.2e-64:345:94//Hs.7736:W81261  
 R-PLACE1005574//ESTs//2.3e-27:231:83//Hs.117771:R99835  
 R-PLACE1005584//ESTs//1.6e-36:188:98//Hs.152050:AA724612  
 45 R-PLACE1005595//ESTs//1.6e-91:453:96//Hs.85079:AI276023  
 R-PLACE1005603//ESTs//8.2e-99:533:93//Hs.96357:AI026927  
 R-PLACE1005611//ESTs//5.2e-28:183:89//Hs.24941:AA261857  
 R-PLACE1005623//ESTs//1.4e-102:505:96//Hs.58382:AA808964  
 R-PLACE1005630  
 50 R-PLACE1005639//ESTs//1.4e-51:256:98//Hs.1975:W72452  
 R-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete cds//1.0e-111:585:93//Hs.8765:  
 AF083255  
 R-PLACE1005656//ESTs//2.7e-88:469:92//Hs.164054:AA528169  
 55 R-PLACE1005666//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//  
 3.3e-24:401:66//Hs.129727:AF035587  
 R-PLACE1005698//ESTs//0.00013:82:79//Hs.116331:AA629355  
 R-PLACE1005727//EST//0.15:206:63//Hs.105002:AA449332  
 R-PLACE1005730//EST//0.0014:129:70//Hs.127931:AA969259

R-PLACE1005739//ESTs, Moderately similar to unknown intracellular protein [M.musculus]//1.3e-42:236:94//Hs.23889:AI341137  
 R-PLACE1005755//ESTs//2.8e-32:308:80//Hs.159821:AA524070  
 R-PLACE1005763//Human mRNA for KIAA0118 gene, partial cds//3.3e-47:268:87//Hs.154326:D42087  
 5 R-PLACE1005799//ESTs, Highly similar to HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III [Caenorhabditis elegans]//7.7e-15:88:98//Hs.109857:AA088385  
 R-PLACE1005802//ESTs//2.8e-19:208:76//Hs.9271:W30941  
 R-PLACE1005803//ESTs//2.6e-75:417:92//Hs.71414:AA131327  
 R-PLACE1005804//EST//6.5e-20:182:70//Hs.149844:AI287693  
 10 R-PLACE1005828//ESTs//3.0e-15:194:77//Hs.106236:N50058  
 R-PLACE1005834//Retinoblastoma 1 (including osteosarcoma)//0.040:435:58//Hs.75770:L41870  
 R-PLACE1005845//EST//5.0e-61:294:99//Hs.133202:AI050965  
 R-PLACE1005850//ESTs//3.4e-82:425:96//Hs.7966:AI203471  
 R-PLACE1005851//ESTs//2.9e-21:165:84//Hs.23607:N98305  
 15 R-PLACE1005876//ESTs//0.48:296:57//Hs.39140:AI041842  
 R-PLACE1005884//ESTs//0.0027:177:66//Hs.150295:AA570558  
 R-PLACE1005898//ESTs//1.7e-98:467:98//Hs.159475:AI339981  
 R-PLACE1005921//ESTs//5.8e-96:480:95//Hs.30822:AA885501  
 R-PLACE1005923//ESTs//1.8e-66:333:96//Hs.150890:AI341793  
 20 R-PLACE1005925//Human Line-1 repeat mRNA with 2 open reading frames//2.8e-27:382:70//Hs.23094:M19503  
 R-PLACE1005932//ESTs, Moderately similar to MNK1 [H.sapiens]//1.1e-70:377:93//Hs.5662:AA868361  
 R-PLACE1005934//ESTs//1.0e-42:251:91//Hs.25092:AA922142  
 R-PLACE1005936//ESTs//1.2e-88:461:94//Hs.94125:N62913  
 R-PLACE1005951//ESTs//1.4e-83:533:86//Hs.21148:AI183729  
 25 R-PLACE1005953  
 R-PLACE1005955//ESTs, Highly similar to HYPOTHETICAL 54.2 KD PROTEIN-IN CDC12-ORC6 INTERGENIC REGION [Saccharomyces cerevisiae]//2.2e-83:494:88//Hs.108117:AI097079  
 R-PLACE1005966//ESTs//1.1e-95:465:97//Hs.98510:AI016239  
 R-PLACE1005968//EST//0.26:103:66//Hs.161300:AI420897  
 30 R-PLACE1005990  
 R-PLACE1006002//Human mRNA for KIAA0355 gene, complete cds//2.0e-45:481:74//Hs.153014:AB002353  
 R-PLACE1006003//ESTs, Highly similar to HYPOTHETICAL 30.3 KD PROTEIN IN APE1/LAP4-CWP1 INTERGENIC REGION [Saccharomyces cerevisiae]//3.1e-112:593:93//Hs.111449:AI192946  
 R-PLACE1006011//ESTs, Moderately similar to NAD(\*) ADP-RIBOSYLTRANSFERASE [D.melanogaster]//5.7e-35 100:596:88//Hs.24284:AA595596  
 R-PLACE1006017//ESTs//4.2e-18:296:68//Hs.133350:AI056276  
 R-PLACE1006037//ESTs, Weakly similar to T23D8.3 [C.elegans]//4.1e-102:491:98//Hs.61164:AI096332  
 R-PLACE1006040//ESTs//1.2e-92:443:98//Hs.111680:N93765  
 R-PLACE1006076//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//2.0e-40 26:213:77//Hs.139007:H74314  
 R-PLACE1006119//ESTs//0.14:257:61//Hs.113149:AA908904  
 R-PLACE1006129//ESTs//3.8e-54:285:97//Hs.18827:W68002  
 R-PLACE1006139//ESTs, Highly similar to HYPOTHETICAL 52.9 KD PROTEIN IN SAP155-YMR31 INTERGENIC REGION [Saccharomyces cerevisiae]//2.6e-99:560:91//Hs.5249:U55977  
 45 R-PLACE1006143//Amylo-1,6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III) //0.038:463:59//Hs.904:U84010  
 R-PLACE1006157//ESTs//0.014:341:58//Hs.121773:AI357886  
 R-PLACE1006159//EST//0.00036:247:61//Hs.140054:AA668925  
 R-PLACE1006164//ESTs//2.6e-31:362:73//Hs.141024:H07128  
 50 R-PLACE1006167//Homo sapiens chromosome 19, cosmid F23149//5.8e-54:286:94//Hs.152894:AC005239  
 R-nnnnnnnnnnnnnnnnn//ESTs, Highly similar to ALPHA-ADAPTIN [Rattus norvegicus]//2.7e-79:393:96//Hs.19121:AI125280  
 R-PLACE1006187//Homo sapiens cyclin E2 mRNA, complete cds//5.1e-118:597:95//Hs.30464:AF091433  
 R-PLACE1006195//ESTS, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//6.8e-94:  
 55 532:91//Hs.105216:AI361807  
 R-PLACE1006196//ESTs//3.2e-66:382:90//Hs.18665:T99507  
 R-PLACE1005205//EST//1.7e-89:448:96//Hs.116665:AA669114  
 R-PLACE1006223//Human RNaseP protein p38 (RPP38) mRNA, complete cds//0.90:304:58//Hs.94986:U77664

R-PLACE1006225//ESTs//7.2e-96:474:97//Hs.91165:AI079555  
 R-PLACE1006236//ESTs//8.8e-105:535:95//Hs.7919:AI341472  
 R-nnnnnnnnnnnn//Homo sapiens BAC clone RG118D07 from 7q31//3.2e-99:497:95//Hs.3781:AC004142  
 R-PLACE1006246//ESTs, Weakly similar to CMP-sialic acid transporter [M.musculus]//1.3e-104:532:95//Hs.  
 5 41151:AI301961  
 R-PLACE1006248//Homo sapiens mRNA for KIAA0648 protein, partial cds//3.0e-97:499:95//Hs.31921:AB014548  
 R-PLACE1006262//ESTs, Moderately similar to !!! ALU SUBFAMILY SC WARNING ENTRY !!! [H.sapiens]//1.6e-  
 07:321:62//Hs.53057:W67839  
 R-PLACE1006288//Voltage-dependent anion channel 1//3.8e-100:605:88//Hs.2060:L06132  
 10 R-PLACE1006318//ESTs//2.4e-102:536:94//Hs.8109:AA005265  
 R-PLACE1006325//ESTs//5.2e-105:518:96//Hs.102319:AI246503  
 R-PLACE1006335//ESTs//5.1e-45:254:93//Hs.153585:R70900  
 R-PLACE1006357//EST//6.5e-09:309:62//Hs.132493:AA923168  
 R-PLACE1006360//Human mRNA for KIAA0090 gene, partial cds//0.0097:381:58//Hs.154797:D42044  
 15 R-PLACE1006368//ESTs//7.9e-85:412:97//Hs.150587:AI079284  
 R-PLACE1006371//ESTs//7.7e-74:442:88//Hs.143671:W61053  
 R-PLACE1006382  
 R-PLACE1006385//ESTs//5.3e-06:346:61//Hs.163706:AA515748  
 R-PLACE1006412//EST//7.7e-46:306:86//Hs.149580:AI281881  
 20 R-PLACE1006414//Homo sapiens UM protein mRNA, complete cds//4.1e-43:551:69//Hs.154103:AF061258  
 R-PLACE1006438//ESTs//1.1e-77:284:86//Hs.24545:AI278629  
 R-PLACE1006445//ESTs//4.4e-53:259:99//Hs.24481:AA573139  
 R-PLACE1006469//ESTs//9.4e-102:482:98//Hs.7218:AA936961  
 R-PLACE1006470//ESTs//1.0:271:57//Hs.144517:AA938297  
 25 R-PLACE1006482//ESTs//4.0e-61:354:92//Hs.51305:T47418  
 R-PLACE1006492//EST//1.8e-09:48:91//Hs.144451:AA827722  
 R-PLACE1006506//ESTs//0.012:161:61//Hs.145333:AI251374  
 R-PLACE1006521//Human mRNA for KIAA0013 gene, complete cds//2.1e-15:415:63//Hs.48824:D87717  
 R-PLACE1006531//ESTs//5.6e-31:213:87//Hs.125153:AA453723  
 30 R-PLACE1006534//ESTs//6.5e-101:512:95//Hs.27763:W46368  
 R-PLACE1006540//ESTs//7.3e-40:320:79//Hs.121659:H02532  
 R-PLACE1006552//EST//0.38:418:56//Hs.140470:AA765214  
 R-PLACE1006598//ESTs//4.0e-80:409:95//Hs.142868:AI128443  
 R-PLACE1006615//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds//  
 35 9.3e-118:590:95//Hs.155377:U97670  
 R-PLACE1006617//ESTs//8.1e-31:246:83//Hs.139128:AA205322  
 R-PLACE1006626//ESTs//0.90:98:68//Hs.96322:AA541615  
 R-PLACE1006629//Human mRNA for KIAA0386 gene, complete cds//5.3e-33:315:78//Hs.101359:AB002384  
 R-PLACE1006640//ESTs//3.7e-26:137:100//Hs.32672:W16522  
 40 R-PLACE1006673//Interleukin 10//8.4e-47:330:83//Hs.2180:M57627  
 R-PLACE1006678//ESTs//1.1e-13:87:98//Hs.34035:D87736  
 R-PLACE1006704//ESTs//2.6e-65:394:89//Hs.30582:D12214  
 R-PLACE1006731//Homo sapiens clone 23923 mRNA sequence//1.9e-102:486:98//Hs.12472:AF038172  
 R-PLACE1006754//EST//1.0e-61:381:89//Hs.14727:T83861  
 45 R-PLACE1006760//Homo sapiens clone 24800 mRNA sequence//3.8e-73:394:93//Hs.7252:AF070622  
 R-PLACE1006779//ESTs//1.4e-69:405:90//Hs.136235:AA262658  
 R-PLACE1006782//EST//1.8e-25:197:86//Hs.137257:N33234  
 R-PLACE1006792//ESTs//1.8e-43:317:84//Hs.139190:N55515  
 R-PLACE1006795//ESTs//6.4e-68:350:95//Hs.11092:AA916335  
 50 R-PLACE1006800//ESTs//1.9e-55:268:100//Hs.126695:AA917989  
 R-PLACE1006805//ESTs//6.6e-91:484:93//Hs.94262:AA768847  
 R-PLACE1006815//ESTs//2.1e-49:364:83//Hs.142031:AA809159  
 R-PLACE1006819//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//  
 1.0e-87:481:92//Hs.141263:H64113  
 55 R-PLACE1006829//ESTs//5.7e-43:332:83//Hs.19906:AA456933  
 R-PLACE1006860//ESTs//0.96:138:63//Hs.136649:AA-828359  
 R-PLACE1006867//ESTs//1.4e-98:478:97//Hs.10299:N35008  
 R-PLACE1006878//EST//8.4e-48:243:97//Hs.54970:N93536

R-PLACE1006883//EST//3.1e-46:300:88//Hs.162404:AA573131  
R-nnnnnnnnnnnnn//ESTs//3.0e-95:496:94//Hs.47546:AA181348  
R-PLACE1006904//ESTs//5.8e-18:304:68//Hs.125816:AA806089  
R-PLACE1006917//Endothelin receptor type B//0.00012:451:60//Hs.82002:D13168  
5 R-PLACE1006932//ESTs//4.6e-56:285:96//Hs.114727:AI379514  
R-PLACE1006935//ESTs//3.6e-12:157:73//Hs.161714:AA229078  
R-nnnnnnnnnnnnn//Human mRNA for KIAA0201 gene, complete cds//3.2e-25:494:63//Hs.36927:D86956  
R-PLACE1006961//Tyrosine aminotransferase//2.5e-46:471:74//Hs.2999:X52520  
R-PLACE1006962//ESTs, Moderately similar to plakophilin 2b [H.sapiens]//9.0e-29:324:68//Hs.154257:AI275982  
10 R-PLACE1006966//ESTs//4.5e-99:470:99//Hs.46913:AI017636  
R-PLACE1006989//ESTs//2.2e-68:353:97//Hs.14394:R61257  
R-PLACE1007014//ESTs//3.4e-86:457:94//Hs.129819:AA838366  
R-PLACE1007021//ESTs//1.6e-93:539:90//Hs.7111:U55971  
R-PLACE1007045//Human Line-1 repeat mRNA with 2 open reading frames//6.6e-83:584:82//Hs.23094:M19503  
15 R-PLACE1007053//ESTs//4.2e-85:550:88//Hs.7984:AI202575  
R-PLACE1007097//ESTs//6.4e-78:493:86//Hs.56406:N91027  
R-PLACE1007105//ESTs//5.3e-70:381:91//Hs.22605:N74202  
R-PLACE1007111//ESTs//8.6e-75:358:99//Hs.145629:AA398646  
R-PLACE1007112//ESTs//6.9e-69:371:94//Hs.71922:AA148417  
20 R-PLACE1007132//ESTs//1.2e-36:373:69//Hs.10762:W28948  
R-PLACE1007140//ESTs//1.7e-70:360:96//Hs.56179:W56794  
R-PLACE1007178//EST//0.68:85:65//Hs.147010:AI184765  
R-PLACE1007226//ESTs//3.1e-78:452:90//Hs.8033:N94998  
R-PLACE1007238//ESTs//5.2e-70:362:95//Hs.85636:AA740619  
25 R-PLACE1007239//Human mRNA for transcription elongation factor S-II, hS-II-T1, complete cds//6.3e-93:534:89//Hs.80598:D50495  
R-PLACE1007242//ESTS//1.2e-80:390:98//Hs.117325:AA699450  
R-PLACE1007243//ESTs, Weakly similar to transporter protein [H. sapiens]//3.7e-73:357:98//Hs.18272:N78499  
R-PLACE1007257//Homo sapiens mRNA for dia-156 protein//4.3e-85:487:91//Hs.121556:Y15909  
30 R-PLACE1007274//ESTs//4.3e-79:430:93//Hs.146023 AI275071  
R-PLACE1007276//ESTs//1.5e-33:338:74//Hs.142850:R38419  
R-PLACE1007282//ESTs//4.8e-98:532:93//Hs.10071:AA100812  
R-PLACE1007286//Human mRNA for KIAA0118 gene, partial cds//2.9e-50:518:74//Hs.154326:D42087  
R-PLACE1007301  
35 R-PLACE1007317  
R-PLACE1007342  
R-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EBBP) mRNA, complete cds//1.2e-66:367:91//Hs.76596:AF096870  
R-PLACE1007367//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.2e-98:  
40 488:96//Hs.24359:AA699594  
R-PLACE1007375//ESTs//2.3e-67:375:92//Hs.33368:AA206614  
R-PLACE1007386//ESTs//0.020:242:62//Hs.42768:AI129945  
R-PLACE1007402//ESTs//1.6e-91:441:97//Hs.26243:AA455877  
R-PLACE1007409//Homo sapiens mitoxantrone resistance protein 1 mRNA, partial sequence//2.4e-113:590:94//  
45 Hs.14387:AF093771  
R-PLACE1007416//ESTs, Weakly similar to DIPEPTIDYL PEPTIDASE IV [H.sapiens]//3.8e-115:579:95//Hs.  
72165:AI243857  
R-PLACE1007450//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//2.7e-38:311:  
80//Hs.97203:U83171  
50 R-PLACE1007452//EST//2.5e-42:386:77//Hs.140562:AA826514  
R-PLACE1007460//ESTs//4.9e-87:434:95//Hs.28472:AI028230  
R-PLACE1007478  
R-PLACE1007484//ESTs//6.8e-08:64:92//Hs.100251:AA535975  
R-PLACE1007488//Dystrophin (muscular dystrophy, Duchenne and Becker types), includes DDX142, DDX164,  
55 DDX206, DDX230, DDX239, DDX268, DDX269, DDX270, DDX272//0.26:411:60//Hs.79012:M18533  
R-PLACE1007507//ESTs//2.2e-11:136:76//Hs.128815:AA678072  
R-PLACE1007511//ESTs, Highly similar to KERATIN, TYPE I CYTOSKELETAL 14 [Homo sapiens]//1.5e-41:261:  
89//Hs.9029:W57657

R-PLACE1007524//ESTs//5.8e-45:297:87//Hs.154923:AA491377  
R-PLACE1007525//Human mRNA for KIAA0118 gene, partial cds//1.9e-44:422:75//Hs.154326:D42087  
R-PLACE1007544//ESTs//8.4e-59:327:93//Hs.27410:N25612  
R-PLACE1007547//EST//0.00010:107:71//Hs.146867:AI161404  
5 R-PLACE1007557//ESTs//1.6e-43:356:79//Hs.44702:AI148840  
R-PLACE1007583//ESTs//1.7e-41:214:97//Hs.155071:AA584257  
R-PLACE1007598//Homo sapiens clone 23939 mRNA sequence//4.8e-104:554:93//Hs.21838:AF038179  
R-PLACE1007618//Lymphocyte cytosolic protein 1 (L-plastin)//0.54:161:65//Hs.76506:J02923  
R-PLACE1007621//Homo sapiens clone 23859 mRNA sequence//4.8e-105:537:94//Hs.151046:AF038176  
10 R-PLACE1007632  
R-PLACE1007645//ESTs//0.99:187:62//Hs.163453:AI344106  
R-PLACE1007649//ESTs//2.2e-108:561:94//Hs.24398:AI262946  
R-PLACE1007677//ESTs, Moderately similar to !!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!! [H.sapiens]//  
9.0e-37:190:97//Hs.23437:AA707331  
15 R-PLACE1007688//ESTs//7.5e-79:409:95//Hs.6166:AI376944  
R-PLACE1007690//ESTs, Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 [Ascaris suum]  
//3.4e-61:384:89//Hs.92918:AA133274  
R-PLACE1007697//ESTs, Highly similar to GCN20 PROTEIN [Saccharomyces cerevisiae]//1.8e-84:501:88//Hs.  
91251:U66685  
20 R-PLACE1007705//Human mRNA for apolipoprotein E receptor 2, complete cds//0.43:307:59//Hs.54481:D86407  
R-PLACE1007706//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds//5.7e-75:374:96//Hs.4812:  
AF061243  
R-PLACE1007725//ESTs, Weakly similar to No definition line found [C.elegans]//3.1e-39:253:88//Hs.108797:  
AA476815  
25 R-PLACE1007729//ESTs//2.7e-44:392:79//Hs.142375:AA398619  
R-PLACE1007730//Homo sapiens mRNA for KIAA0685 protein, complete cds//6.7e-94:556:89//Hs.153121:  
AB014585  
R-PLACE1007737//ESTs//1.1e-41:345:80//Hs.114671:N39322  
R-PLACE1007743//ESTs//2.8e-17:98:100//Hs.124258:AA976778  
30 R-PLACE1007746//ESTs//5.3e-69:413:90//Hs.5297:AA156903  
R-PLACE1007791//ESTS, Weakly similar to TEICHOIC ACID BIOSYNTHESIS PROTEIN A [Bacillus subtilis]//  
8.6e-27:143:98//Hs.144194:AA706337  
R-PLACE1007807//Human Line-1 repeat mRNA with 2 open reading frames//9.9e-45:428:76//Hs.23094:M 9503  
R-PLACE1007810//ESTs//5.9e-15:143:82//Hs.126257:AI279044  
35 R-PLACE1007829//ESTs//2.2e-22:190:84//Hs.142707:W24050  
R-PLACE1007843//ESTs//5.3e-110:556:95//Hs.107287:AI308839  
R-PLACE1007846//Human Line-1 repeat mRNA with 2 open reading frames//1.7e-95:525:91//Hs.23094:M19503  
R-PLACE1007852//ESTs//4.5e-14:174:75//Hs.153419:N52017  
R-PLACE1007858//Homo sapiens mRNA for KIAA0766 protein, complete cds//2.1e-111:574:94//Hs.28020:  
40 AB018309  
R-PLACE1007866//EST//1.8e-48:262:96//Hs.141009:H01178  
R-PLACE1007877//ESTs//1.2e-94:478:96//Hs.5999:AI207832  
R-PLACE1007897//ESTs//2.3e-92:437:99//Hs.122843:AI189060  
R-PLACE1007908//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//2.8e-89:460:95//Hs.  
45 92381:AB007956  
R-PLACE1007946//ESTs//2.8e-28:172:78//Hs.126784:AA521510  
R-PLACE1007954//ESTs//6.1e-72:366:95//Hs.27842:AI217966  
R-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds//3.9e-103:509:96//Hs.  
5671:AF084530  
50 R-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds//7.2e-89:  
465:93//Hs.78106:AF079529  
R-PLACE1007969//ESTs, Weakly similar to F35C12.2 [C.elegans]//1.4e-113:534:99//Hs.44268:AA455900  
R-PLACE1007990//ESTs, Highly similar to DOSAGE COMPENSATION REGULATOR [Drosophila melanogaster]  
//3.8e-97:493:95//Hs.6141:U69564  
55 R-PLACE1008000//ESTs//0.00013:241:65//Hs.44369:AI206835  
R-PLACE1008002//ESTs//2.2e-83:397:98//Hs.28780:AI263612  
R-PLACE1008044//ESTs, Moderately similar to NUCLEAR PORE COMPLEX PROTEIN NUP107 [R.norvegicus]  
//2.0e-115:575:95//Hs.92395:AA779854

R-PLACE1008045//EST//2.6e-89:465:94//Hs.47374:N51935  
 R-PLACE1008080//EST//0.27:118:65//Hs.144110:AI054269  
 R-PLACE1008095//ESTs//5.5e-23:268:73//Hs.152525:AA516469  
 R-PLACE1008111//ESTs, Weakly similar to oxidoreductase [H.sapiens]//4.4e-108:537:96//Hs.28877:AI309334  
 5 R-PLACE1008122//ESTs//6.5e-103:531:94//Hs.34737:AI028617  
 R-PLACE1008129//ESTs//0.76:96:66//Hs.65373:AA883511  
 R-PLACE1008132//ESTs//5.9e-05:113:72//Hs.13014:W26381  
 R-PLACE1008177//ESTs//7.2e-107:557:93//Hs.132851:AI028266  
 R-PLACE1008181//ESTs//5.3e-97:473:97//Hs.57483:AA776267  
 10 R-PLACE1008198//ESTs//3.9e-16:120:85//Hs.9142:AA662107  
 R-nnnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0530 protein, partial cds//1.6e-104:551:93//Hs.10801:AB011102  
 R-PLACE1008209//ESTs//L2e-72:366:96//Hs.92308:AI052701  
 R-PLACE1008231//ESTs//1.2e-70:363:94//Hs.25094:R80871  
 R-PLACE1008244//ESTs//1.3e-98:543:92//Hs.25130:AA218990  
 15 R-PLACE1008273//ESTs//6.1e-16:153:79//Hs.115987:AA483808  
 R-nnnnnnnnnnnnnn  
 R-PLACE1008280//ESTs//1.3e-66:353:94//Hs.156376:AI338705  
 R-PLACE1008309//ESTs//2.8e-100:511:95//Hs.45080:N49852  
 R-PLACE1008329//V-myc avian myelocytomatosis viral oncogene homolog//0.53:206:62//Hs.79070:K02276  
 20 R-PLACE1008330//ESTs, Weakly similar to EOSINOPHIL LYSOPHOSPHOLIPASE [H.sapiens]//8.6e-79:297:91//  
 Hs.146477:AI128445  
 R-PLACE1008331//ESTs//0.98:156:62//Hs.108548:AA081656  
 R-PLACE1008356//Homo sapiens mRNA for KIAA0679 protein, partial cds//2.1e-99:556:90//Hs.5734:AB014579  
 R-PLACE1008368//EST//0.0027:198:63//Hs.160868:AI359052  
 25 R-PLACE1008369//ESTs//5.4e-28:167:92//Hs.19530:AA480009  
 R-PLACE1008392//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//2.0e-  
 41:448:72//Hs.139007:H74314  
 R-PLACE1008398//ESTs, Highly similar to Mig-6//1.4e-103:529:94//Hs.11169:AA156242  
 R-PLACE1008401//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.2e-81:  
 30 536:87//Hs.7570:W31010  
 R-nnnnnnnnnnnnnn//Homo sapiens mRNA for p115, complete cds//5.1e-103:521:95//Hs.7763:D86326  
 R-PLACE1008405//ESTs//1.2e-89:485:92//Hs.138241:AA767440  
 R-PLACE1008424//ESTs//6.7e-97:508:93//Hs.6709:AI379778  
 R-PLACE1008426//ESTs//5.5e-30:174:92//Hs.7946:AA651757  
 35 R-PLACE1008429//ESTs//2.1e-12:188:71//Hs.140769:AA931562  
 R-PLACE1008437//ESTs//7.1e-54:266:98//Hs.13068:AA001928  
 R-PLACE1008455//ESTs//4.7e-69:471:85//Hs.28337:AA210761  
 R-PLACE1008457//EST//8.6e-14:202:71//Hs.149887:AI289387  
 R-PLACE1008465//ESTs//3.8e-80:426:93//Hs.153146:AI299636  
 40 R-PLACE1008488//ESTs//7.9e-73:388:94//Hs.97268:AA292180  
 R-PLACE1008524//ESTs//7.4e-107:545:95//Hs.10441:N62816  
 R-PLACE1008531//ESTs//3.8e-68:427:87//Hs.56607:H23560  
 R-PLACE1008532  
 R-PLACE1008533//ESTs//2.5e-52:318:88//Hs.7274:AA476850  
 45 R-PLACE1008568//ESTs//3.2e-99:486:97//Hs.84414:AI423223  
 R-PLACE1008584//EST//2.2e-18:154:68//Hs.141498:N50064  
 R-PLACE1008621//ESTS, Weakly similar to line-1 protein ORF1 [H.sapiens]//8.6e-67:483:82//Hs.140416:  
 AA778649  
 R-nnnnnnnnnnnnnn  
 50 R-PLACE1008626//ESTs//4.7e-73:372:95//Hs.23491:AA642454  
 R-PLACE1008627//ESTS//1.6e-90:475:93//Hs.102401:AI004972  
 R-PLACE1008629//ESTs//8.0e-93:492:93//Hs.20843:AA699512  
 R-PLACE1008630//ESTs//1.0e-94:453:98//Hs.34840:AI279612  
 R-PLACE1008643//Human mRNA for KIAA0355 gene, complete cds//2.8e-49:422:79//Hs.153014:AB002353  
 55 R-PLACE10086507//Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA, complete cds//7.9e-90:434:97//Hs.  
 147967:AF044333  
 R-PLACE1008693//ISLET AMYLOID POLYPEPTIDE PRECURSOR//1.8e-41:505:71//Hs.51048:X68830  
 R-PLACE1008696//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//1.7e-51:316:

76//Hs.1361:M55053  
 R-PLACE1008715//EST//0.63:114:64//Hs.121353:AA758600  
 R-PLACE1008748//ESTs, Weakly similar to !!!! ALU CLASS B WARNING ENTRY !!!! [H.sapiens]//2.3e-40:281:  
 83//Hs.142209:AA873303  
 5 R-PLACE1008757//ESTs//1.4e-45:226:99//Hs.22822:H06408  
 R-PLACE1008790//ESTs//0.035:67:76//Hs.153554:AI286313  
 R-PLACE1008798//ESTs//4.9e-59:285:99//Hs.49018:N79930  
 R-PLACE1008807//ESTs//1.7e-82:413:96//Hs.130745:AA573217  
 R-PLACE1008808//Homo sapiens putative checkpoint control protein HRAD1 mRNA, complete cds//1.1e-98:499:  
 10 95//Hs.7179:AF011905  
 R-PLACE1008813//ESTs, Weakly similar to coded for by C. elegans cDNA crn10e3 [C.elegans]//4.2e-92:490:93//  
 Hs.110454:H11810  
 R-PLACE1008851//ESTs//2.4e-84:421:95//Hs.158893:AI378428  
 R-nnnnnnnnnnnnn  
 15 R-PLACE1008867//ESTs//1.1e-77:400:95//Hs.44198:AI093502  
 R-PLACE1008887//Oxytocin receptor//1.1e-43:601:67//Hs.2820:X64878  
 R-PLACE1008902//ESTs//0.023:208:61//Hs.154164:AI246893  
 R-PLACE1008920//Homo sapiens mRNA for KIAA0765 protein, partial cds//2.6e-56:344:89//Hs.62318:AB018308  
 R-PLACE1008925//ESTs//0.17:294:57//Hs.105113:AA457018  
 20 R-PLACE1008934//ESTs//2.0e-61:339:92//Hs.100448:AA622653  
 R-PLACE1008941//ESTs, Moderately similar to ATP-BINDING CASSETTE TRANSPORTER 2 [Mus musculus]//  
 1.3e-19:488:63//Hs.15780:U66680  
 R-PLACE1008947//ESTs//1.3e-81:385:99//Hs.71574:AI376573  
 R-PLACE1009020//ESTs//2.9e-79:419:94//Hs.121816:AA775419  
 25 R-PLACE1009027//Homo sapiens mRNA for doublecortin//3.1e-82:434:94//Hs.34780:AJ003112  
 R-PLACE1009039//ESTs//2.8e-83:448:92//Hs.129179:AA988520  
 R-PLACE1009045//ESTs//1.6e-64:318:97//Hs.103423:AA814195  
 R-PLACE1009048//ESTs//2.7e-17:403:63//Hs.149343:AI249139  
 R-PLACE1009050//ESTs//2.0e-88:475:92//Hs.122925:AA909008  
 30 R-PLACE1009060//ESTs, Highly similar to HYPOTHETICAL 98.3 KD PROTEIN R10E12.1 IN CHROMOSOME  
 III [Caenorhabditis elegans]//1.2e-112:555:96//Hs.9663:AA527142  
 R-PLACE1009090//ESTs//5.0e-13:175:75//Hs.140608:N53448  
 R-PLACE1009094//Human splicing factor SRP30c mRNA, complete cds//0.98:161:63//Hs.77608:AL021546  
 R-PLACE1009099//ESTs, Highly similar to MKR2 PROTEIN [Mus musculus]//0.037:63:84//Hs.39943:AA203136  
 35 R-PLACE1009110//EST//5.8e-17:307:65//Hs.117264:AA682549  
 R-PLACE1009111//ESTs//1.9e-57:349:90//Hs.11260:N98983  
 R-PLACE1009130//ESTs, Weakly similar to hypothetical protein 2 [H.sapiens]//6.5e-97:501:94//Hs.11123:  
 AA703945  
 R-PLACE1009150//LAMIN B1//0.064:393:60//Hs.89497:L37747  
 40 R-PLACE1009155//TESTs, Moderately similar to ovarian-specific protein [R.norvegicus]//2.5e-36:163:82//Hs.  
 93332:AA811920  
 R-PLACE1009158//ESTs//0.30:149:65//Hs.155796:R80005  
 R-PLACE1009166//ESTs//3.3e-34:292:77//Hs.140255:AA708322  
 R-PLACE1009172//EST//8.9e-21:364:67//Hs.142557:AA464948  
 45 R-PLACE1009174//ESTs//2.9e-18:274:70//Hs.139241:AA283707  
 R-PLACE1009183//ESTs//2.3e-44:297:87//Hs.136839:H93717  
 R-PLACE10091867//ESTs, Weakly similar to No definition line found [C.elegans]//1.5e-109:572:94//Hs.54943:  
 Z78396  
 R-PLACE1009190//ESTs//2.6e-53:318:90//Hs.25245:AA176701  
 50 R-PLACE1009200//H.sapiens mRNA for sortilin//3.2e-33:195:92//Hs.104247:X98248  
 R-PLACE1009230//ESTs//3.0e-31:153:92//Hs.124116:AA772680  
 R-PLACE1009246//ESTs//2.7e-90:488:92//Hs.10706:AA909018  
 R-PLACE1009308//ESTs//0.022:46:97//Hs.36545:AA075423  
 R-PLACE1009319//ESTs//7.7e-99:533:92//Hs.109654:N91279  
 55 R-PLACE1009328//Human Line-1 repeat mRNA with 2 open reading frames//7.3e-82:578:82//Hs.23094:M19503  
 R-PLACE1009335//EST//1.3e-64:311:99//Hs.130558:AI004397  
 R-PLACE1009338//ESTs//6.0e-70:386:93//Hs.3542:AI015782  
 R-PLACE1009368//ESTs//1.4e-18:107:98//Hs.133303:W04760

R-PLACE1009375//ESTs//8.9e-36:313:76//Hs.24608:AA161260  
R-PLACE1009388//EST//4.4e-11:101:83//Hs.147074:AI188883  
R-PLACE1009398//ESTs//5.7e-63:335:93//Hs.149003:AI243186  
R-nnnnnnnnnnnnnn//ESTs//3.6e-94:452:98//Hs.103177:W72798  
5 R-PLACE1009410//ESTs//2.2e-112:553:96//Hs.61779:AA195255  
R-PLACE1009434//EST//3.4e-15:109:74//Hs.103742:U48632  
R-PLACE1009443//EST//7.5e-61:302:98//Hs.157787:AI361269  
R-PLACE1099444//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA//6.6e-85:479:90//Hs.76987:AF012872  
R-PLACE1009459//ESTs//9.3e-86:437:95//Hs.104871:AI161427  
10 R-PLACE1009476//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-67A1//1.3e-42:266:89//Hs.155049:  
AC004531  
R-PLACE1009477//ESTs//2.0e-50:367:82//Hs.152788:AA630925  
R-PLACE1009493//ESTs//4.5e-14:150:78//Hs.143918:AA699596  
R-PLACE1009524//ESTs//2.9e-97:454:99//Hs.7189:AA767698  
15 R-PLACE1009539//ESTs//9.1e-94:454:97//Hs.154706:AI262131  
R-PLACE1009542//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//1.4e-10:  
289:63//Hs.77579:AF013263  
R-PLACE1009571//ESTs//2.1e-23:125:100//Hs.41767:AA732326  
R-PLACE1009581//ESTS, Weakly similar to FIBRINOGEN ALPHA AND ALPHA-E CHAIN PRECURSORS [H.  
20 sapiens]//0.0012:56:91//Hs.12151:AA001818  
R-PLACE1009595//Homo sapiens mRNA for KIAA0635 protein, complete cds//6.0e-42:547:70//Hs.69157:  
AB014535  
R-PLACE1009596//ESTs//1.9e-102:588:90//Hs.142395:AI374735  
R-PLACE1009607//ESTs//0.0093:107:70//Hs.70932:AA126482  
25 R-PLACE1009613//ESTs//7.5e-101:488:97//Hs.5905:AA946680  
R-PLACE1009621//EST//0.99:261:60//Hs.149030:AI243338  
R-PLACE1009622//ESTs//8.0e-93:508:92//Hs.20967:AI422858  
R-PLACE1009637//EST//8.7e-90:442:97//Hs.121372:AA758701  
R-PLACE1009639//EST//8.5e-49:279:93//Hs.117447:R27213  
30 R-PLACE1009659//Homo sapiens mRNA for KIAA0587 protein, complete cds//3.3e-109:589:92//Hs.21862:  
AB011159  
R-PLACE1009665//ESTs, Weakly similar to line-1 protein ORF1 [H.sapiens]//9.9e-62:483:79//Hs.140416:  
AA778649  
R-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds//6.6e-63:310:97//Hs.109590:AF062534  
35 R-PLACE1009708//ESTs//3.Oe-94:471:96//Hs.40091:N48582  
R-PLACE1009721//ESTs, Weakly similar to MSF1 PROTEIN [S.cerevisiae]//4.2e-98:529:92//Hs.3945:AA004210  
R-PLACE1009731//TESTs, Weakly similar to immune associated protein 38 [M.musculus]//6.8e-85:489:89//Hs.  
26194:AA033989  
R-PLACE1009763//Homo sapiens UBA3 (UBA3) mRNA, complete cds//2.0e-117:598:95//Hs.154320:AF046024  
40 R-PLACE1009794//ESTs//7.9e-102:529:95//Hs.42927:N20989  
R-nnnnnnnnnnnn//Human DNA sequence from clone 1189B24 on chromosome Xq25-26.3. Contains NADH-Ubi-  
quione Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, CI-MLRQ), Tubulin Beta and Proto-oncogene  
Tyrosine-protein Kinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part of a novel gene  
similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8. Contains ESTs and GSSs//1.e-  
45 113:549:97//Hs.16411:AL030996  
R-PLACE1009845//ESTs//9.5e-106:560:93//Hs.117751:AI056868  
R-PLACE1009879//ESTs//1.8e-61:399:86//Hs.141012:R68748  
R-PLACE1009886//EST//0.54:153:64//Hs.144281:AA081328  
R-PLACE1009888//ESTs//2.7e-105:520:97//Hs.108646:AA613031  
50 R-nnnnnnnnnnnn//ESTs, Weakly similar to similar to mouse MMR1 [C.elegans]//1.6e-114:594:94//Hs.67466:  
AI219740  
R-PLACE1009921//ESTs//7.6e-05:291:60//Hs.124786:AA825563  
R-PLACE1009924//EST//1.2e-42:216:98//Hs.31742:H20276  
R-PLACE1009925//ESTs//5.4e-30:154:100//Hs.114605:AI04317  
55 R-PLACE1009935//ESTs//1.4e-83:417:97//Hs.131755:AA496543  
R-PLACE1009947//Keratin 9//1.0:273:61//Hs.2783:Z29074  
R-PLACE1009971//ESTs//1.5e-87:424:98//Hs.13781:AI160540  
R-PLACE1009992//ESTs//1.3e-87:531:87//Hs.55044:AA460698

R-PLACE1009995//ESTs//1.3e-103:575:91//Hs.71218:C75347  
R-PLACE1009997//Small inducible cytokine A5 (RANTES)//1.1e-42:286:86//Hs.155464:AF088219  
R-PLACE1010023//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]//1.7e-17:137:86//Hs.7049:  
AI141736  
5 R-PLACE1010031//ESTs//0.22:191:62//Hs.127787:AA832204  
R-PLACE1010053//ESTs, Moderately similar to spermatid perinuclear RNA-binding protein Spur [M.musculus]//  
7.6e-104:546:94//Hs.8215:AA521150  
R-PLACE1010069//ESTs//0.99:173:59//Hs.21415:AI150905  
R-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds//1.5e-88:543:88//Hs.  
10 11183AF065482  
R-PLACE1010076//ESTs//3.4e-106:530:95//Hs.28005:AA604375  
R-PLACE1010083//ESTs//4.1e-65:395:88//Hs.6103:AA496424  
R-PLACE1010089//ESTs//1.6e-70:348:97//Hs.9011:AA418615  
R-PLACE1010096//ESTs, Highly similar to hypothetical protein, 100K [R.norvegicus]//2.8e-104:565:92//Hs.11469:  
15 U69567  
R-PLACE1010102//ESTs//7.7e-50:311:89//Hs.5518:AI052015  
R-PLACE1010105//ESTs//6.0e-94:483:94//Hs.62684:AA806103  
R-PLACE1010106//ESTs, Weakly similar to putative p150 [H.sapiens]//1.6e-107:575:93//Hs.48301:AA122270  
R-PLACE1010134//EST//8.5e-59:314:94//Hs.135005:AI095130  
20 R-PLACE1010148//A-KINASE ANCHOR PROTEIN 79//0.52:351:56//Hs.48714:M90359  
R-PLACE1010152//ESTs//1.9e-40:240:90//Hs.17054:AI139897  
R-PLACE1010181//ESTs//3.6e-64:307:99//Hs.154163:AJ003313  
R-PLACE1010194//ESTs//2.7e-70:366:96//Hs.5301:T58466  
R-PLACE1010202//ESTs//0.57:120:67//Hs.58873:W95037  
25 R-PLACE1010231  
R-PLACE1010261//EST//6.9e-50:251:98//Hs.148208:AA897478  
R-PLACE1010270//ESTs//1.9e-87:430:96//Hs.25252:AI079545  
R-PLACE1010274//ESTs//1.9e-57:439:81//Hs.30078:H04535  
R-PLACE1010293//ESTs//8.1e-41:310:81//Hs.146811:AA410788  
30 R-PLACE1010321//ESTs//5.7e-50:246:99//Hs.151445:AA351081  
R-PLACE1010324//ESTs//0.00025:377:60//Hs.97430:AA398568  
R-PLACE1010329//Small inducible cytokine A5 (RANTES)//2.4e-40:300:82//Hs.155464:AF088219  
R-PLACE1010341//EST, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//9.9e-  
32:190:77//Hs.152369:AA504818  
35 R-PLACE1010362//ESTs//8.2e-86:404:99//Hs.25625:AA669327  
R-PLACE1010364//ESTs//1.5e-105:556:93//Hs.12229:AA149594  
R-PLACE1010383//Homo sapiens mRNA for putative lipoic acid synthetase, partial//4.9e-35:166:86//Hs.53531:  
AJ224162  
R-PLACE1010401//ESTs//2.3e-85:450:93//Hs.23193:AA418152  
40 R-PLACE1010481//ESTs//0.012:280:59//Hs.5579:AI392816  
R-PLACE1010491//Homo sapiens Cre binding protein-like 2 mRNA, complete cds//2.4e-89:438:96//Hs.13313:  
AF039081  
R-PLACE1010492  
R-PLACE1010522//EST//0.43:82:68//Hs.89303:AA284031  
45 R-nnnnnnnnnnnnn//ESTs//3.4e-36:228:89//Hs.128724:AA215455  
R-PLACE1010562//ESTs//4.8e-68:408:90//Hs.17244:W86306  
R-PLACE1010579//EST//0.015:193:63//Hs.67093:C14033  
R-PLACE1010580//ESTs//2.4e-93:445:98//Hs.127325:AA234116  
R-PLACE1010599  
50 R-PLACE1010616//ESTs//2.9e-101:497:97//Hs.142197:AA573418  
R-PLACE1010622//ESTs//7.1e-23:157:91//Hs.159877:N57895  
R-PLACE1010624//ESTs//1.4e-89:428:98//Hs.116561:AA658475  
R-PLACE1010628//ESTS, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//6.4e-74:  
391:95//Hs.163495:W57637  
55 R-PLACE1010629//ESTs//5.8e-75:359:99//Hs.123630:AI250805  
R-PLACE1010630//ESTs//9.5e-101:519:94//Hs.77873:AA731719  
R-PLACE1010631//Homo sapiens mRNA for KIAA0530 protein, partial cds//8.3e-94:497:93//Hs.10801:AB011102  
R-PLACE1010661//ESTs, Highly similar to TESTIS-SPECIFIC PROTEIN PBS13 [Mus musculus]//4.8e-83:467:

	91//Hs.22383:R51067
R-PLACE1010662//ESTs, Weakly similar to UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR [D.melanogaster]/8.3e-103:538:94//Hs.105794:AA701659	
R-PLACE1010702//Homo sapiens DNA from chromosome 19, BAC 33152//4.8e-46:531:71//Hs.55452:AC003973	
R-PLACE1010714//Human organic anion transporting polypeptide (OATP) mRNA, complete cds//0.0074:351:60//Hs.46440:U21943	
R-PLACE1010720//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds//1.2e-56:300:95//Hs.50758:AF092564	
R-PLACE1010739//Homo sapiens mRNA for oligophrenin 1//2.6e-84:501:88//Hs.158122:AJ001189	
R-PLACE1010743	
R-PLACE1010761//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//5.2e-94:442:96//Hs.3688:AF069250	
R-PLACE1010771//ESTs//3.8e-54:264:99//Hs.27299:AI074024	
R-PLACE1010786//ESTs, Highly similar to MYOSIN HEAVY CHAIN IB [Acanthamoeba castellanii]/7.6e-111:575:94//Hs.10260:AI126627	
R-PLACE1010800//ESTs//1.9e-109:557:95//Hs.11460:AA057558	
R-PLACE1010802//ESTs//0.00021:428:5 8//Hs.70258:AI091203	
R-PLACE1010811//ESTs//7.4e-73:394:93//Hs.48499:AA428896	
R-PLACE1010833//ESTs//9.0e-33:274:78//Hs.24391:W27472	
R-PLACE1010856//ESTs//5.8e-41:351:81//Hs.17401:W81048	
R-PLACE1010857//ESTs, Weakly similar to T14B4.2 gene product [C.elegans]/1.4e-71:326:92//Hs.3385:N25917	
R-PLACE1010870//ESTs//5.8e-57:303:96//Hs.30503:H05090	
R-PLACE1010877//Homo sapiens mRNA for KIAA0610 protein, partial cds//2.3e-101:501:96//Hs.118087:AB011182	
R-PLACE1010891	
R-PLACE1010896//EST//0.0039:249:57//Hs.126090:AA867983	
R-PLACE1010900//Human Xq28 mRNA, complete cds//3.3e-07:106:76//Hs.20136:U46023	
R-PLACE1010916//Plasminogen activator inhibitor, type II (arginine-serpin)//0.25:190:61//Hs.75716:Y00630	
R-PLACE1010917//ESTs//1.3e-82:452:92//Hs.68055:AA081093	
R-PLACE1010925//ESTs//1.1e-92:471:95//Hs.17448:AI125479	
R-PLACE1010926//Homo sapiens mRNA for KIAA0554 protein, partial cds//1.3e-66:402:89//Hs.74750:AB011126	
R-nnnnnnnnnnnnnnnnnnn//Homo sapiens intersectin short form mRNA, complete cds//8.9e-82:441:93//Hs.66392:AF064244	
R-PLACE1010944	
R-PLACE1010947//ESTs//6.7e-15:102:91//Hs.116808:AA211519	
R-PLACE1010954//Small inducible cytokine A5 (RANTES)//8.8e-51:278:93//Hs.155464:AF088219	
R-PLACE1010960//ESTs, Highly similar to ACTIN-LIKE PROTEIN 13E [Drosophila melanogaster]/1.0e-103:565:92//Hs.23259:AA532437	
R-PLACE1010965//EST//6.3e-80:447:91//Hs.139529:AA219580	
R-PLACE1011026//ESTs//4.6e-99:463:99//Hs.149732:AI199846	
R-PLACE1011032//ESTs//6.3e-56:295:94//Hs.143576:AI147867	
R-PLACE1011041//ESTs//5.3e-27:168:91//Hs.7936:AA923249	
R-nnnnnnnnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0581 protein, partial cds//9.4e-102:563:91//Hs.41143:AB011153	
R-PLACE1011054//EST//1.1e-15:245:69//Hs.112648:AA609135	
R-PLACE1011056//Small inducible cytokine A5 (RANTES)//3.5e-38:285:82//Hs.155464:AF088219	
R-PLACE1011057//ESTs//3.5e-81:410:96//Hs.96499:AA252537	
R-PLACE1011090//ESTS, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]/1.6e-54:398:84//Hs.108740:W20094	
R-PLACE1011109//EST//1.3e-48:321:85//Hs.146794:AI149478	
R-PLACE1011111 4//ESTs//5.4e-90:475:94//Hs.69331:AA099587	
R-PLACE1011133//ESTs, Highly similar to 40 KD PROTEIN [Borna disease virus]/3.0e-105:552:93//Hs.31257:AA875998	
R-PLACE1011143//ESTs//0.40:127:65//Hs.118701:AA420795	
R-PLACE1011160//Homa sapiens mRNA for HRIHFB2038, partial cds//7.7e-97:534:91//Hs.28719:AB015333	
R-PLACE1011165//ESTs//1.0:135:69//Hs.32163:AI374673	
R-PLACE1011185//ESTs, Weakly similar to !!!! ALU CLASS B WARNING ENTRY !!!! [H.sapiens]/3.4e-85:442:95//Hs.136910:AA810782	
R-PLACE1011203//EST//0.0047:268:60//Hs.68832:AA088438	

R-PLACE1011219//ESTs//7.6e-96:504:93//Hs.124834:AI138671  
 R-PLACE1011221//ESTs//5.2e-23:241:78//Hs.26761:AA203299  
 R-PLACE1011229//ESTs//1.9e-90:461:95//Hs.132288:AI027693  
 R-PLACE1011263//ESTs//6.6e-56:321:93//Hs.158787:W79602  
 5 R-PLACE1011273//ESTs//0.016:131:65//Hs.140466:AA766772  
 R-PLACE1011291//EST//8.7e-47:267:91//Hs.158806:AI376913  
 R-PLACE1011296//EST//2.7e-38:225:92//Hs.160934:AI376849  
 R-PLACE1011310//ESTs//9.1e-37:196:96//Hs.39328:H71807  
 R-PLACE1011325//Human clone 23721 mRNA sequence//0.0012:486:58//Hs.83572:U79291  
 10 R-PLACE1011332//ESTs//8.4e-44:217:99//Hs.101365:R60578  
 R-PLACE1011340//ESTs, Weakly similar to TEICHOIC ACID BIOSYNTHESIS PROTEIN A [Bacillus subtilis]//3.4e-92:452:97//Hs.144194:AA706337  
 R-PLACE1011375//ESTs//2.2e-35:195:96//Hs.106486:H11376  
 R-PLACE1011399//ESTs//0.00096:224:67//Hs.151643:AA001194  
 15 R-PLACE1011419//ESTs//4.9e-50:267:95//Hs.7045:AA167337  
 R-nnnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0530 protein, partial cds//4.8e-114:600:94//Hs.10801:AB011102  
 R-PLACE1011452//Homo sapiens mRNA for KIAA0707 protein, partial cds//3.7e-32:310:76//Hs.138488:AB014607  
 20 R-PLACE1011465//ESTs//4.5e-86:471:93//Hs.144519:R70887  
 R-PLACE1011472//Homo sapiens mRNA for KIAA0712 protein, complete cds//2.6e-104:515:96//Hs.111138:AB018255  
 R-PLACE1011492//ESTs//1.7e-96:488:95//Hs.116555:AA639278  
 R-PLACE1011503//Homo sapiens clone 23597 mRNA sequence//1.0:193:60//Hs.28197:AF035294  
 25 R-PLACE1011520//ESTs//6.8e-99:477:97//Hs.85077:AA968576  
 R-PLACE1011563//ESTs//1.4e-94:514:92//Hs.16471:AA206421  
 R-PLACE1011567//EST//2.8e-89:417:100//Hs.149770:AI285985  
 R-PLACE1011576//Zinc finger protein 91 (HPF7, HTF10)//4.7e-55:267:81//Hs.8597:L11672  
 R-PLACE1011586//Myosin, heavy polypeptide 11, smooth muscle//0.98:168:61//Hs.78344:AF001548  
 30 R-PLACE1011635//ESTs//2.5e-67:332:98//Hs.108194:AA780067  
 R-PLACE1011641//ESTs//2.5e-71:J38:100//Hs.153085:AA993965  
 R-PLACE1011643//EST//1.9e-18:181:78//Hs.160879:AI361900  
 R-PLACE1011649//Homo sapiens clone 24432 mRNA sequence//2.5e-73:414:91//Hs.78019:AF070535  
 R-PLACE1011650//EST//5.8e-18:118:92//Hs.124486:AA846036  
 35 R-PLACE1011664//Restin (Reed-Steinberg cell-expressed intermediate filament-associated protein)//0.50:178:62//Hs.31638:X64838  
 R-PLACE1011675  
 R-PLACE1011682//ESTs//2.4e-90:465:94//Hs.57830:AI312025  
 R-PLACE1011719//Human Line-1 repeat mRNA with 2 open reading frames//8.5e-57:410:83//Hs.23094:M19503  
 40 R-PLACE1011725//ESTs//2.0e-70:340:98//Hs.161725:AA251392  
 R-PLACE1011729//ESTs//7.5e-19:180:79//Hs.119516:AA443426  
 R-PLACE1011749//Myelin oligodendrocyte glycoprotein {alternative products}//7.3e-40:361:77//Hs.53217:Z48051  
 R-PLACE1011762//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//3.0e-60:319:76//Hs.103948:K00627  
 45 R-PLACE1011778//ESTs//8.0e-70:372:94//Hs.46765:AA521080  
 R-PLACE1011783//Calcium modulating ligand//8.4e-41:279:85//Hs.13572:AF068179  
 R-PLACE1011858//ESTs//2.6e-69:396:91//Hs.55220:D11563  
 R-PLACE1011874//Human mRNA for KIAA0033 gene, partial cds//1.2e-53:439:80//Hs.22271:D26067  
 R-PLACE1011875//ESTs//9.0e-88:420:98//Hs.70897:AA987648  
 50 R-PLACE1011891//ESTs//3.9e-17:97:100//Hs.84698:AA725913  
 R-PLACE1011896//ESTs//2.8e-23:176:84//Hs.121540:AI275497  
 R-PLACE1011922//ESTs//6.6e-35:415:73//Hs.10972:AA164268  
 R-PLACE1011923//Homo sapiens serum-inducible kinase mRNA, complete cds//2.3e-99:546:92//Hs.3838:AF059617  
 55 R-PLACE1011962//ESTs//3.3e-49:294:90//Hs.106800:AI031969  
 R-PLACE1011964//ESTs, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [H.sapiens]//2.6e-06:284:63//Hs.124102:AA701285  
 R-PLACE1011982//ESTs//2.9e-51:291:93//Hs.20792:R14890

R-PLACE1011995//ESTs//4.5e-39:304:81//Hs.138852:AA284247  
R-PLACE1012031//Homo sapiens mRNA for KIAA0713 protein, partial cds//8.0e-106:540:95//Hs.88756:  
AB018256

5 R-PLACE2000003//ESTs//2.0e-103:488:98//Hs.8341:AA490069  
R-PLACE2000007//ESTs//2.4e-110:564:95//Hs.65135:W89120  
R-PLACE2000011//Homo sapiens clone 614 unknown mRNA, complete sequence//4.8e-105:524:95//Hs.21811:  
AF091080

10 R-PLACE2000015//ESTs//7.1e-111:543:96//Hs.32178:AA083211  
R-PLACE2000017//EST//8.2e-46:404:79//Hs.133006:AI049504  
R-PLACE2000021//EST//4.5e-19:221:71//Hs.150830:AI302868  
R-PLACE2000033//Human melanoma antigen recognized by T-cells (MART-1) mRNA//1.6e-43:355:79//Hs.  
15 154069:U06452  
R-PLACE2000034//ESTs//2.2e-21:314:70//Hs.107697:W29013  
R-PLACE2000039//H.sapiens mRNA for translin associated protein X//2.9e-45:514:72//Hs.96247:X95073  
R-PLACE2000047//Homo sapiens class-I MHC-restricted T cell associated molecule (CRTAM) mRNA, complete  
cds//4.1e-45:358:81//Hs.159523:AF001622

20 R-PLACE2000050//ESTs//4.5e-65:322:98//Hs.155820:N67652  
R-PLACE2000061//Homo sapiens mRNA for KIAA0575 protein, complete cds//9.2e-41:429:72//Hs.153468:  
AB011147

25 R-PLACE2000062//Human mRNA for KIAA0392 gene, partial cds//2.0e-43:296:86//Hs.40100:AB002390  
R-PLACE2000072//Homo sapiens ZNF202 alpha (ZNF202) mRNA, complete cds//6.2e-111:550:95//Hs.9443:  
AF027219  
R-PLACE2000097//Calcium modulating ligand//6.2e-47:372:80//Hs.13572:AF068179

30 25 R-PLACE2000100//ESTs//8.8e-42:281:86//Hs.150727:AI292236  
R-PLACE2000103//ESTs//4.7e-97:518:93//Hs.118727:W26941  
R-PLACE2000111//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds//0.00043:127:71//Hs.  
42400:AF022789  
R-PLACE2000115//ESTs//7.8e-93:458:96//Hs.104520:AA481662

35 R-PLACE2000132//ESTs//3.8e-69:409:91//Hs.98502:AA433988  
R-PLACE2000136//ESTs//6.2e-05:274:61//Hs.114067:AA701558  
R-PLACE2000140//Homo sapiens mRNA for KIAA0562 protein, complete cds//4.7e-44:302:85//Hs.118401:  
AB011134

40 R-PLACE2000164//ESTs//6.3e-106:506:98//Hs.16390:AI052357  
R-PLACE2000170//Small inducible cytokine A5 (RANTES)//3.7e-42:326:79//Hs.155464:AF088219  
R-PLACE2000172//ESTs//9.6e-43:232:94//Hs.6709:AI379778  
R-PLACE2000176//EST//1.6e-24:154:91//Hs.157734:AI360292  
R-PLACE2000187//Human mRNA for KIAA0033 gene, partial cds//2.0e-49:292:90//Hs.22271:D26067

45 R-PLACE2000216//ESTS//0.0041:166:64//Hs.159476:AI382378  
R-PLACE2000223//ESTs//0.49:171:60//Hs.86154:AA207191  
R-PLACE2000235//ESTs//2.9e-39:264:85//Hs.136839:H93717  
R-PLACE2000246//NAD(P)H:menadione oxidoreductase//4.0e-44:331:82//Hs.80706:M81600  
R-PLACE2000264//Human mRNA for KIAA0365 gene, partial cds//4.0e-38:311:81//Hs.84123:AB002363  
R-PLACE2000274//ESTs, Weakly similar to dynein-related protein [H.sapiens]//1.9e-87:422:98//Hs.9740:  
AI004779

50 45 R-PLACE2000302//ESTs, Highly similar to THREONYL-TRNA SYNTHETASE, CYTOPLASMIC [Homo sapiens]//  
4.8e-68:380:92//Hs.107365:AA720664  
R-PLACE2000305//ESTs//2.6e-43:413:75//Hs.I18732:AI344055  
R-PLACE2000317//ESTs//2.8e-92:501:92//Hs.28432:R83380  
R-PLACE2000335//ESTs//4.3e-32:300:77//Hs.163035:AA748058  
R-PLACE2000342//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds//0.00071:117:73//Hs.  
42400:AF022789

55 R-PLACE2000347//ESTs//1.6e-30:214:86//Hs.135272:AI347618  
R-PLACE2000359//Zinc finger protein 139 (clone pHZ-37)//5.5e-42:288:86//Hs.140090:U09848  
R-PLACE2000366//Thromboxane A2 receptor//6.7e-53:392:82//Hs.89887:D38081  
R-PLACE2000371//ESTs//3.6e-81:409:97//Hs.155138:AA158731  
R-PLACE2000373//Homo sapiens mRNA for KIAA0734 protein, partial cds//0.89:186:62//Hs.101516:AB018277  
R-PLACE2000379//ESTs//3.4e-10:228:64//Hs.57842:W63781  
R-PLACE2000394//ESTs//6.7e-41:462:74//Hs.107657:AA126814

R-PLACE2000398//ESTs//4.2e-33:373:74//Hs.155184:AA573189  
R-PLACE2000399  
R-PLACE2000404//ESTs, Highly similar to LEUCYL-TRNA SYNTHETASE, CYTOPLASMIC [Saccharomyces cerevisiae]//4.2e-109:540:96//Hs.6762:AA088424  
5 R-PLACE2000411//ESTs//1.6e-89:459:95//Hs.117589:N25941  
R-PLACE2000419//ESTs, Weakly similar to F25H9.6 [C.elegans]//1.6e-97:436:95//Hs.24647:W19739  
R-PLACE2000425//Homo sapiens PEC-205 mRNA, complete cds//2.2e-44:287:88//Hs.153563:AF011333  
R-PLACE2000427//ESTs, Weakly similar to coded for by C. elegans cDNA CEESI42F [C.elegans]//3.0e-113:543:  
97//Hs.16933:AA976002  
10 R-PLACE2000433//ESTs//1.8e-46:311:85//Hs.145032:AA343523  
R-PLACE2000435//ESTs//2.9e-33:243:87//Hs.90964:AA393986  
R-PLACE2000438//ESTs//2.8e-09:66:96//Hs.59548:AI279887  
R-PLACE2000450//Human mRNA for KIAA0392 gene, partial cds//3.3e-39:394:74//Hs.40100:AB002390  
R-PLACE2000455//ESTs//1.2e-62:301:99//Hs.151708:AA554714  
15 R-PLACE2000458//ESTs//6.8e-92:473:96//Hs.115897:AA156638  
R-PLACE2000465//ESTs//1.3e-45:435:76//Hs.141635:N79228  
R-PLACE2000477//ESTs//2.6e-100:536:94//Hs.77822:AA532642  
R-PLACE3000044//ESTs//9.1e-114:558:97//Hs.13035:AA151838  
20 R-PLACE3000029//Homo sapiens mRNA for KIAA0575 protein, complete cds//6.3e-64:350:86//Hs.153468:  
AB011147  
R-PLACE3000059//EST//0.028:175:61//Hs.159873:R92763  
R-PLACE3000070//ESTs//3.8e-16:200:74//Hs.138771:N70979  
R-PLACE3000103//ISLET AMYLOID POLYPEPTIDE PRECURSOR//3.7e-48:468:75//Hs.51048:X68830  
R-PLACE3000119//ESTs//1.2e-45:330:83//Hs.35254:AI133727  
25 R-PLACE3000124//EST//3.1e-75:391:96//Hs.161515:N71739  
R-PLACE3000136//ESTs//8.3e-18:152:84//Hs.10043:D81792  
R-PLACE3000142//ESTs//0.047:183:62//Hs.43102:AA131369  
R-PLACE3000147//ESTs//6.6e-53:310:90//Hs.8230:W07142  
R-PLACE3000148//EST//1.9e-16:184:76//Hs.146570:AI139815  
30 R-PLACE3000155//ESTS//1.2e-19:192:79//Hs.131350:AA805223  
R-PLACE3000156//ESTs, Highly similar to ENV POLYPROTEIN [Avian spleen necrosis virus]//4.8e-36:262:88//  
Hs.31532:H18272  
R-PLACE3000157  
R-PLACE3000158//Small inducible cytokine A5 (RANTES)//8.2e-39:296:81//Hs.155464:AF088219  
35 R-PLACE3000160  
R-PLACE3000169//ESTs//1.5e-64:329:97//Hs.129864:R20798  
R-PLACE3000194  
R-PLACE3000197//ESTs//1.4e-3 8:197:98//Hs.146341:AI269930  
R-PLACE3000199//ESTs, Highly similar to APOLIPOPROTEIN E PRECURSOR [Sus scrofa]//0.018:261:61//Hs.  
40 131370:AA927516  
R-PLACE3000207//EST//1.3e-15:154:78//Hs.136617:AA630476  
R-PLACE3000208//ESTS//1.6e-18:151:82//Hs.155498:W27084  
R-PLACE3000218//ESTs//1.8e-85:463:93//Hs.7849:AI129964  
R-PLACE3000220//ESTs//6.4e-44:308:84//Hs.136839:H93717  
45 R-PLACE3000226//ESTs//L3e-49:269:95//Hs.9059:AI359014  
R-PLACE3000230//EST//2.3e-34:258:83//Hs.4382:T02878  
R-PLACE3000242//Human trophinin mRNA, complete cds//1.1e-63:546:78//Hs.76313:U04811  
R-PLACE3000244//ESTs, Highly similar to NEGATIVE REGULATOR OF MITOSIS [Emericella nidulans]//7.5e-  
110:549:95//Hs.13692:AA632002  
50 R-PLACE3000254//Human mRNA for KIAA0309 gene, partial cds//2.4e-29:174:94//Hs.87908:AB002307  
R-PLACE3000271//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//2.3e-62:287:  
82//Hs.97203:U83171  
R-PLACE3000276//ESTs//7.5e-07:187:64//Hs.80720:AA031782  
55 R-PLACE3000304//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIP) mRNA, com-  
plete cds//4.0e-59:456:80//Hs.108966:U48696  
R-PLACE3000310//ISLET AMYLOID POLYPEPTIDE PRECURSOR//6.0e-45:302:86//Hs.51048:X68830  
R-PLACE3000320//Interleuldn 10//9.6e-42:288:85//Hs.2180:M57627  
R-PLACE3000322//ESTs, Highly similar to ARGININOSUCCINATE LYASE [Homo sapiens]//5.8e-34:190:95//Hs.

114531:N74103  
R-PLACE3000331//Homo sapiens mRNA for KIAA0772 protein, complete cds//3.7e-32:239:84//Hs.15519:  
AB018315  
R-PLACE3000339//ESTs//1.3e-109:548:96//Hs.7871:AI041837  
5 R-PLACE3000341//EST//1.1e-11:231:68//Hs.131328:AA922688  
R-PLACE3000350//Human mRNA for adipogenesis inhibitory factor//8.0e-40:291:76//Hs.1721:X58377  
R-PLACE3000352//EST//1.8e-72:343:100//Hs.144871:AI202380  
R-PLACE3000353//ESTs//2.0e-75:395:95//Hs.107260:W52683  
R-PLACE3000362//EST//2.8e-80:381:99//Hs.136233:AA261888  
10 R-PLACE3000363  
R-PLACE3000365//EST//4.8e-50:307:88//Hs.149580:AI281881  
R-PLACE3000373//ESTs//5.8e-60:422:83//Hs.142826:W87430  
R-PLACE3000388//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.0e-  
35:427:73//Hs.138795:R98534  
15 R-PLACE3000399//ESTs//6.5e-05:162:66//Hs.149440:AI274570  
R-PLACE3000400//ESTs//8.3e-05:310:63//Hs.17697:AA287528  
R-PLACE3000401//ESTs//4.6e-60:326:80//Hs.139555:N48230  
R-PLACE3000402//Homo sapiens clone 24629 mRNA sequence//0.50:227:62//Hs.142570:AF052I60  
R-PLACE3000405//Human HsLIM15 mRNA for HsLim15, complete cds//5.3e-43:315:82//Hs.37181:D64108  
20 R-PLACE3000406//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//4.4e-47:302:87//  
Hs.73614:U83460  
R-PLACE3000413//ESTs//1.6e-116:571:97//Hs.10235:H93077  
R-PLACE3000416//Small inducible cytokine A5 (RANTES)//1.8e-41:300:85//Hs.155464:AF088219  
R-PLACE3000425//Homo sapiens 4F5S mRNA, complete cds//1.6e-46:307:85//Hs.32567:AF073519  
25 R-PLACE3000455//ESTs//1.0:160:64//Hs.156045:AA884461  
R-PLACE3000475//Human signal transducing adaptor molecule STAM mRNA, complete cds//6.1e-84:440:92//Hs.  
153487:U43899  
R-PLACE3000477//ESTs//2.4e-113:568:96//Hs.24557:AA142980  
R-PLACE4000009//ESTs//1.5e-72:361:96//Hs.10119:AA700227  
30 R-PLACE4000014//Homo sapiens mRNA for KIAA0809 protein, partial cds//8.8e-85:433:95//Hs.105399:  
AB018352  
R-PLACE4000034//ESTs//7.0e-110:550:96//Hs.76607:AA156240  
R-PLACE4000049//EST//0.028:87:75//Hs.89303:AA284031  
R-PLACE4000052//ESTs//5.6e-116:553:98//Hs.19067:AA521292  
35 R-PLACE4000063//ESTs//5.0e-80:388:98//Hs.135028:AI096444  
R-PLACE4000089//ESTs//2.3e-97:479:97//Hs.102425:AA807547  
R-PLACE4000093//ESTs//1.5e-82:391:99//Hs.160730:AI142739  
R-PLACE4000100  
R-PLACE4000106//Homo sapiens mRNA for KIAA0462 protein, partial cds//2.7e-98:419:91//Hs.129937:  
40 AB007931  
R-PLACE4000128//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.8e-  
11:184:71//Hs.154278:N45985  
R-PLACE4000129//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0500//5.2e-21:118:100//Hs.  
118164:AB007969  
45 R-PLACE4000147//EST//1.6e-23:175:79//Hs.162236:AA551582  
R-PLACE4000156//Homo sapiens mRNA for KIAA0575 protein, complete cds//3.0e-47:306:88//Hs.153468:  
AB011147  
R-PLACE4000192//ESTs, Weakly similar to similar to Human zinc finger protein(ZNF142) [H.sapiens]//6.7e-31:  
232:82//Hs.16493:T92186  
50 R-PLACE4000222//ESTs//2.2e-53:195:85//Hs.141575:AA211734  
R-PLACE4000233//ESTs//2.9e-81:456:93//Hs.124964:R81949  
R-PLACE4000247//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.5e-72:307:85//Hs.113283:AF018080  
R-PLACE4000250//Small inducible cytokine A5 (RANTES)//7.1e-43:301:83//Hs.155464:AF088219  
R-PLACE4000252//EST//1.6e-40:275:85//Hs.162197:AA535216  
55 R-PLACE4000261//EST//0.0063:384:58//Hs.136284:AA400442  
R-PLACE4000269//ESTs//7.3e-67:345:97//Hs.5000:R44586  
R-PLACE4000270//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//2.1e-37:  
352:77//Hs.77579:AF013263

R-PLACE4000300//EST//0.26:103:68//Hs.144438:AA780782  
R-PLACE4000320//EST//2.7e-44:298:85//Hs.162404:AA573131  
R-PLACE4000323//ESTs//8.8e-38:178:79//Hs.155475:AA761454  
R-PLACE4000326//ESTs//7.4e-103:516:96//Hs.55042:AA150460  
5 R-PLACE4000344//ESTs//9.9e-94:463:96//Hs.100057:AA001414  
R-PLACE4000367//ESTs//0.81:102:73//Hs.107692:H38478  
R-PLACE4000369//ESTs//1.5e-69:390:92//Hs.13733:AA418656  
R-PLACE4000379//ESTs//1.3e-67:373:91//Hs.48569:AA905425  
R-PLACE4000387//EST, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//1.9e-  
10 44:379:78//Hs.152369:AA504818  
R-PLACE4000392//ESTs, Weakly similar to line-1 protein ORF1 [H.sapiens]//2.3e-70:482:83//Hs.140416:  
AA778649  
R-PLACE4000401//ESTs//1.3e-18:151:84//Hs.150355:AI273502  
R-PLACE4000411//ESTs//1.1e-108:543:96//Hs.23901:AA169780  
15 R-PLACE4000445//ESTs, Weakly similar to C05D9.6 gene product [C.elegans]//2.6e-111:530:98//Hs.12003:  
AA643063  
R-PLACE4000465//Cytochrome P450, subfamily 1 (aromatic compound-inducible), polypeptide 2//8.5e-58:409:  
72//Hs.1361:M55053  
R-PLACE4000489//ESTs//5.0e-70:342:98//Hs.72865:AI380932  
20 R-PLACE4000494//EST&//1.4e-109:525:98//Hs.22539:AI334210  
R-PLACE4000522//ESTs//6.3e-88:471:93//Hs.8121:AA521290  
R-PLACE4000548//ESTs//3.3e-86:441:96//Hs.5070:AA149527  
R-PLACE4000558//Human putative monocarboxylate transporter (MCT) mRNA, complete cds//5.7e-46:425:76//  
Hs.23590:U59185  
25 R-THYRO1000026//ESTs//2.6e-42:331:82//Hs.137875:AA993532  
R-THYRO1000034//ESTs//2.1e-43:214:100//Hs.153018:AI243524  
R-THYRO1000035//ESTs//7.6e-52:325:90//Hs.49817:AA001249  
R-THYRO1000040//ESTs//1.7e-94:459:98//Hs.48712:AI027889  
R-THYRO1000070//ESTs//6.7e-43:283:86//Hs.37573:H59651  
30 R-THYRO1000072//ESTs//1.3e-57:313:96//Hs.127827:H13438  
R-THYRO1000085//ESTs//1.1e-90:439:98//Hs.150539:AA908435  
R-THYRO1000092//Human mRNA for KIAA0355 gene, complete cds//1.3e-41:344:79//Hs.153014:AB002353  
R-THYRO1000107//Interieuldn 10//2.8e-43:292:84//Hs.2180:M57627  
R-THYRO1000111//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//  
35 1.0e-52:413:80//Hs.140385:AA773359  
R-THYRO1000121//EST//0.24:78:74//Hs.156632:AI345108  
R-THYRO1000124//ESTs//2.8e-86:428:96//Hs.141634:AI122764  
R-THYRO1000129//Homo sapiens TED protein (TED) mRNA, complete cds//6.8e-90:449:96//Hs.87619:  
AF087142  
40 R-THYRO1000132//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//5.2e-  
49:486:77//Hs.24164:N95217  
R-THYRO1000156//ESTs//6.1e-36:344:75//Hs.70279:AA757426  
R-THYRO1000163//Homo sapiens LIM protein mRNA, complete cds//4.8e-38:278:84//Hs.154103:AF061258  
R-THYRO1000173//ESTs, Highly similar to CLATHRIN COAT ASSEMBLY PROTEIN AP47 [Mus musculus]//1.1e-  
45 111:554:96//Hs.18894:AA910946  
R-THYRO1000186//ESTs//1.0e-44:339:83//Hs.155184:AA573189  
R-THYRO1000187//Small inducible cytokine A5 (RANTES)//1.1e-41:305:81//Hs.155464:AF088219  
R-THYRO1000190//Small inducible cytokine A5 (RANTES)//2.3e-44:301:85//Hs.155464:AF088219  
R-THYRO1000197//Homo sapiens mRNA for poly(A)-specific ribonuclease//3.6e-110:535:97//Hs.43445:  
50 AJ005698  
R-THYRO1000199//Homo sapiens mRNA for KIAA0652 protein, complete cds//4.3e-115:559:97//Hs.79672:  
AB014552  
R-THYRO1000206//ESTs//3.1e-90:507:90//Hs.32456:W29063  
R-THYRO1000221//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING  
55 ENTRY !!!! [H.sapiens]//1.1e-72:357:98//Hs.140002:AA635349  
R-THYRO1000241//Homo sapiens mRNA for KIAA0688 protein, complete cds//7.8e-69:524:82//Hs.141874:  
AB014588  
R-THYRO1000242//ESTs//4.2e-27:222:85//Hs.77554:W87927

R-THYRO1000253//Sialophorin (gpL115, leukosialin, CD43)//7.3e-40:318:80//Hs.80738:X52075  
R-THYRO1000270//ESTs//1.9e-99:531:94//Hs.17767:N62925  
R-THYRO1000279//EST//2.7e-54:266:99//Hs.149527:AI280674  
R-THYRO1000288//Homo sapiens mRNA for Hs Ste24p, complete cds//3.5e-100:566:91//Hs.25846:AB016068  
5 R-THYRO1000320//POLYPOSIS LOCUS PROTEIN 1//1.0:321:58//Hs.74648:M73547  
R-THYRO1000327//Autocrine motility factor receptor//9.2e-54:289:93//Hs.80731:M63175  
R-THYRO1000343//Homo sapiens mRNA for KIAA0790 protein, partial cds//3.4e-113:559:96//Hs.12002:  
AB018333  
R-THYRO1000358//Human selenium-binding protein (hSBP) mRNA, complete cds//1.5e-48:317:87//Hs.7833:  
10 U29091  
R-THYRO1000368//ESTs//4.7e-88:430:98//Hs.146085:AA021064  
R-nnnnnnnnnnnnn//ESTs//1.0:253:57//Hs.128783:AA436250  
R-THYRO1000387//Homo sapiens ubiquitin conjugating enzyme G2 (UBE2G2) mRNA, complete cds//4.6e-69:  
294:84//Hs.151614:AF032456  
15 R-THYRO1000394//Thromboxane A2 receptor//4.1e-40:232:87//Hs.89887:D38081  
R-THYRO1000395//ESTs//3.3e-20:160:83//Hs.101570:AA505429  
R-THYRO1000401//ESTs//1.3e-109:516:99//Hs.78524:AI140601  
R-THYRO1000438//ESTs//2.1e-48:360:83//Hs.141203:H52638  
R-THYRO1000452//ESTs, Weakly similar to No definition line found [C.elegans]//8.5e-40:239:90//Hs.84009:  
20 AI309761  
R-THYRO1000471//ESTs//3.3e-36:302:80//Hs.70279:AA757426  
R-THYRO1000484//Homo sapiens mRNA for KIAA0737 protein, complete cds//2.2e-49:479:75//Hs.17630:  
AB018280  
R-THYRO1000488//Homa sapiens mRNA for HRIHFB2038, partial cds//4.1e-89:471:94//Hs.28719:AB015333  
25 R-THYRO1000501//ESTs//L5e-46:287:89//Hs.125300:R62360  
R-THYRO1000502//ESTs//1.7e-08:63:96//Hs.116319:AI208005  
R-THYRO1000505//ESTs, Weakly similar to KIAA0281 [H. sapiens]//3.9e-57:286:96//Hs.105861:AI206965  
R-THYRO1000558//ESTs//1.7e-95:454:99//Hs.125063:AA648511  
R-THYRO1000569//ESTs//3.2e-89:463:94//Hs.20555:W22193  
30 R-THYRO1000570//ESTs//2.8e-97:471:97//Hs.8245:AA115485  
R-nnnnnnnnnnnn//Homo sapiens protein associated with Myc mRNA, complete cds//2.6e-108:533:97//Hs.151411:  
AF075587  
R-THYRO1000596//ESTs//3.1e-99:527:94//Hs.6084:AA045247  
R-THYRO1000602//EST//6.9e-50:381:83//Hs.161917:AA483223  
35 R-THYRO1000605//ESTs, Weakly similar to monocytic leukaemia zinc finger protein [H.sapiens]//1.2e-96:483:96//  
Hs.21907:N24415  
R-THYRO1000625//ESTs//5.6e-36:257:84//Hs.139657:AA191742  
R-THYRO1000637  
R-THYRO1000641//ESTs, Weakly similar to ERYTHROCYTE BAND 7 INTEGRAL MEMBRANE PROTEIN [H.  
40 sapiens]//4.9e-46:245:95//Hs.97398:AA398634  
R-THYRO1000658//ESTs//5.8e-48:281:90//Hs.142259:AA828840  
R-nnnnnnnnnnnn//ESTs//1.5e-82:389:99//Hs.155573:AA487384  
R-THYRO1000666//ESTs//1.4e-26:179:88//Hs.98382:AA779866  
R-THYRO1000676//EST//6.4e-05:88:77//Hs.133424:AI061063  
45 R-THYRO1000684//ESTs//1.9e-69:374:94//Hs.144617:R77109  
R-THYRO1000699//ESTs//1.7e-58:394:86//Hs.26373:AA700713  
R-THYRO1000712  
R-THYRO1000734//EST//2.0e-06:95:73//Hs.156201:AA724287  
R-THYRO1000748//EST//4.1e-12:155:74//Hs.118694:AA148713  
50 R-THYRO1000756//ESTs, Weakly similar to CMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-AL-  
PHA-2,3-SIALYLTRANSFERASE [H.sapiens]//8.1e-82:497:87//Hs.109672:W22624  
R-THYRO1000777  
R-THYRO1000783//EST//5.6e-100:470:99//Hs.123515:AA812932  
R-THYRO1000787//EST//8.0e-34:175:99//Hs.99607:AA463897  
55 R-THYRO1000793//ESTs//2.2e-106:505:99//Hs.50929:AA443144  
R-THYRO1000796//ESTs//4.3e-44:445:75//Hs.55855:AA621381  
R-THYRO1000805//EST//2.6e-32:407:67//Hs.123424:AA813594  
R-THYRO1000815//Human mRNA for KIAA0033 gene, partial cds//2.0e-56:307:87//Hs.22271:D26067

	R-THYRO1000829
	R-THYRO1000843//Interleukin 10//1.1e-44:285:87//Hs.2180:M57627
	R-THYRO1000852//EST//2.3e-20:157:85//Hs.149580:AI281881
	R-THYRO1000855//ESTs//2.6e-44:359:81//Hs.140329:AA714011
5	R-THYRO1000865//Protein kinase, interferon-inducible double stranded RNA dependent//2.8e-44:374:79//Hs.73821:M35663
	R-THYRO1000895//ESTs//1.0e-32:196:85//Hs.138630:H97871
	R-THYRO1000916//ESTs//4.6e-99:492:96//Hs.152442:AA528234
10	R-THYRO1000926//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds//3.1e-110:566:94//Hs.78106:AF079529
	R-THYRO1000934//ESTs//7.4e-102:535:95//Hs.58194:W72182
	R-THYRO1000951//ESTs//4.2e-11:91:89//Hs.6278:T15859
	R-THYRO1000952//ESTs//3.9e-93:489:94//Hs.48928:AA211761
15	R-THYRO1000974//Homo sapiens ribosomal protein L33-like protein mRNA, complete cds//1.1e-60:321:95//Hs.14454:AF047440
	R-THYRO1000975//EST//9.8e-49:303:89//Hs.149580:AI281881
	R-THYRO1000983//ESTs, Highly similar to UBIQUITIN-CONJUGATING ENZYME E2-17 KD 11 [Arabidopsis thaliana]//1.6e-90:474:93//Hs.106616:AI027524
20	R-THYRO1000984//ESTs//5.9e-97:481:96//Hs.142457:AI202777
	R-THYRO1000988//EST//3.5e-42:241:83//Hs.162404:AA573131
	R-THYRO1001003//ESTs, Weakly similar to ubiquitin-conjugating enzyme [H.sapiens]//3.0e-57:341:91//Hs.44049:AA521489
	R-THYRO1001031//ESTs//5.5e-47:322:85//Hs.136839:H93717
25	R-THYRO1001033//ESTs//5.7e-89:427:98//Hs.71508:AA809070
	R-THYRO1001062//EST//1.5e-46:291:89//Hs.161917:AA483223
	R-THYRO1001093//ESTs//2.7e-80:468:90//Hs.124601:AA203497
	R-THYRO1001100
	R-THYRO1001120//ESTs, Moderately similar to fractionated X-irradiation-induced 29 thymoma [M.musculus]//6.6e-86:491:89//Hs.89135:AI138834
30	R-THYRO1001121//Homo sapiens mRNA for beta-tubulin folding cofactor D//2.6e-82:429:94//Hs.12570:AJ006417
	R-THYRO1001133//ESTs//2.9e-39:242:90//Hs.152340:AA521399
	R-THYRO1001134//ESTs//1.8e-102:521:95//Hs.108408:N31922
35	R-THYRO1001142//ESTs//0.26:84:69//Hs.153434:AI287853
	R-THYRO1001173//Human mRNA for KIAA0238 gene, partial cds//0.0012:305:62//Hs.82042:D87075
	R-THYRO1001177
	R-THYRO1001189//H.sapiens F11 mRNA//1.5e-59:260:83//Hs.159639:X77744
	R-THYRO1001204//ESTs, Weakly similar to TH1 protein [D.melanogaster]//1.0e-75:431:91//Hs.5184:AA709151
40	R-THYRO1001213//ESTs//1.3e-75:409:92//Hs.140213:AA828932
	R-THYRO1001262//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//1.3e-48:349:83//Hs.139107:K00629
	R-THYRO1001271//PUTATIVE PROTEIN PHOSPHATASE 2C//1.0:128:64//Hs.118728:D13640
	R-THYRO1001290//ESTs//2.1e-89:424:99//Hs.118152:AA702561
	R-THYRO1001313//ESTs//3.5e-17:139:87//Hs.15827:H16269
	R-THYRO1001320//ESTs//1.4e-61:403:79//Hs.139555:N48230
45	R-THYRO1001321//Hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome)//8.5e-05:326:60//Hs.82314:M31642
	R-nnnnnnnnnnnnnn//ESTs//0.16:422:5.9//Hs.23876:AA082935
	R-THYRO1001347//ESTs, Weakly similar to C35A5.8 [C.elegans]//1.1e-106:562:94//Hs.15032:AA774250
50	R-THYRO1001363//ESTs//1.4e-99:508:95//Hs.5028:D51033
	R-THYRO1001365
	R-THYRO1001374
	R-THYRO001401//Human HsLIM15 mRNA for HsLiml5, complete cds//2.5e-48:467:75//Hs.37181:D64108
	R-THYRO1001403//Interleukin 10//2.1e-46:305:85//Hs.2180:M57627
	R-THYRO1001405//ESTs//4.8e-25:197:84//Hs.6907:W72733
55	R-THYRO1001406//EST//0.0023:117:66//Hs.162931:AA633197
	R-THYRO1001411//ESTs//6.1e-77:421:93//Hs.22973:R40979
	R-THYRO1001426//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0508//9.1e-49:305:86//Hs.159187:AB007977



EP 1 074 617 A2

	R-Y79AA1000328//ESTs//1.9e-76:448:91//Hs.16470:AA121635
	R-Y79AA1000342//ESTs, Weakly similar to MATRIN 3 [H.sapiens]//2.0e-37:239:88//Hs.23476:AA401210
	R-Y79AA1000346//ESTs//7.9e-12:139:76//Hs.115987:AA483808
5	R-Y79AA1000349//ESTs, Moderately similar to spermatid perinuclear RNA-binding protein Spnr [M.musculus]//4.4e-66:339:97//Hs.8215:AA521150
	R-Y79AA1000355//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//3.2e-44:279:88//Hs.139007:H74314
	R-Y79AA1000368//ESTs//3.8e-97:513:94//Hs.68090:AA641018
10	R-Y79AA1000405//ESTs//4.4e-47:267:94//Hs.125304:R51613
	R-Y79AA1000410//ESTs//7.4e-49:359:82//Hs.158107:AA707758
	R-Y79AA1000420//EST//0.17:99:69//Hs.160859:AI352292
	R-Y79AA1000469//ESTs, Highly similar to ancient ubiquitous 46 kDa protein AUP46 precursor [M.musculus]//3.1e-60:362:88//Hs.6381:AI188509
15	R-Y79AA1000480//ESTs//1.0e-75:433:91//Hs.78110:AA741320
	R-Y79AA1000538//EST//7.9e-48:307:87//Hs.149580:AI281881
	R-Y79AA1000539//Human kinesin-like spindle protein HKSP (HKSP) mRNA, complete cds//0.95:172:62//Hs.41723:U37426
	R-Y79AA1000540//ESTs//1.5e-97:534:93//Hs.67991:AA147848
20	R-Y79AA1000560//ESTs, Highly similar to ALPHA-ADAPTIN [Rattus norvegicus]//8.2e-97:482:97//Hs.19121:AI125280
	R-Y79AA1000574//ESTs, Weakly similar to M04B2.4 [C.elegans]//1.3e-107:564:93//Hs.16361:AI147455
	R-Y79AA1000627//Homo sapiens zinc finger protein (ZF5128) mRNA, complete cds//3.4e-99:517:94//Hs.60580:AF060503
25	R-Y79AA1000705//ESTs, Weakly similar to HYPOTHETICAL 128.5 KD HELICASE IN ATS1-TPD3 INTERGENIC REGION [Saccharomyces cerevisiae]//8.1e-27:140:100//Hs.129049:H28818
	R-Y79AA1000734//Homo sapiens peroxisomal biogenesis factor (PEX11b) mRNA, complete cds//8.7e-114:586:95//Hs.83023:AF093670
	R-Y79AA1000748//ESTs, Weakly similar to HYPOTHETICAL 61.3 KD PROTEIN F25B5.5 IN CHROMOSOME III [C.elegans]//9.8e-111:563:95//Hs.19845:AI005330
30	R-Y79AA1000752//Homo sapiens (huc) mRNA, complete cds//0.97:235:59//Hs.1701:L26405
	R-Y79AA1000774//ESTs//5.9e-109:559:95//Hs.17138:N91463
	R-Y79AA1000782//Human mRNA for KIAA0246 gene, partial cds//1.6e-18:107:100//Hs.84753:D87433
	R-Y79AA1000784//EST//0.80:87:67//Hs.158558:AI368359
35	R-Y79AA1000794//ESTs//2.7e-99:498:96//Hs.25441:AA580512
	R-Y79AA1000800//ESTs//1.2e-97:532:93//Hs.77822:AA532642
	R-nnnnnnnnnnnn//Carboxypeptidase E//0.018:354:59//Hs.75360:X51405
	R-Y79AA1000805
	R-Y79AA1000824//ESTs//0.99:276:61//Hs.153992:AA280227
40	R-Y79AA1000827//ESTs//1.2e-55:326:92//Hs.158127:AI334650
	R-Y79AA1000850//Homo sapiens small optic lobes homolog (SOLH) mRNA, complete cds//0.016:386:59//Hs.55836:U85647
	R-Y79AA1000962//EST//0.024:177:63//Hs.25214:R37079
	R-Y79AA1000968
	R-Y79AA1000969//ESTs//2.9e-70:251:98//Hs.120858:AA417181
45	R-Y79AA1000976//ESTs//7.8e-56:299:95//Hs.120125:M86049
	R-Y79AA1000985
	R-Y79AA1001023//ESTs//5.7e-66:379:90//Hs.64616:W22851
	R-Y79AA1001041//ESTs//8.6e-06:54:100//Hs.8980:AA629067
	R-Y79AA1001048//ESTs//4.4e-97:461:99//Hs.7010:AA837407
50	R-Y79AA1001061//ESTs//3.8e-105:493:99//Hs.128419:AI271325
	R-Y79AA1001068//Homo sapiens mRNA for KIAA0563 protein, complete cds//4.8e-53:279:83//Hs.15731:AB011135
	R-Y79AA1001077//ESTs//1.9e-51:339:87//Hs.11197:AA309047
	R-Y79AA1001078//ESTs//8.3e-98:528:92//Hs.24608:AA161260
55	R-Y79AA1001105//ESTs//6.0e-77:393:96//Hs.30837:H08155
	R-Y79AA1001145//ESTs//1.7e-13:285:64//Hs.128259:AA343015
	R-Y79AA1001167
	R-Y79AA1001177//EST//1.2e-05:92:76//Hs.65277:T15884

R-Y79AA1001185  
R-Y79AA1001211//ESTs//1.3e-70:344:97//Hs.49760:AA741051  
R-Y79AA1001216//ESTs//5.8e-63:416:88//Hs.8595:W60933  
R-Y79AA1001228//ESTs//9.3e-101:483:98//Hs.13916:AI025750  
5 R-Y79AA1001233//EST//0.00027:232:62//Hs.132431:AA909674  
R-Y79AA1001236//Homo sapiens mRNA for JM23 protein, complete coding sequence (clone IMAGE 34581 and  
IMAGE 45355 and LLNLc110I133Q7 (RZPD Berlin))//1.1e-110:549:95//Hs.23170:AJ005892  
R-Y79AA1001281//ESTs//3.6e-98:466:99//Hs.104442:AA481271  
R-Y79AA1001299//Human In1 mRNA, complete cds//9.6e-25:133:100//Hs.155626:U04847  
10 R-Y79AA1001312//ESTs//3.4e-92:454:97//Hs.127319:AI191149  
R-Y79AA1001323//ESTs//1.6e-67:422:89//Hs.118559:AA887084  
R-Y79AA1001384//ESTs//3.1e-104:496:98//Hs.153692:AA604143  
R-Y79AA1001391//ESTs//2.2e-77:418:94//Hs.118608:AA101819  
15 R-Y79AA1001394//ESTs//2.1e-78:409:95//Hs.23413:AA579859  
R-Y79AA1001402//EST//9.3e-08:128:75//Hs.141607:N63891  
R-Y79AA1001493//ESTs, Highly similar to UBIQUITIN-CONJUGATING ENZYME E2-17 KD 11 [Arabidopsis thal-  
iana]//4.4e-109:553:95//Hs.106616:AI027524  
R-Y79AA1001511//ESTs//4.9e-49:271:92//Hs.109045:AA523704  
R-Y79AA1001533//ESTs, Moderately similar to RNA polymerase I associated factor [M.musculus]//6.2e-46:260:  
20 94//Hs.24884:AA176812  
R-nnnnnnnnnnnnnn//EST//0.62:126:67//Hs.137020:AA868563  
R-Y79AA1001548//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA//3.5e-95:517:91//Hs.76987:AF012872  
R-Y79AA1001555//Collagen, type XI, alpha 1//1.0:157:64//Hs.82772:J04177  
R-Y79AA1001585//ESTs//1.9e-90:430:98//Hs.48333:AA704508  
25 R-Y79AA1001594//ESTs//9.6e-23:122:100//Hs.63795:AI126237  
R-Y79AA1001603//ESTs//1.0e-50:193:100//Hs.25635:AI336204  
R-Y79AA1001613//ESTs, Weakly similar to zinc finger protein [H.sapiens]//7.2e-81:400:97//Hs.13323:AA897542  
R-Y79AA1001647//ESTs//6.8e-92:479:95//Hs.154270:N26486  
R-Y79AA1001665//ESTs, Weakly similar to 50S RIBOSOMAL PROTEIN L20 [E.coli]//2.5e-19:112:97//Hs.26252:  
30 AA643235  
R-Y79AA1001679//ESTs, Highly similar to LAMBDA-CRYSTALLIN [Oryctolagus cuniculus]//9.7e-99:553:92//Hs.  
108896:R54040  
R-nnnnnnnnnnnnnn  
R-Y79AA1001696//ESTs//1.4e-84:478:91//Hs.6606:AA211783  
35 R-Y79AA1001705//ESTs//6.7e-107:546:95//Hs.106805:AA418490  
R-Y79AA1001711//Human DNA sequence from clone 1119D9 on chromosome 20p12. Contains part of a gene for  
a PAK1 LIKE Serine/Threonine-Protein Kinase and part of the PLCB4 gene for Phopholipase C, beta (1-Phos-  
phatidylinositol -4,5-Bisphosphate Phosphodiesterase Beta 4). Contains ESTs, STSs and GSSs//0.0085:251:63//  
Hs.21864:AL031652  
40 R-Y79AA1001781//ESTs, Weakly similar to partial CDS [C.elegans]//9.4e-87:427:97//Hs.18645:AI023798  
R-nnnnnnnnnnnnnn//ESTs//1.1e-112:558:97//Hs.109755:AA180809  
R-Y79AA1001827//ESTs, Weakly similar to Similar to S.cerevisiae YD9335.03c protein [H.sapiens]//8.1e-95:530:  
91//Hs.72444:W23217  
R-Y79AA1001846//EST//2.8e-41:312:81//Hs.162236:AA551582  
45 R-Y79AA1001848//Human adhalin (DAG2) mRNA, complete cds//0.54:221:58//Hs.99931:L34355  
R-Y79AA1001866//ESTs//2.2e-102:498:97//Hs.130683:AI278630  
R-Y79AA1001874//ESTs//1.9e-76:377:98//Hs.79707:AA354094  
R-Y79AA1001875//ESTs//0.64:152:63//Hs.156159:AI333652  
R-Y79AA1001923//EST//0.19:180:58//Hs.148290:AA908404  
50 R-Y79AA1002027//ESTs//1.6e-104:497:98//Hs.21275:N73275  
R-Y79AA1002083//Homo sapiens mRNA for KIAA0563 protein, complete cds//0.69:93:73//Hs.15731:AB011135  
R-Y79AA1002089//Homo sapiens PYRJN (MEFV) mRNA, complete cds//1.1e-46:392:80//Hs.113283:AF018080  
R-Y79AA1002093//Homo sapiens GT198 mRNA, complete ORF//1.2e-12:80:100//Hs.78185:L38933  
R-Y79AA1002103//ESTs//1.3e-52:535:76//Hs.142167:AI417785  
55 R-Y79AA1002115//ESTs//4.2e-101:519:96//Hs.23977:AA115275  
R-Y79AA1002125//ESTs//9.8e-68:363:94//Hs.72085:AA193399  
R-Y79AA1002139//ESTs//1.2e-100:498:96//Hs.72020:AA149858  
R-Y79AA1002204//ESTs//2.1e-83:434:95//Hs.22979:R43725

R-nnnnnnnnnnnn//ESTs//1.7e-55:478:76//Hs.154554:AA552715  
 R-Y79AA1002209//ESTs, Weakly similar to similar to tyrosyl-tRNA synthetase. [C.elegans]//3.5e-108:553:95//Hs.  
 5 50441:AA747428  
 R-Y79AA1002210//ESTs//4.2e-16:92:100//Hs.54862:AA248349  
 R-Y79AA1002211//ESTs, Weakly similar to PHOSPHATIDYLETHANOLAMINE-BINDING PROTEIN [H.sapiens]//  
 10 6.5e-86:518:90//Hs.25682:AA857843  
 R-Y79AA1002220//EST//1.3e-68:326:100//Hs.131052:AI016274  
 R-Y79AA1002229//ESTs//1.9e-98:467:98//Hs.132002:AI039977  
 R-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds//2.0e-118:564:98//Hs.100729:  
 15 AB014592  
 R-Y79AA1002246//ESTs, Weakly similar to PROTEIN KINASE C, BRAIN ISOZYME [D.melanogaster]//9.0e-102:  
 20 507:96//Hs.25895:AI341537  
 R-Y79AA1002258//Homo sapiens mRNA for KIAA0655 protein, partial cds//2.4e-93:453:97//Hs.96731:AB014555  
 R-Y79AA1002298//ESTs//0.022:241:62//Hs.118272:N90288  
 25 R-Y79AA1002307//Homo sapiens mRNA for KIAA0634 protein, partial cds//8.1e-110:403:99//Hs.30898:  
 AB014534  
 R-Y79AA1002311//EST//2.6e-27:214:85//Hs.144721:AI187985  
 R-Y79AA1002351//ESTs//5.6e-100:489:97//Hs.30318:AA913371  
 R-Y79AA1002361  
 30 R-Y79AA1002399//ESTs//0.029:149:65//Hs.43872:N26908  
 R-Y79AA1002407//ESTs//2.8e-117:552:99//Hs.99519:AI042000  
 R-Y79AA1002416//ESTs//2.6e-107:531:96//Hs.6716:AA502753  
 R-Y79AA100243//EST//6.6e-23:128:98//Hs.128417:AA975026  
 R-nnnnnnnnnnnn//ESTs, Highly similar to CELL DIVISION CONTROL PROTEIN 68 [Saccharomyces cerevisiae]  
 35 //4.4e-62:390:88//Hs.143930:AI207821  
 R-Y79AA1002472//ESTs//1.1e-39:234:78//Hs.117969:H94870  
 R-Y79AA1002482//ESTs//3.4e-45:312:85//Hs.146811:AA410788  
 R-Y79AA1002487//ESTs//1.7e-80:427:94//Hs.49210:N66499

## 30 Homology Search Result Data 6

**[0314]** Data obtained by the homology search for full-length nucleotide sequences and deduced amino acid sequences. In the result of the search shown below, both units, aa and bp, are used as length units for the sequences to be compared. Each data includes Clone name, Definition in hit data, P value, Length of sequence to be compared, Homology, and Accession number (No.) of hit data. These items are shown in this order and separated by a double-slash mark, //.

40 C-HEMBA1000005//DNAJ PROTEIN HOMOLOG MTJ1//1.9E-250//554aa//85%//Q61712  
 C-HEMBA1000030  
 C-HEMBA1000046  
 C-HEMBA1000050  
 C-HEMBA1000076  
 C-HEMBA1000156//NEUROFILAMENT TRIPLET M PROTEIN (160 KD NEUROFILAMENT PROTEIN) (NF-M).//  
 45 1.9E-12//368aa//24%//P08553  
 C-HEMBA1000158//HEPATOCYTE NUCLEAR FACTOR 3.-GAMMA (HNF-3G).//5E-16//166aa//36%//P35584  
 C-HEMBA1000168//CYLICIN I (MULTIPLE-BAND POLYPEPTIDE I).//2.9E-14//303aa//25%//P35662  
 C-HEMBA1000185//RAS-RELATED PROTEIN RAL-A.//3.4E-12//125aa//31%//P48555  
 C-HEMBA1000193  
 C-HEMBA1000227  
 50 C-HEMBA1000288  
 C-HEMBA1000302  
 C-HEMBA1000304  
 C-HEMBA1000307//CARNITINE DEFICIENCY-ASSOCIATED PROTEIN EXPRESSED IN VENTRICLE 1//5.2E-  
 49//107aa//91 %//035594  
 55 C-HEMBA1000369//Novel human mRNA similar to mouse gene PICK1 (TR:Q62083).//0//1950bp//98%//  
 AL049654  
 C-HEMBA1000387  
 C-HEMBA1000392

C-HEMBA1000460  
 C-HEMBA1000488//RING CANAL PROTEIN (KELCH PROTEIN).//3.3E-45//481aa//29%//Q04652  
 C-HEMBA1000491//RAS-LIKE PROTEIN 2.//2E-22//188aa//31%//P22279  
 C-HEMBA1000501  
 5 C-HEMBA1000508  
 C-HEMBA1000520  
 C-HEMBA1000531//HEAT SHOCK 70 KD PROTEIN COGNATE 1 (HEAT SHOCK 70 KD PROTEIN 70C) (FRAGMENTS).//2.6E-12//73aa//41%//P02826  
 C-HEMBA1000534  
 10 C-HEMBA1000555  
 C-HEMBA1000568  
 C-HEMBA1000588  
 C-HEMBA1000608//HYPOTHETICAL PROTEIN KIAA0411 (FRAGMENT).//1.8E-55//179aa//61%//O43295  
 C-HEMBA1000636  
 15 C-HEMBA1000682  
 C-HEMBA1000686  
 C-HEMBA1000719  
 C-HEMBA1000727  
 C-HEMBA1000752  
 20 C-HEMBA1000817  
 C-HEMBA1000851  
 C-HEMBA1000867  
 C-HEMBA1000869  
 C-HEMBA1000872  
 25 C-HEMBA1000910//MELANOMA-ASSOCIATED ANTIGEN B1 (MAGE-B1 ANTIGEN) (MAGE-XP ANTIGEN)//1.6E-30//127aa//40%//P43366  
 C-HEMBA1000918  
 C-HEMBA1000919//HYPOTHETICAL 65.5 KD TRP-ASP REPEATS CONTAINING PROTEIN F02E8.5 IN CHROMOSOME X.//1E-10//288aa//23%//Q19124  
 30 C-HEMBA1000946  
 C-HEMBA1000968  
 C-HEMBA1000971  
 C-HEMBA1000975  
 C-HEMBA1001009  
 35 C-HEMBA1001022  
 C-HEMBA1001043//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID)(FRAGMENT).//1.4E-12//131aa//38%//Q01485  
 C-HEMBA1001052  
 C-HEMBA1001080  
 40 C-HEMBA1001085  
 C-HEMBA1001088//PINCH PROTEIN (PARTICULARLY INTERESTING NEW CYS-HIS PROTEIN).//3.5E-50//176aa//57%//P48059  
 C-HEMBA1001109  
 C-HEMBA1001122  
 45 C-HEMBA1001133  
 C-HEMBA1001137//ZINC FINGER PROTEIN 33A (ZINC FINGER PROTEIN KOX31) (KIAA0065) (HA0946) (FRAGMENT).//1.5E-116//197aa//58%//Q06730  
 C-HEMBA1001140  
 C-HEMBA1001174//ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 5.//6.8E-79//179aa//80%//P51646  
 50 C-HEMBA1001197//Homo sapiens mRNA for KIAA0871 protein, complete cds.//9.5E-257//1307bp//94%//AB020678  
 C-HEMBA1001235  
 C-HEMBA1001257//Homo sapiens mRNA 2-methylacyl-CoA racemase.//0//1672bp//99%//AJ130733  
 C-HEMBA1001281  
 55 C-HEMBA1001286//COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR.//0.00000002//198aa//29%//Q60401  
 C-HEMBA1001303  
 C-HEMBA1001310

C-HEMBA1001326  
C-HEMBA1001351//Homo sapiens VAMP-associated protein of 33 kDa (VAP-33) mRNA, complete cds.//1.4E-133//614bp//99%//AF057358  
C-HEMBA1001387//GTP-BINDING PROTEIN TC10.//2.9E-64//104aa//82%//P17081  
5 C-HEMBA1001388  
C-HEMBA1001398  
C-HEMBA1001405  
C-HEMBA1001407  
C-HEMBA1001413  
10 C-HEMBA1001415  
C-HEMBA1001446  
C-HEMBA1001450  
C-HEMBA1001455  
C-HEMBA1001510//CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-6 (FRAGMENT).//1.7E-16//  
15 63aa//61%//P18850  
C-HEMBA1001526//PERIPLASMIC [FE] HYDROGENASE 1 (EC 1.18.99.1).//4.9E-37//399aa//29%//P29166  
C-HEMBA1001533  
C-HEMBA1001579//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1662bp//99%//AB020657  
C-HEMBA1001581  
20 C-HEMBA1001595//SEPTIN 2 HOMOLOG (FRAGMENT).//4.9E-156//348aa//83%//Q14141  
C-HEMBA1001635//TESTIS SPECIFIC PROTEIN A (ZINC FINGER PROTEIN TSGA).//1.6E-10//155aa//28%//  
Q63679  
C-HEMBA1001661//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//4.6E-36//  
365aa//33%//P33450  
25 C-HEMBA1001702  
C-HEMBA1001714//Homo sapiens mRNA; cDNA DKFZp564G0422 (from clone DKFZp564G0422).//0//1845bp//  
99%//AL050386  
C-HEMBA1001731  
C-HEMBA1001744//SCY1PROTEIN.//9.9E-32//481aa//25%//P53009  
30 C-HEMBA1001809//IMMEDIATE-EARLY PROTEIN IE180.//3.8E-11//206aa//36%//P11675  
C-HEMBA1001815  
C-HEMBA1001819//ZINC FINGER PROTEIN 184 (FRAGMENT).//2.9E-135//459aa//52%//Q99676  
C-HEMBA1001847//ZINC FINGER PROTEIN 29 (ZFP-29).//7.6E-64//221aa//55%//Q07230  
C-HEMBA1001864  
35 C-HEMBA1001869//TRITHORAX PROTEIN.//0.000096//166aa//27%//P20659  
C-HEMBA1001896//DIMETHYLGlycine DEHYDROGENASE PRECURSOR (EC 1.5.99.2) (ME2GLYDH).//  
9.3E-36//395aa//26%//Q63342  
C-HEMBA1001987  
C-HEMBA1002018  
40 C-HEMBA1002049  
C-HEMBA1002084  
C-HEMBA1002125  
C-HEMBA1002161//MYOSIN HEAVY CHAIN, CARDIAC MUSCLE BETA ISOFORM.//1.4E-51//180aa//56%//  
P79293  
45 C-HEMBA1002177//TRANSCRIPTION FACTOR GATA-4 (GATA BINDING FACTOR-4).//6E-13//190aa//36%//  
P43694  
C-HEMBA1002191  
C-HEMBA1002199  
C-HEMBA1002212//TYROSINE-PROTEIN KINASE 2 (EC 2.7.1.112) (FRAGMENT).//3E-17//267aa//29%//  
50 P18161  
C-HEMBA1002237  
C-HEMBA1002265  
C-HEMBA1002267//Sus scrofa decorin mRNA, complete cds.//1.1E-46//302bp//90%//AF125537  
C-HEMBA1002349  
55 C-HEMBA1002363//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//0//  
1847bp//99%//AF092563  
C-HEMBA1002419//TRICHOHYALIN.//1.9E-09//299aa//24%//P22793  
C-HEMBA1002430

C-HEMBA1002439  
C-HEMBA1002458//OVARIAN GRANULOSA CELL 13.0 KD PROTEIN HGR74..//4.2E-24//109aa//55%//Q00994  
C-HEMBA1002460  
C-HEMBA1002462  
5 C-HEMBA1002469//DXS8237E PROTEIN (FRAGMENT).//3.5E-50//199aa//61%//P98175  
C-HEMBA1002475//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//1.1E-12//285aa//  
31%//P17437  
C-HEMBA1002477  
C-HEMBA1002495//LIGHT-MEDIATED DEVELOPMENT PROTEIN DET1..//6.8E-53//257aa//36%//P48732  
10 C-HEMBA1002515  
C-HEMBA1002542  
C-HEMBA1002569//Homo sapiens protein associated with Myc mRNA, complete cds..//6.8E-305//951bp//99%//  
AF075587  
C-HEMBA1002583  
15 C-HEMBA1002609//Homo sapiens mRNA for KIAA0597 protein, partial cds..//1.4E-253//1149bp//99%//AB011169  
C-HEMBA1002624//Homo sapiens mRNA for KIAA0808 protein, complete cds..//0//1539bp//99%//AB018351  
C-HEMBA1002688  
C-HEMBA1002696  
C-HEMBA1002750  
20 C-HEMBA1002768//Homo sapiens mRNA for Cdc42-interacting protein 4 (CIP4)..//1E-80//882bp//61%//AJ000414  
C-HEMBA1002770//Homo sapiens mRNA for KIAA0829 protein, partial cds..//0//1532bp//99%//AB020636  
C-HEMBA1002777  
C-HEMBA1002794  
C-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cds..//8.2e-314//1437bp//99%//  
25 AF071185  
C-HEMBA1002818//Homo sapiens, mRNA for fibulin-4..//2E-304//1383bp//99%//AJ132819  
C-HEMBA1002850  
C-HEMBA1002863  
C-HEMBA1002876//HYPOTHETICAL 26.4 KD PROTEIN EED8.8 IN CHROMOSOME II..//1.5E-44//188aa//  
30 52%//Q09297  
C-HEMBA1002935//Homo sapiens mRNA for KIAA0576 protein, partial cds..//0//1483bp//100%//AB011148  
C-HEMBA1002937  
C-HEMBA1002939//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN)..//2E-34//300aa//34%//  
P16157  
35 C-HEMBA1002951//Homo sapiens mRNA for KIAA0903 protein, partial cds..//0//1752bp//99%//AB020710  
C-HEMBA1002954  
C-HEMBA1002971  
C-HEMBA1002973//CAMP-DEPENDENT 3',5'-CYCLIC PHOSPHODIESTERASE 4B (EC 3.1.4.17) (DPDE4)..//  
1.2E-27//63aa//100%//P14646  
40 C-HEMBA1002997//CENTROMERIC PROTEIN E (CENP-E PROTEIN)..//3.8E-25//5 34aa//24%//Q02224  
C-HEMBA1003033  
C-HEMBA1003035  
C-HEMBA1003041  
C-HEMBA1003046//MITOCHONDRIAL PROCESSING PROTEASE BETA SUBUNIT PRECURSOR (EC  
45 3.4.24.64) (BETA-MPP) (P-52)..//2.5E-263//489aa//99%//Q075439  
C-HEMBA1003067  
C-HEMBA1003096  
C-HEMBA1003117  
C-HEMBA1003129  
50 C-HEMBA1003136//MANNOSE-1-PHOSPHATE GUANYLTRANSFERASE (EC 2.7.7.13) (ATP-MANNOSE-  
1-PHOSPHATE GUANYLYLTRANSFERASE) (NDP-HEXOSE PYROPHOSPHORYLASE)..//8.5E-51//221aa//  
33%//P41940  
C-HEMBA1003148//Homo sapiens mRNA full-length insert cDNA clone EUROIMAGE 381801..//0//1583bp//99%//  
AL079278  
55 C-HEMBA1003175  
C-HEMBA1003179//PROBABLE TRNA (5-METHYLAMINOMETHYL-2-THIOURIDYLATE)-METHYLTRANS-  
FERASE (EC 2.1.1.61)..//5.9E-74//134aa//53%//P44551  
C-HEMBA1003199

C-HEMBA1003222  
C-HEMBA1003235//TROPOMYOSIN//0.0000023//109aa//33%//Q02088  
C-HEMBA1003250//PROTEIN KINASE APK1A (EC 2.7.1.-).//7.2E-41//245aa//42%//Q06548  
C-HEMBA1003257  
5 C-HEMBA1003281//POLIOVIRUS RECEPTOR PRECURSOR//6E-11//239aa//32%//P32506  
C-HEMBA1003286//Homo sapiens mRNA for beta-1,4-galactosyltransferase IV, complete cds//5.4E-229//  
1043bp//99%//AB024436  
C-HEMBA1003291//Homo sapiens mRNA for KIAA0537 protein, complete cds//0//791bp//99%//AB011109  
C-HEMBA1003322  
10 C-HEMBA1003327  
C-HEMBA1003369//CENTROMERIC PROTEIN E (CENP-E PROTEIN).//0.0000002//248aa//23%//Q02224  
C-HEMBA1003370  
C-HEMBA1003380  
C-HEMBA1003395  
15 C-HEMBA1003402  
C-HEMBA1003408//Homo sapiens mRNA for KIAA0905 protein, complete cds//0//1732bp//98%//AB020712  
C-HEMBA1003417//Homo sapiens mRNA; cDNA DKFZp586C021 (from clone DKFZp586C021).//1.6e-312//  
1414bp//99%//AL050287  
C-HEMBA1003418//TRICHOHYALIN//8.7E-19//281aa//31%//P37709  
20 C-HEMBA1003433//Homo sapiens gene for NBS1, complete cds//0//511bp//94%//AB013139  
C-HEMBA1003447  
C-HEMBA1003461  
C-HEMBA1003463  
C-HEMBA1003528  
25 C-HEMBA1003545//INSULIN GENE ENHANCER PROTEIN ISL-2 (ISLET-2).//8.8E-189//360aa//96%//P50480  
C-HEMBA1003555//NUCLEOTIDE-BINDING PROTEIN (NBP).//2.1E-68//251aa//52%//P53384  
C-HEMBA1003560//GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(O) GAMMA-2 SUBUNIT (G GAM-  
MA-I).//1.2E-31//71aa//100%//P16874  
C-HEMBA1003568//52 KD RO PROTEIN (SJOGLREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)).//7.9E-  
30 49//279aa//32%//P19474  
C-HEMBA1003569//METASTASIS-ASSOCIATED PROTEIN MTA1.//6.9E-206//445aa//74%//Q13330  
C-HEMBA1003581//TALIN.//4.4E-45//52aa//98%//P26039  
C-HEMBA1003591//CHLOROPLAST 28 KD RIBONUCLEOPROTEIN PRECURSOR (28RNP).//4.4E-10//118aa//  
35 35%//P19682  
C-HEMBA1003615  
C-HEMBA1003617//Homo sapiens HRIHFB2157 mRNA, partial cds//8.2E-178//501bp//97%//AB015344  
C-HEMBA1003621  
C-HEMBA1003662//TBX2 PROTEIN (T-BOX PROTEIN 2).//1.2E-75//151aa//99%//Q13207  
C-HEMBA1003690//HISTONE DEACETYLASE HDA1.//2.1E-59//249aa//47%//P53973  
40 C-HEMBA1003711  
C-HEMBA1003807  
C-HEMBA1003864  
C-HEMBA1003953//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAGMENT).//3.8E-16//  
89aa//46%//P16372  
45 C-HEMBA1003959  
C-HEMBA1003989  
C-HEMBA1004074  
C-HEMBA1004097//Mus musculus putative transcription factor mRNA, complete cds//8.5E-221//1188bp//78%//  
AF091234  
50 C-HEMBA1004146  
C-HEMBA1004199//Homo sapiens mRNA for KIAA0928 protein, partial cds//0//1893bp//98%//AB023145  
C-HEMBA1004207//Homo sapiens leptin receptor short form (db) mRNA, complete cds//0//1892bp//99%//U50748  
C-HEMBA1004227//Rattus norvegicus protein phosphatase 2C mRNA, complete cds//5.7E-217//1217bp//88%//  
AF095927  
55 C-HEMBA1004246  
C-HEMBA1004276//Homo sapiens AP-4 adaptor complex beta4 subunit mRNA, complete cds//4.8E-257//738bp//  
99%//AF092094  
C-HEMBA1004289

C-HEMBA1004509//Homo sapiens CGI-21 protein mRNA, complete cds.//0//1512bp//96%//AF132955  
 C-HEMBA1004534//Homo sapiens gamma-filamin (ABPL) mRNA, complete cds.//1.2e-316//1445bp//99%//  
 AF089841  
 5 C-HEMBA1004596  
 C-HEMBA1004693  
 C-HEMBA1004736  
 C-HEMBA1004753  
 C-HEMBA1004756//Human transporter protein (g17) mRNA, complete cds.//9.1E-34//515bp//66%//U49082  
 C-HEMBA1004758//Homo sapiens transcription factor SL1 mRNA, complete cds.//2.6E-246//1249bp//94%//  
 10 L39060  
 C-HEMBA1004763  
 C-HEMBA1004768//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//5.4E-111//314aa//58%//P08547  
 C-HEMBA1004771  
 C-HEMBA1004776  
 15 C-HEMBA1004795//CDC4-LIKE PROTEIN (FRAGMENT).//3.8E-69//198aa//66%//P50851  
 C-HEMBA1004806  
 C-HEMBA1004847//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//8.2E-154//317aa//94%//  
 Q00004  
 C-HEMBA1004850  
 20 C-HEMBA1004863//Homo sapiens mRNA; cDNA DKFZp586M2022 (from clone DKFZp586M2022).//0//1443bp//  
 100%//AL080114  
 C-HEMBA1004923  
 C-HEMBA1004929  
 C-HEMBA1004930//26S PROTEASOME SUBUNIT S5B (KIAA0072) (HA1357).//3.3E-27//65aa//100%//Q16401  
 25 C-HEMBA1004933  
 C-HEMBA1004954  
 C-HEMBA1004972//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H).//  
 0.00000096//286aa//23%//P12036  
 C-HEMBA1005475  
 30 C-HEMBA1005581//Homo sapiens SLIT2 (SUL2) mRNA, complete cds.//0//1721bp//100%//AF133270  
 C-HEMBA1006248//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAGMENT).//8.6E-23//  
 151aa//37%//P16372  
 C-HEMBA1006310//Rattus norvegicus cytosolic sorting protein PACS-1a (PACS-1) mRNA, complete cds.//3.7E-  
 225//1189bp//88%//AF076183  
 35 C-HEMBA1006344//RADIXIN.//1.5E-31//333aa//28%//P26043  
 C-HEMBA1006377  
 C-HEMBA1006467  
 C-HEMBA1006474//40 KD PROTEIN.//1.4E-39//292aa//34%//Q01552  
 C-HEMBA1006530  
 40 C-HEMBA1006737//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID) (FRAGMENT).//  
 0.000000043//111aa//40%//Q01485  
 C-HEMBA1006795  
 C-HEMBA1006877//OXYSTEROL-BINDING PROTEIN.//2E-59//378aa//39%//P16258  
 C-HEMBA1006936  
 45 C-HEMBA1007018//Homo sapiens dynein light chain-A mRNA, complete cds.//1.5E-267//1215bp//99%//  
 AP078849  
 C-HEMBA1007342  
 C-HEMBB1000008  
 C-HEMBB1000018  
 50 C-HEMBB1000024  
 C-HEMBB1000025  
 C-HEMBB1000036  
 C-HEMBB1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//2.8E-187//  
 1582bp//80%//AF084928  
 55 C-HEMBB1000083//MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC  
 2.7.1.117) (MLCK) [CONTAINS: TELOKIN].//1.9E-22//426aa//25%//P11799  
 C-HEMBB1000103  
 C-HEMBB1000119//Homo sapiens ASMTL gene.//0//1891bp//99%//Y15521

C-HEMBB1000136  
 C-HEMBB1000215  
 C-HEMBB1000226//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE EED8.5//  
 2.7E-12//112aa//47%//Q09530  
 5 C-HEMBB1000244  
 C-HEMBB1000266//HYPOTHETICAL 54.5 KD TRP-ASP REPEATS CONTAINING PROTEIN ZC302.2 IN CHRO-  
 MOSOME V//6.1E-09//242aa//26%//Q23256  
 C-HEMBB1000338  
 C-HEMBB1000339  
 10 C-HEMBB1000391  
 C-HEMBB1000438  
 C-HEMBB1000449  
 C-HEMBB1000589  
 C-HEMBB1000591  
 15 C-HEMBB1000623  
 C-HEMBB1000630  
 C-HEMBB1000631//LONGEVITY-ASSURANCE PROTEIN 1 (LONGEVITY ASSURANCE FACTOR 1)//4.1E-19//  
 232aa//28%//P78970  
 C-HEMBB1000632//GUANINE NUCLEOTIDE RELEASING PROTEIN (GNRP)//2.2E-28//273aa//31%//P27671  
 20 C-HEMBB1000671  
 C-HEMBB1000673  
 C-HEMBB1000705  
 C-HEMBB1000706  
 C-HEMBB1000725//Rattus norvegicus GTPase Rab8b (Rab8b) mRNA, complete cds//6.2E-130//692bp//93%//  
 25 U53475  
 C-HEMBB1000763//Homo sapiens CGI-89 protein mRNA, complete cds//0//1676bp//96%//AF151847  
 C-HEMBB1000781//Homo sapiens mitogen-activated protein kinase kinase kinase MEKK2 mRNA, complete cds//  
 1.2E-126//613bp//97%//AF111105  
 C-HEMBB1000789//PUTATIVE 90.2 KD ZINC FINGER PROTEIN IN CCA1-ADK2 INTERGENIC REGION//5.1E-  
 30 54//232aa//43%//P39956  
 C-HEMBB1000807  
 C-HEMBB1000810  
 C-HEMBB1000848  
 C-HEMBB1000852  
 35 C-HEMBB1000870  
 C-HEMBB1000887  
 C-HEMBB1000908  
 C-HEMBB1000927//Homo sapiens calsenilin mRNA, complete cds//1.1E-70//595bp//76%//AF120102  
 C-HEMBB1000947//Homo sapiens clone HAW 100 putative ribonuclease III mRNA, complete cds//0//2292bp//  
 40 99%//AF116910  
 C-HEMBB1000973//Mus musculus schlafen3 (Slfn3) mRNA, complete cds//3.4E-120//580bp//67%//AF099974  
 C-HEMBB1000975  
 C-HEMBB1000985//MEPP PROTEIN (MURINE IAP-PROMOTED PLACENTA-EXPRESSED PROTEIN)//8.6E-  
 18//178aa//30%//P28575  
 45 C-HEMBB1000991  
 C-HEMBB1001011//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2)//1.4E-73//230aa//45%//  
 P51523  
 C-HEMBB1001014  
 C-HEMBB1001024  
 50 C-HEMBB1001056//PROLIFERATING-CELL NUCLEOLAR ANTIGEN P120 (PROLIFERATION-ASSOCIATED  
 NUCLEOLAR PROTEIN P120)//2.9E-19//264aa//34%//P46087  
 C-HEMBB1001058//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//3.6E-52//331bp//  
 80%//AF010144  
 C-HEMBB1001068//Homo sapiens lirrin-beta2 mRNA, partial cds//2.4E-307//1447bp//97%//AF034803  
 55 C-HEMBB1001096  
 C-HEMBB1001105  
 C-HEMBB1001117  
 C-HEMBB1001126

C-HEMBB1001137//Homo sapiens mRNA for putative phospholipase, complete cds./0//3069bp//99%//AB019435  
 C-HEMBB1001151//Rattus norvegicus golgi stacking protein homolog GRASP55 mRNA, complete cds./4.2E-210//1835bp//76%//AF110267  
 5 C-HEMBB1001153  
 C-HEMBB1001169  
 C-HEMBB1001175//ANKYRIN./6.9E-11//169aa/31%//Q02357  
 C-HEMBB1001182  
 C-HEMBB1001199  
 C-HEMBB1001210//Homo sapiens mRNA for KIAA0970 protein, complete cds./0//1816bp//99%//AB023187  
 10 C-HEMBB1001242//Homo sapiens topoisomerase-related function protein (TRF4-2) mRNA, partial cds./1.8E-284//713bp//100%//AF089897  
 C-HEMBB1001288//Homo sapiens CGI-32 protein mRNA, complete cds./1.8E-274//642bp//99%//AF132966  
 C-HEMBB1001289  
 C-HEMBB1001294//GTP-BINDING PROTEIN TC10./1.2E-79//196aa/80%//P17081  
 15 C-HEMBB1001314//Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-3) mRNA, complete cds./1.3E-129//724bp//86%//U92703  
 C-HEMBB1001331  
 C-HEMBB1001339//DXS8237E PROTEIN (FRAGMENT).//0.0000046//124aa/37%//P98175  
 C-HEMBB1001346//Homo sapiens phenylalanine-tRNA synthetase (FARS1) mRNA, nuclear gene encoding mitochondrial protein, complete cds./1.1E-58//292bp//99%//AF097441  
 20 C-HEMBB1001369  
 C-HEMBB1001384//Homo sapiens COP9 complex subunit 4 mRNA, complete cds./0//1586bp//99%//AF100757  
 C-HEMBB1001387  
 C-MAMMA1002317  
 25 C-MAMMA1002319  
 C-MAMMA1002385//RIBONUCLEOPROTEIN RB97D./0.00000015//206aa/29%//Q02926  
 C-NT2RM1000080//UNC-1 PROTEIN./5.9E-25//211aa/31%//Q21190  
 C-NT2RM1000242  
 C-NT2RM1000257//MAGO NASHI PROTEIN./7.9E-69//143aa/91%//P49028  
 30 C-NT2RM1000280//VACUOLAR ATP SYNTHASE SUBUNIT D (EC 3.6.1.34) (V-ATPASE D SUBUNIT) (V-ATPASE 28 KD ACCESSORY PROTEIN).//1.5E-106//118aa/97%//P39942  
 C-NT2RM1000669  
 C-NT2RM1000781  
 C-NT2RM1000867//Homo sapiens HSPC033 mRNA, complete cds./6.3E-172//798bp//99%//AF092138  
 35 C-NT2RM1001008  
 C-NT2RM1001044//Homo sapiens HSPC031 mRNA, complete cds./0.000000002//980bp//95%//AF085360  
 C-NT2RM1001074  
 C-NT2RM1001115//ENDOCHITINASE 2 PRECURSOR (EC 3.2.1.14).//0.0000056//239aa/27%//  
 40 C-NT2RM2000006//Human DNA sequence from clone 796F18 on chromosome 1p36.11-36.33 Contains a pseudogene similar to MMS2, ESTs and GSSs, complete sequence./0//1740bp//99%//AL031291  
 C-NT2RM2000013//DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE III SUBUNIT 2).//2.2E-144//362aa/71%//P25167  
 C-NT2RM2000030//DYNEIN INTERMEDIATE CHAIN, CYTOSOLIC (DH IC) (CYTOPLASMIC DYNEIN INTERMEDIATE CHAIN).//0.00000043//136aa/31%//P54703  
 45 C-NT2RM2000032  
 C-NT2RM2000042  
 C-NT2RM2000092//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 8 (EC 3.1.2.15) (UBIQUITIN THIOESTERASE 8) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 8) (DEUBIQUITINATING ENZYME 8).//1.3E-36//160aa/40%//P50102  
 50 C-NT2RM2000093  
 C-NT2RM2000101  
 C-NT2RM2000191//Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds./0//1574bp//99%//AF067223  
 C-NT2RM2000192  
 55 C-NT2RM2000239  
 C-NT2RM2000250//Homo sapiens mRNA; cDNA DKFZp564L232 (from clone DKFZp564L232).//4.2e-314//1416bp//100%//AL080069  
 C-NT2RM2000259

C-NT2RM2000260//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).//3.6E-19//181-aa//34%//  
P14918  
C-NT2RM2000287  
C-NT2RM2000322//Homo sapiens mRNA for KIAA0859 protein, complete cds.//3.4E-294//863bp//99%//  
5 AB020666  
C-NT2RM2000359//Homo sapiens mRNA for KIAA0560 protein, complete cds.//0//1637bp//99%//AB011132  
C-NT2RM2000363//BREAKPOINT CLUSTER REGION PROTEIN.//1.8E-14//245aa//29%//P11274  
C-NT2RM2000368//Homo sapiens protein kinase C-binding protein RACK7 mRNA, partial cds.//0//1506bp//99%//  
U48251  
10 C-NT2RM2000371//POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE (EC 2.7.7.8) (POLYNUCLE-  
OTIDE//1.7E-68//419aa//36%//P50849  
C-NT2RM2000374  
C-NT2RM2000395  
C-NT2RM2000402//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHE-  
15 ROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPO-  
NENT).//1.6E-54//344aa//33%//P32802  
C-NT2RM2000407  
C-NT2RM2000422//SODIUM- AND CHLORIDE-DEPENDENT TRANSPORTER NTT73.//1E-222//237aa//89%//  
Q08469  
20 C-NT2RM2000452//HYPOTHETICAL 63.6 KD PROTEIN IN YPT52-GCN3 INTERGENIC REGION.//0.0000001//  
157aa//28%//P36113  
C-NT2RM2000469//NITROGEN PERMEASE REACTIVATOR PROTEIN (EC 2.7.1.-).//0.0000089//377aa//24%//  
P22211  
C-NT2RM2000490//SYNAPTOTAGMIN(P65).//1.8E-13//166aa//34%//P41823  
25 C-NT2RM2000502  
C-NT2RM2000504//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//0//1673bp//99%//AF061243  
C-NT2RM2000522//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//1.3E-12//282aa//  
32%//P17437  
C-NT2RM2000540  
30 C-NT2RM2000567  
C-NT2RM2000569  
C-NT2RM2000577//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE-TRNA LIGASE) (ILERS).//  
1.7E-187//741aa//46%//P73505  
C-NT2RM2000581//Homo sapiens mRNA for KIAA0214 protein, complete cds.//0//3001bp//99%//D86987  
35 C-NT2RM2000588//HISTONE DEACETYLASE HDA1.//2.8E-60//384aa//40%//P53973  
C-NT2RM2000594//Homo sapiens DNA cytosine-5 methyltransferase 3 beta 3 (DNMT3B) mRNA, complete cds.//  
0//2712bp//99%//AF156487  
C-NT2RM2000599//Homo sapiens F-box protein Lilina (LILINA) mRNA, complete cds.//4.9E-70//838bp//69%//  
AF179221  
40 C-NT2RM2000624//SPLICING FACTOR, ARGinine/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR  
SRP75).//4.4E-32//319aa//35%//Q08170  
C-NT2RM2000635//Homo sapiens mRNA for KIAA0729 protein, partial cds.//0//3791bp//99%//AB018272  
C-NT2RM2000636//Homo sapiens mRNA for KIAA0658 protein, partial cds.//0//2530bp//99%//AB014558  
C-NT2RM2000639  
45 C-NT2RM2000649//Homo sapiens mRNA for KIAA0676 protein, partial cds.//0//1543bp//99%//AB014576  
C-NT2RM2000669  
C-NT2RM2000691//ACTIN-LIKE PROTEIN 3 (ACTIN-2).//3.7E-142//285aa//90%//P32391  
C-NT2RM2000714//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP1).//3.8E-23//184aa//  
36%//Q15404  
50 C-NT2RM2000718//Homo sapiens HRIHFB2436 mRNA, partial cds.//4.4E-231//1065bp//99%//AB015342  
C-NT2RM2000740//POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L.//5.7E-53//266aa//43%//  
P41877  
C-NT2RM2000795  
55 C-NT2RM2000821//COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETACOP).//9.5E-279//545aa//  
98%//P23514  
C-NT2RM2000837  
C-NT2RM2000951//Homo sapiens XYLB mRNA for xylulokinase, complete cds.//1.7E-200//927bp//99%//  
AB015046

C-NT2RM2000952  
 C-NT2RM2000984  
 C-NT2RM2001004  
 5 C-NT2RM2001035//CCR4-ASSOCIATED FACTOR 1 (CAF1).//8.2E-154//285aa//99%//Q60809  
 C-NT2RM2001065  
 C-NT2RM2001100//HYPOTHETICAL 39.7 KD PROTEIN C34E10.2 IN CHROMOSOME III.//2.4E-15//266aa//  
 26%//P46577  
 C-NT2RM2001131  
 C-NT2RM2001141  
 10 C-NT2RM2001152  
 C-NT2RM2001177//Homo sapiens mRNA; cDNA DKFZp586G1822 (from clone DKFZp586G1822).//2.1E-293//  
 1335bp//99%//AL080109  
 C-NT2RM2001194  
 C-NT2RM2001196//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//1.3E-20//267aa//35%//P05143  
 15 C-NT2RM2001201//EUkARYOTIC TRANSLATION INITIATION FACTOR 5 (EIF5).//0.00000015//95aa//35%//  
 P48724  
 C-NT2RM2001221//KALIRIN (PAM COOH-TERMINAL INTERACTOR PROTEIN 10) (PCI1P10).//3.6E-10//177aa//  
 32%//P97924  
 C-NT2RM2001238//GLUTAMINASE, KIDNEY ISOFORM PRECURSOR (EC 3.5.1.2) (GLS) (L-GLUTAMINE AMI-  
 20 DOHYDROLASE).//1.3E-180//328aa//99%//P13264  
 C-NT2RM2001243  
 C-NT2RM2001247  
 C-NT2RM2001256//PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR).//1.6E-166//312aa//98%//  
 P53995  
 25 C-NT2RM2001291  
 C-NT2RM2001306//Homo sapiens mRNA; cDNA DKFZp564I052 (from clone DKFZp564I052).//0//1694bp//99%//  
 AL080063  
 C-NT2RM2001312  
 C-NT2RM2001319  
 30 C-NT2RM2001324//ZYXIN.//6.8E-55//200aa//41%//Q04584  
 C-NT2RM2001345//VEGETABLE INCOMPATIBILITY PROTEIN HET-E1.//0.000000029//334aa//22%//000808  
 C-NT2RM2001370  
 C-NT2RM2001393  
 C-NT2RM2001420  
 35 C-NT2RM2001424//Homo sapiens mRNA; cDNA DKFZp586D0920 (from clone DKFZp586D0920).//0//1621bp//  
 100%//AL050146  
 C-NT2RM2001499//LOW-AFFINITY CATIONIC AMINO ACID TRANSPORTER-2 (CAT-2) (CAT2).//7.4E-121//  
 437aa//57%//P52569  
 C-NT2RM2001504  
 40 C-NT2RM2001524  
 C-NT2RM2001544  
 C-NT2RM2001547//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//6.9E-27//  
 90aa//42%//P38660  
 C-NT2RM2001575//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SSA)) (RO(SS-A)).//4.3E-  
 45 61//312aa//44%//P19474  
 C-NT2RM2001582  
 C-NT2RM2001886//Homo sapiens mRNA for KIAA0710 protein, complete cds.//0//1000bp//100%//AB014610  
 C-NT2RM2001896//CELL DIVISION PROTEIN FTSJ.//5.1E-26//204aa//34%//P28692  
 50 C-NT2RM2001903//Homo sapiens mRNA for KIAA0462 protein, partial cds.//0//2390bp//99%//AB007931  
 C-NT2RM2001930  
 C-NT2RM2001935  
 C-NT2RM2001936//32.3 KD PROTEIN IN CWP1-MBR1 INTERGENIC REGION.//2.7E-27//216aa//34%//P28320  
 C-NT2RM2001950//HYPOTHETICAL 105.9 KD PROTEIN IN AAC3-RFC5 INTERGENIC REGION.//0.0000001//  
 212aa//23%//P38250  
 55 C-NT2RM2001982  
 C-NT2RM2001989//NUCLEOLAR PROTEIN NOP4 (NUCLEOLAR PROTEIN NOP77).//1.9E-39//253aa//35%//  
 P37838  
 C-NT2RM2001997//PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (EC 5.3.4.1).//1.3E-10//232aa//

28%//Q12730  
 C-NT2RM2001998//HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOME I./.3.1E-12//206aa//  
 30%//Q09782  
 C-NT2RM2002004//LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG).//  
 5 0.00000029//83aa//44%//P40796  
 C-NT2RM2002014//HYPOTHETICAL 81.4 KD PROTEIN IN GREB-FEOA INTERGENIC REGION./.1.1E-89//  
 425aa//41%//P46837  
 C-NT2RM2002030//Homo sapiens mRNA for Glutamine:fructose-6-phosphate amidotransferase, complete cds./.  
 10 0//1959bp//99%//AB016789  
 C-NT2RM2002049  
 C-NT2RM2002055//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS13./.0.00000099//338aa//  
 24%//Q07878  
 C-NT2RM2002088//PUTATIVE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN X (HNRNP X) (CBP).//  
 15 5E-62//104aa//57%//Q61990  
 C-NT2RM2002091  
 C-NT2RM2002100//Homo sapiens mRNA for ATP-dependent RNA helicase, partial./.0//1807bp//99%//AJ010840  
 C-NT2RM2002109//Homo sapiens glioma amplified on chromosome 1 protein (GAC1) mRNA, complete cds./.0//  
 1868bp//99%//AF030435  
 20 C-NT2RM2002128//PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).//4.9E-13//487aa//  
 26%//P49695  
 C-NT2RM2002142//GASTRULATION SPECIFIC PROTEIN G12//8E-31//105aa//47%//P47805  
 C-NT2RM2002178//Homo sapiens mRNA; cDNA DKFZp434E0335 (from clone DKFZp434E0335).//0//1683bp//  
 99%//AL117402  
 25 C-NT2RM4000024//DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE (EC 2.7.7.6) (RNA  
 POLYMERASE III SUBUNIT 2).//7.1E-155//381aa//72%//P25167  
 C-NT2RM4000061  
 C-NT2RM4000104//ZINC FINGER PROTEIN 135./.1.5E-81//251aa//53%//P52742  
 C-NT2RM4000139//R.norvegicus trg mRNA./.2.3E-114//1161bp//72%//X68101  
 30 C-NT2RM4000169//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1./.4.8E-13//686aa//23%//  
 P25386  
 C-NT2RM4000191//PUTATIVE ATP-DEPENDENT RNA HELICASE PL10./.9.2E-75//439aa//41%//P16381  
 C-NT2RM4000197  
 C-NT2RM4000210//Homo sapiens mRNA for KIAA0712 protein, complete cds./.0//1926bp//100%//AB018255  
 35 C-NT2RM4000229//Gallus gallus actin filament-associated protein (AFAP-110) mRNA, complete cds./.1.1E-27//  
 633bp//64%//L20303  
 C-NT2RM4000290//Human transducin-like enhancer protein (TLE3) mRNA, complete cds./.2.2E-276//1124bp//  
 97%//M99438  
 C-NT2RM4000344//Homo sapiens mRNA for ATP-dependent metalloprotease YME1L./.0//2030bp//99%//  
 AJ132637  
 40 C-NT2RM4000349//Homo sapiens HSPC028 mRNA, complete cds./.0//1827bp//99%//AF083246  
 C-NT2RM4000354//LETHAL(2)DENTICLELESS PROTEIN (DTL83 PROTEIN).//1.5E-21//208aa//35%//Q24371  
 C-NT2RM4000386//Mus musculus mRNA for Ten-m3, complete cds./.0//2156bp//86%//AB025412  
 C-NT2RM4000395  
 C-NT2RM4000421//Homo sapiens mRNA for nuclear transport receptor./.0//1730bp//99%//AJ133769  
 45 C-NT2RM4000457//HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMOSOME I./.8E-20//393aa//  
 24%//Q10297  
 C-NT2RM4000471//Homo sapiens cysteine desulfurase (nifS) mRNA, complete cds./.0//2092bp//99%//AF097025  
 C-NT2RM4000486//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CONTAINS:  
 50 BASIC PEPTIDE IB-6; PEPTIDE P-H].//4.8E-11//242aa//31%//P04280  
 C-NT2RM4000496//SAP1 PROTEIN./.8.3E-53//434aa//29%//P39955  
 C-NT2RM4000511  
 C-NT2RM4000515//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H)  
 (FRAGMENT).//1.1E-11//394aa//24%//P16884  
 C-NT2RM4000520  
 55 C-NT2RM4000585  
 C-NT2RM4000595//Homo sapiens leucine-rich repeats containing F-box protein FBL3 mRNA, complete cds./.  
 1.1E-285//1293bp//99%//AF186273  
 C-NT2RP1000018//Homo sapiens mRNA for KIAA0687 protein, partial cds./.0//1940bp//95%//AB014587

**EP 1 074 617 A2**

C-NT2RP1000035//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
C-NT2RP1000040  
C-NT2RP1000063  
C-NT2RP1000086//H.sapiens mRNA for zinc finger protein, Hsal2.//0//1162bp//99%//X98834  
5 C-NT2RP1000101  
C-NT2RP1000111//COP1 REGULATORY PROTEIN.//4E-116//296aa//51%//P93471  
C-NT2RP1000112  
C-NT2RP1000124  
C-NT2RP1000130//HEPATOMA-DERIVED GROWTH FACTOR (HDGF).//4.5E-50//181aa//60%//P51859  
10 C-NT2RP1000163//Homo sapiens mRNA for KIAA0948 protein, complete cds.//0//1889bp//98%//AB023165  
C-NT2RP1000170  
C-NT2RP1000191  
C-NT2RP1000202//ANKYRIN.//1E-25//302aa//34%//Q02357  
C-NT2RP1000243  
15 C-NT2RP1000259  
C-NT2RP1000272//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds.//5.8E-114//616bp//  
93%//AF067730  
C-NT2RP1000326//Homo sapiens metaxin 2 (MTX2) mRNA, nuclear gene encoding mitochondrial protein, com-  
plete cds.//1.3E-275//1249bp//99%//AF053551  
20 C-NT2RP1000333//ANTI-SILENCING PROTEIN 1.//8.7E-47//155aa//58%//P32447  
C-NT2RP1000348//REDUCED VIABILITY UPON STARVATION PROTEIN 161.//1.7E-15//162aa//30%//P25343  
C-NT2RP1000357  
C-NT2RP1000376//Homo sapiens mRNA; cDNA DKFZp434A102 (from clone DKFZp434A102).//0//2265bp//  
95%//AL080187  
25 C-NT2RP1000413//Homo sapiens mRNA for KIAA0587 protein, complete cds.//0//1056bp//99%//AB011159  
C-NT2RP1000416  
C-NT2RP1000439//Xenopus laevis chromosome condensation protein XCAP-G mRNA, complete cds.//1.8E-94//  
1019bp//63%//AF111423  
C-NT2RP1000443//QUINONE OXIDOREDUCTASE (EC 1.6.5.5) (NADPH:QUINONE REDUCTASE) (ZETA-  
CRYSTALLIN).//2.4E-10//227aa//25%//Q08257  
30 C-NT2RP1000470//PUTATIVE ATP-DEPENDENT RNA HELICASE T26G10.1 IN CHROMOSOME III.//2.6E-94//  
254aa//47%//P34580  
C-NT2RP1000478//TUBULIN BETA-5 CHAIN (CLASS-V).//4.5E-240//445aa//97%//P09653  
C-NT2RP1000481  
35 C-NT2RP1000493//Homo sapiens mRNA for KIAA0017 protein, complete cds.//0//2728bp//99%//D87686  
C-NT2RP1000547//COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (FRAGMENT).//1.1E-  
27//193aa//35%//P49020  
C-NT2RP1000574//HOMEobox PROTEIN MEIS2 (MEIS1-RELATED PROTEIN 1).//3.5E-75//151aa//94%//  
P97367  
40 C-NT2RP1000581  
C-NT2RP1000630//NECDIN.//2.4E-44//227aa//41%//P25233  
C-NT2RP1000688  
C-NT2RP1000695  
C-NT2RP1000733//Human mRNA for GSPT1-TK protein,complete cds.//0//2057bp//99%//E14379  
45 C-NT2RP1000738//Homo sapiens Wolf-Hirschhorn syndrome candidate 2 protein (WHSC2) mRNA, complete  
cds.//0//2186bp//99%//AF101434  
C-NT2RP1000782//PLATELET-ENDOTHELIAL TETRASPA<sup>N</sup> ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYC-  
OPROTEIN SFA-1) (CD151 ANTIGEN).//1.2E-30//232aa//30%//O35566  
C-NT2RP1000825//GTPASE-ACTIVATING PROTEIN RHOGAP (RHO-RELATED SMALL GTPASE PROTEIN  
50 ACTIVATOR) (CDC42 GTPASE-ACTIVATING PROTEIN) (P50-RHOGAP).//8.2E-83//334aa//50%//Q07960  
C-NT2RP1000833//Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds.//0//1494bp//  
99%//AF067223  
C-NT2RP1000846  
C-NT2RP1000851  
55 C-NT2RP1000856//PLATELET-ENDOTHELIAL TETRASPA<sup>N</sup> ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYC-  
OPROTEIN SFA-1) (CD151 ANTIGEN).//1.2E-30//232aa//30%//O35566  
C-NT2RP1000915//AUTOANTIGEN NGP-1.//1.7E-19//343aa//25%//Q13823  
C-NT2RP1000947//Human E2 ubiquitin conjugating enzyme UbcH5B (UBCH5B) mRNA, complete cds.//4.6E-

105//504bp//99<%//U39317  
 C-NT2RP1000954//RING CANAL PROTEIN (KELCH PROTEIN).//1.4E-23//370aa//28%//Q04652  
 C-NT2RP1000958//AUTOANTIGEN NGP-1.//1.4E-19//343aa//25%//Q13823  
 C-NT2RP1000959//Human acidic ribosomal phosphoprotein P0 mRNA, complete cds.//2.5E-236//966bp//99%//  
 5 M17885  
 C-NT2RP1000966//NUCLEOLIN (PROTEIN C23).//8.9E-299//554aa//99%//P19338  
 C-NT2RP1000980  
 C-NT2RP1000988  
 C-NT2RP1001011//Drosophila melanogaster putative 43 kDa protein (TH1) mRNA, complete cds.//2.2E-78//  
 10 1529bp//61%//L01790  
 C-NT2RP1001014  
 C-NT2RP1001395  
 C-NT2RP1001410//PUTATIVE GTP-BINDING PROTEIN W08E3.3.//8.9E-141//396aa//67%//P91917  
 C-NT2RP1001424  
 15 C-NT2RP1001449  
 C-NT2RP1001457//Homo sapiens partial mRNA for beta-transducin family protein (putative).//1.2E-137//629bp//  
 100%//AJ005257  
 C-NT2RP1001466  
 C-NT2RP1001475  
 20 C-NT2RP1001482  
 C-NT2RP1001494//MALE STERILITY PROTEIN 2.//7.2E-40//261aa//27%//Q08891  
 C-NT2RP1001543//MYO-INOSITOL-1-PHOSPHATE SYNTHASE (EC 5.5.1.4) (IPS).//1.6E-166//506aa//60%//  
 P42803  
 C-NT2RP1001546//PLATELET-ENDOTHELIAL TETRASPAAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYC-  
 25 OPROTEIN SFA-1) (CD151 ANTIGEN).//1.6E-30//232aa//30%//035566  
 C-NT2RP1001569//SIGNAL RECOGNITION PARTICLE RECEPTOR BETA SUBUNIT (SR-BETA).//5.8E-121//  
 271aa//89%//P47758  
 C-NT2RP1001616  
 C-NT2RP1001665//CALMODULIN.//0.00000051//83aa//30%//P02594  
 30 C-NT2RP2000006//DNAJ PROTEIN (40 KD HEAT SHOCK CHAPERONE PROTEIN) (HSP40).//9.8E-17//79aa//  
 55%//O34136  
 C-NT2RP2000007  
 C-NT2RP2000008//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//2.4E-177//726aa//47%//  
 P51523  
 35 C-NT2RP2000032//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP1).//1.8E-22//184aa//  
 34%//Q01730  
 C-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds.//  
 0//1390bp//98%//AF061749  
 C-NT2RP2000054  
 40 C-NT2RP2000056//PROTEIN-TYROSINE PHOSPHATASE EPSILON PRECURSOR (EC 3.1.3.48) (R-PTP- EP-  
 SILON).//9.4E-16//45aa//100%//P49446  
 C-NT2RP2000067  
 C-NT2RP2000070//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//3.4E-51//  
 383aa//32%//P33450  
 45 C-NT2RP2000079  
 C-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cds.//0//2286bp//100%//AB018338  
 C-NT2RP2000091  
 C-NT2RP2000097  
 C-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds.//0//2244bp//99%//AB018356  
 50 C-NT2RP2000120  
 C-NT2RP2000126//POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L.//2.5E-117//541aa//42%//  
 P41877  
 C-NT2RP2000133//Homo sapiens mRNA for KIAA0989 protein, partial cds.//0//2286bp//99%//AB023206  
 C-NT2RP2000147//CLATHRIN COAT ASSEMBLY PROTEIN AP47 (CLATHRIN COAT ASSOCIATED PROTEIN  
 55 AP47) (GOLGI ADAPTOR AP-1-47 KD PROTEIN) (HA1 47 KD SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN  
 ASSEMBLY PROTEIN COMPLEX 1 MEDIUM CHAIN).//4.4E-226//423aa//99%//P35585  
 C-NT2RP2000153//GAR2 PROTEIN.//9.8E-23//311aa//28%//P41891  
 C-NT2RP2000157//MLO2 PROTEIN.//2.6E-11//62aa//40%//Q09329

C-NT2RP2000161//Homo sapiens mRNA for KIAA1008 protein, complete cds.//3.4e-315//1430bp//99%//  
 AB023225  
 C-NT2RP2000173  
 C-NT2RP2000175  
 5 C-NT2RP2000195  
 C-NT2RP2000205  
 C-NT2RP2000208//Homo sapiens mRNA for KIAA0892 protein, partial cds.//0//2898bp//99%//AB020699  
 C-NT2RP2000224//INSULIN RECEPTOR SUBSTRATE-1 (IRS1).//0.000043//103aa//28%//P35568  
 C-NT2RP2000232  
 10 C-NT2RP2000233  
 C-NT2RP2000239  
 C-NT2RP2000248//UDP-N-ACETYLGLUCOSAMINE-PEPTIDE N-ACETYLGLUCOSAMINYLTRANSFERASE  
 110 KD SUBUNIT (EC 2.4.1.-) (O-GLCNAC TRANSFERASE P110 SUBUNIT).//3.4E-21//210aa//33%//P56558  
 C-NT2RP2000270  
 15 C-NT2RP2000274  
 C-NT2RP2000283  
 C-NT2RP2000288//HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMOSOME I.//1.6E-27//576aa//  
 25%//Q10297  
 C-NT2RP2000297//ZINC FINGER PROTEIN 184 (FRAGMENT).//3.3E-186//256aa//60%//Q99676  
 20 C-NT2RP2000298  
 C-NT2RP2000310//Human proline-dehydrogenase/proline oxidase (PRODH) mRNA, complete cds.//4.3E-279//  
 1193bp//99%//U82381  
 C-NT2RP2000328  
 C-NT2RP2000329//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//2E-111//  
 25 226aa//92%//P08760  
 C-NT2RP2000346//MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD116.//6.3E-115//  
 674aa//46%//P17564  
 C-NT2RP2000369  
 C-NT2RP2000412  
 30 C-NT2RP2000414//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN F (HNRNP F).//4.3E-228//415aa//  
 100%//P52597  
 C-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//0//1757bp//  
 99%//AF102265  
 C-NT2RP2000438  
 35 C-NT2RP2000448//KES1 PROTEIN.//8.7E-54//392aa//38%//P35844  
 C-NT2RP2000503  
 C-NT2RP2000510  
 C-NT2RP2000516  
 C-NT2RP2000603  
 40 C-NT2RP2000617  
 C-NT2RP2000634//Homo sapiens mRNA for KIAA0614 protein, partial cds.//0//2482bp//99%//AB014514  
 C-NT2RP2000656  
 C-NT2RP2000658  
 45 C-NT2RP2000668//SERINE/THREONINE PROTEIN KINASE PKPA (EC 2.7.1.-).//1.3E-27//349aa//32%//Q01577  
 C-NT2RP2000704  
 C-NT2RP2000710//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA LIGASE).//2.7E-100//  
 488aa//44%//O32038  
 C-NT2RP2000764//NIFS PROTEIN.//6.6E-36//252aa//42%//P12623  
 C-NT2RP2000809//Homo sapiens mRNA for KIAA0873 protein, partial cds.//0//3347bp//99%//AB020680  
 50 C-NT2RP2000812//DILUTE MYOSIN HEAVY CHAIN, NON-MUSCLE (MYOSIN 5A).//0.000000056//179aa//  
 29%//Q99104  
 C-NT2RP2000814//GELATION FACTOR (ACTIN BINDING PROTEIN 120) (ABP-120).//0.00000011//96aa//29%//  
 P13466  
 C-NT2RP2000816//MAGNESIUM-CHELATASE 30 KD SUBUNIT.//0.000000079//172aa//28%//P26174  
 55 C-NT2RP2000819  
 C-NT2RP2000841  
 C-NT2RP2000845  
 C-NT2RP2000863

EP 1 074 617 A2

C-NT2RP2000880//PROBABLE TRANSLATION INITIATION FACTOR IF-2./0//694aa//99%//060841  
C-NT2RP2000892  
C-NT2RP2000931//MATRIN 3./2.4E-289//467aa//95%//P43244  
C-NT2RP2000932//Homo sapiens mRNA; cDNA DKFZp5640043 (from clone DKFZp5640043).//0//2487bp//99%//  
5 AL050390  
C-NT2RP2000938  
C-NT2RP2000943//Homo sapiens mRNA for KIAA0755 protein, complete cds./0//3458bp//99%//AB018298  
C-NT2RP2000965//Homo sapiens mRNA for fls353, complete cds./0//1989bp//96%//AB024704  
C-NT2RP2000985  
10 C-NT2RP2001036  
C-NT2RP2001044  
C-NT2RP2001056//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488./0//2749bp//99%//  
AB007957  
C-NT2RP2001065  
15 C-NT2RP2001070//PUTATIVE PYRIDOXAMINE 5'-PHOSPHATE OXIDASE (EC 1.4.3.5) (PNP/PMP OXIDASE).//  
5.8E-46//222aa//45%//Q20939  
C-NT2RP2001081//SYNAPTOTAGMIN IV./4.2E-118//430aa//54%//P50232  
C-NT2RP2001094  
C-NT2RP2001119  
20 C-NT2RP2001127//Homo sapiens mRNA for PLU-1 protein./0//2514bp//99%//AJ132440  
C-NT2RP2001218  
C-NT2RP2001245//MYOSIN HEAVY CHAIN, NONMUSCLE (CELLULAR MYOSIN HEAVY CHAIN) (NMMHC).//  
2.2E-10//366aa//28%//P14105  
C-NT2RP2001381  
25 C-NT2RP2001397//Homo sapiens mRNA; cDNA DKFZp434B174 (from clone DKFZp434B174).//0//1495bp//  
100%//AL080146  
C-NT2RP2001427  
C-NT2RP2001601//Homo sapiens mRNA for KIAA0797 protein, partial cds./0//1748bp//99%//AB018340  
C-NT2RP2001675  
30 C-NT2RP2001721  
C-NT2RP2001907  
C-NT2RP2001969  
C-NT2RP2001976//Mus musculus calmodulin-binding protein SHA1 (Sha1) mRNA, complete cds./4.7E-177//  
1538bp//74%//AF062378  
35 C-NT2RP2002046  
C-NT2RP2002154  
C-NT2RP2002208  
C-NT2RP2002270//AF-9 PROTEIN./0.00000012//74aa//36%//P42568  
C-NT2RP2002312//Homo sapiens mRNA for CDS2 protein./0//2333bp//99%//Y16521  
40 C-NT2RP2002325//Homo sapiens mRNA for Pex11p, complete cds./8.4E-254//1158bp//99%//AB015594  
C-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant mRNA, complete cds./4.3E-240//  
1105bp//99%//AF038958  
C-NT2RP2002426  
45 C-NT2RP2002479//Homo sapiens mRNA for ABC transporter 7 protein, complete cds./0//2180bp//99%//  
AB005289  
C-NT2RP2002537//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X./6.2E-19//288aa//26%//  
Q11073  
C-NT2RP2002595//PROBABLE CALCIUM-BINDING PROTEIN ALG-2 (PMP41) (ALG-257).//7.5E-35//181aa//  
42%//P12815  
50 C-NT2RP2002618//PROTEIN ARGININE N-METHYLTRANSFERASE 2 (EC 2.1.1.-).//1.7E-51//326aa//38%//  
P55345  
C-NT2RP2002621  
C-NT2RP2002672  
C-NT2RP2002701//HYPOTHETICAL 38.1 KD PROTEIN C2F12.15C IN CHROMOSOME II./1.9E-14//210aa//  
55 30%//O14345  
C-NT2RP2002769  
C-NT2RP2002862//60S ACIDIC RIBOSOMAL PROTEIN P0 (LIGHT-INDUCED 34 KD PROTEIN).//8.8E-10//  
203aa//27%//P29764

C-NT2RP2002928//Homo sapiens pre-mRNA splicing factor (PRP17) mRNA, complete cds./.1.9E-136//623bp//  
100%//AF038392  
C-NT2RP2002954  
C-NT2RP2002959//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN- PROTEIN  
5 LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2).//4.6E-80//147aa//100%//P51669  
C-NT2RP2002980//30S RIBOSOMAL PROTEIN S10.//0.00000001//98aa//36%//P10129  
C-NT2RP2002986//Homo sapiens mRNA for Kelch motif containing protein, complete cds./.0//2209bp//99%//  
AB026190  
C-NT2RP2003108  
10 C-NT2RP2003117  
C-NT2RP2003121//Mus musculus enhancer of polycomb (Epc1) mRNA, complete eds./.2.3E-82//642bp//68%//  
AF079765  
C-NT2RP2003125//RING CANAL PROTEIN (KELCH PROTEIN).//2.4E-38//539aa//25%//004652  
C-NT2RP2003177  
15 C-NT2RP2003194  
C-NT2RP2003265//Homo sapiens CGI-53 protein mRNA, complete cds./.0//1580bp//99%//AF151811  
C-NT2RP2003295//Homo sapiens RMP mRNA for RPB5 mediating protein, complete cds./.0//1526bp//99%//  
AB006572  
C-NT2RP2003329//PUTATIVE ADENYLYLATE CYCLASE REGULATORY PROTEIN./.3.6E-14//332aa//32%//  
20 P26337  
C-NT2RP2003367  
C-NT2RP2003433//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT./.5E-131//269aa//91%//P38378  
C-NT2RP2003446  
C-NT2RP2003533  
25 C-NT2RP2003543//HYPOTHETICAL TRNA/RRNA METHYLTRANSFERASE SLR1673 (EC 2.1.1.-).//1.7E-17//  
148aa//34%//P74261  
C-NT2RP2003596  
C-NT2RP2003629  
C-NT2RP2003687  
30 C-NT2RP2003714//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//5.4E-29//85aa//72%//  
Q05481  
C-NT2RP2003737//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN-PROTEIN  
LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2).//1.7E-75//147aa//93%//P51669  
C-NT2RP2003793  
35 C-NT2RP2003952//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE) (ARGININE AMI-  
NOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV) (AP-B).//1.5E-23//200aa//30%//O09175  
C-NT2RP2003986  
C-NT2RP2004042  
C-NT2RP2004316//Homo sapiens chromosome 1 clone J549L20, WORKING DRAFT SEQUENCE, in unordered  
40 pieces./.8.2E-202//926bp//100%//AL096820  
C-NT2RP2004389//PROBABLE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN S9 PRECURSOR./.9.3E-15//  
126aa//39%//P38120  
C-NT2RP2004392//MNN4 PROTEIN./.1.4E-11//143aa//27%//P36044  
C-NT2RP2004463  
45 C-NT2RP2004602  
C-NT2RP2004614//Homo sapiens mRNA for KIAA0922 protein, partial cds./.0//2040bp//99%//AB023139  
C-NT2RP2004655//Homo sapiens mRNA for leucine rich protein./.8.5E-233//1061bp//99%//AJ006291  
C-NT2RP2004689//HYPOTHETICAL 192.5 KD PROTEIN C6G9.10C IN CHROMOSOME 1./.5.6E-64//616aa//  
33%//Q92355  
50 C-NT2RP2004791//PUTATIVE LEUCYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.4) (LEUCINE-- TRNA  
LIGASE) (LEURS).//9.5E-73//153aa//59%//Q10490  
C-NT2RP2004799//PROBABLE SUCCINYL-COA LIGASE [GDP-FORMING], BETA-CHAIN PRECURSOR (EC  
6.2.1.4) (SUCCINYL-COA SYNTHETASE, BETA CHAIN) (SCS-BETA).//3.7E-135//414aa//62%//P53588  
C-NT2RP2004802  
55 C-NT2RP2004841  
C-NT2RP2004936  
C-NT2RP2004959//P54 PROTEIN PRECURSOR./.0.00000095//297aa//20%//P13692  
C-NT2RP2004999

C-NT2RP2005000  
C-NT2RP2005001//Homo sapiens mRNA for KIAA0615 protein, complete cds.//0//1694bp//99%//AB014515  
C-NT2RP2005012//Homo sapiens mRNA for SEC63 protein.//0//1693bp//99%//AJ011779  
C-NT2RP2005037//ANTI-SILENCING PROTEIN 1./.3.3E-47//155aa//59%//P32447  
5 C-NT2RP2005126//H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein).//0//2388bp//98%//  
X98743  
C-NT2RP2005140  
C-NT2RP2005147  
C-NT2RP2005159  
10 C-NT2RP2005239//Homo sapiens cysteine desulfurase (nifS) mRNA, complete cds.//0//2087bp//99%//AF097025  
C-NT2RP2005270  
C-NT2RP2005276//Homo sapiens mRNA for Acyl-CoA synthetase 3, complete cds.//0//2122bp//99%//D89053  
C-NT2RP2005293  
15 C-NT2RP2005315//Homo sapiens mRNA for KIAA0676 protein, partial cds.//0//1515bp//99%//AB014576  
C-NT2RP2005358//Homo sapiens methyl-CpG binding domain-containing protein MBD3 (MBD3) mRNA, com-  
plete cds.//0//2199bp//99%//AF072247  
C-NT2RP2005393//AUTOANTIGEN NGP-1./.7.2E-39//224aa//35%//Q13823  
C-NT2RP2005436//SPLICING FACTOR, ARGinine/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR  
SRP75).//1.2E-13//185aa//38%//Q08170  
20 C-NT2RP2005441  
C-NT2RP2005453  
C-NT2RP2005464  
C-NT2RP2005465//MITOCHONDRIAL CARRIER PROTEIN RIM2./.3E-44//252aa//41%//P38127  
C-NT2RP2005472  
25 C-NT2RP2005495  
C-NT2RP2005498//PROTEIN PHOSPHATASE PP2A, 55 KD REGULATORY SUBUNIT, ALPHA ISOFORM (PRO-  
TEIN PHOSPHATASE PP2A B SUBUNIT ALPHA ISOFORM) (ALPHA-PR55).//5.2E-81//166aa//88%//P36876  
C-NT2RP2005509//Homo sapiens CGI-45 protein mRNA, complete cds.//0//1825bp//99%//AF151803  
C-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//0//  
30 3994bp//99%//AF092563  
C-NT2RP2005525//Mus musculus kanadapin mRNA, complete cds.//2.4E-304//1687bp//85%//AF035526  
C-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds.//0//2856bp//99%//AB007963  
C-NT2RP2005549//PUTATIVE LACTOYLGLUTATHIONE LYASE (EC 4.4.1.5) (METHYLGlyOXALASE) (AL-  
35 DOKETOMUTASE) (GLYOXALASE I) (GLX I) (KETONE-ALDEHYDE MUTASE) (S-D-LACTOYLGLUTATHIONE  
METHYLGlyOXAL LYASE).//2E-20//181aa//36%//Q39366  
C-NT2RP2005555  
C-NT2RP2005557//Homo sapiens clone 486790 diphosphoinositol polyphosphate phosphohydrolase mRNA,  
complete cds.//1E-46//576bp//70%//AF062529  
C-NT2RP2005620//Homo sapiens epsin 2a mRNA, complete cds.//8.9e-313//1455bp//98%//AF062085  
40 C-NT2RP2005622  
C-NT2RP2005635//PROBABLE NH(3)-DEPENDENT NAD(+) SYNTHETASE (EC 6.3.5.1).//1E-11//128aa//36%//  
P47623  
C-NT2RP2005637  
C-NT2RP2005640  
45 C-NT2RP2005654//CYSTEINE STRING PROTEIN (CCCS1).//1.2E-13//74aa//45%//P56101  
C-NT2RP2005669//Homo sapiens mRNA for DEDD protein.//3.9E-209//957bp//99%//AJ010973  
C-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds.//4.4E-200//908bp//  
99%//AF089814  
C-NT2RP2005683  
50 C-NT2RP2005690  
C-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds.//0//1684bp//99%//AB018342  
C-NT2RP2005723//HNRNP ARGinine N-METHYLTRANSFERASE (EC 2.1.1.-) (ODP1 PROTEIN).//  
0.000000003//169aa//28%//P38074  
C-NT2RP2005748  
55 C-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds.//0//1968bp//99%//  
AF068868  
C-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//0//1966bp//99%//  
AF082516

EP 1 074 617 A2

C-NT2RP2005763//EUKARYOTIC INITIATION FACTOR 4A (EIF-4A).//1.7E-61//374aa//38%//P47943  
C-NT2RP2005767//G.gallus PB1 gene./5E-163//1158bp//81%//X90849  
C-NT2RP2005773//Homo sapiens pyrroline 5-carboxylate reductase isoform (P5CR2) mRNA, complete cds./2.7E-180//656bp//99%//AF151351  
5 C-NT2RP2005775//NEUROLYSIN PRECURSOR (EC 3.4.24.16) (NEUROTENSIN ENDOPEPTIDASE) (MITO-CHONDRIAL OLIGOPEPTIDASE M) (MICROSOMAL ENDOPEPTIDASE) (MEP) (SOLUBLE ANGIOTENSIN-BINDING PROTEIN) (SABP).//2.1E-213//249aa//85%//Q02038  
C-NT2RP2005781  
C-NT2RP2005804  
10 C-NT2RP2005835//SHP1 PROTEIN./1.8E-28//208aa//32%//P34223  
C-NT2RP2005853  
C-NT2RP2005868  
C-NT2RP2005886  
C-NT2RP2005890  
15 C-NT2RP2005901//Homo sapiens mRNA for KIAA0971 protein, complete cds./0//1977bp//99%//AB023188  
C-NT2RP2005933//NUCLEOPORIN NUP57 (NUCLEAR PORE PROTEIN NUP57).//5E-11//155aa//34%//P48837  
C-NT2RP2006038  
C-NT2RP2006043//SPLICING FACTOR, ARGinine/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//1.5E-13//185aa//38%//Q08170  
20 C-NT2RP2006052  
C-NT2RP2006069  
C-NT2RP2006071  
C-NT2RP2006100//Homo sapiens mRNA; cDNA DKFZp564B102 (from clone DKFZp564B102).//0//1759bp//99%//AL049970  
25 C-NT2RP2006106  
C-NT2RP2006141  
C-NT2RP2006186//Homo sapiens mRNA for KIAA0654 protein, partial cds./3.3E-189//899bp//97%//AB014554  
C-NT2RP2006196  
C-NT2RP2006200  
30 C-NT2RP2006219//H.sapiens mRNA for DGCR6 protein./1.1E-214//1026bp//97%//X96484  
C-NT2RP2006237  
C-NT2RP2006238  
C-NT2RP2006275//MICROTUBULE-ASSOCIATED PROTEIN 1B [CONTAINS: LIGHT CHAIN LC1].//2E-59//388aa//32%//P46821  
35 C-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds./2.8E-274//1236bp//99%//AF035262  
C-NT2RP2006333  
C-NT2RP2006365  
C-NT2RP2006393  
40 C-NT2RP2006436//ANTERIOR-RESTRICTED HOMEobox PROTEIN (RATHKE POUCH HOMEO BOX).//0.0000034//50aa//50%//Q61658  
C-NT2RP2006456  
C-NT2RP2006464//Homo sapiens mRNA for AND-1 protein./0//2181bp//99%//AJ006266  
C-NT2RP2006467  
C-NT2RP2006472  
45 C-NT2RP2006565//Sus scrofa mRNA for SCAMPI protein./0//1276bp//84%//Y15710  
C-NT2RP2006571//CYTOCHROME P450 2G1 (EC 1.14.14.1) (CYP11G1) (P450-NMB) (OLFACTIVE).//4.2E-134//486aa//50%//P24461  
C-NT2RP2006573//2',3'-CYCLIC NUCLEOTIDE 3'-PHOSPHODIESTERASE (EC 3.1.4.37) (CNP).//0.0000055//169aa//25%//P09543  
50 C-NT2RP3000031//Homo sapiens mRNA for KIAA0901 protein, complete cds./0//2547bp//99%//AB020708  
C-NT2RP3000072  
C-NT2RP3000142//Homo sapiens mRNA for KIAA0592 protein, partial cds./0//1404bp//97%//AB011164  
C-NT2RP3000220  
C-NT2RP3000251  
55 C-NT2RP3000252//Homo sapiens GTP-binding protein NGB mRNA, complete cds./0//2388bp//99%//AF120334  
C-NT2RP3000312  
C-NT2RP3000320//Homo sapiens partial mRNA for putative p621 protein which interacts with transcription factor Sp1./0//1544bp//100%//AJ242978

C-NT2RP3000333  
 C-NT2RP3000348  
 C-NT2RP3000350//PROBABLE GTP-BINDING PROTEIN  
 HP0303.//0.00000028//185aa//31%//O25074  
 5 C-NT2RP3000359//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//2E-111//  
 226aa//92%//P08760  
 C-NT2RP3000361//Homo sapiens mRNA, complete cds, similar to yeast pre-mRNA splicing factors, Prp1/Zer1  
 and Prp6.//0//2072bp//98%//AB019219  
 10 C-NT2RP3000366//RAS-RELATED PROTEIN RAB-18.//2.1E-107//206aa//99%//P35293  
 C-NT2RP3000397//PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE (DEAH BOX PROTEIN 13)//  
 1.7E-139//679aa//41%//O43143  
 C-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cds.//0//2364bp//99%//AF071185  
 C-NT2RP3000484  
 15 C-NT2RP3000527//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//4.8E-28//536aa//27%//P28160  
 C-NT2RP3000531//POLIOVIRUS RECEPTOR PRECURSOR (CD155 ANTIGEN).//1.9E-12//192aa//30%//  
 P15151  
 C-NT2RP3000596/TRICHOHYALIN.//2.5E-17//304aa//28%//Q07283  
 C-NT2RP3000599  
 20 C-NT2RP3000632//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3E-140//499aa//46%//P51523  
 C-NT2RP3000644  
 C-NT2RP3000661  
 C-NT2RP3000665  
 C-NT2RP3000690  
 25 C-NT2RP3000759//ADP-RIBOSYLATION FACTOR.//7E-28//176aa//34%//Q94650  
 C-NT2RP3000825//NEUROGENIC LOCUS NOTCH 3 PROTEIN.//2.5E-36//417aa//31%//Q61982  
 C-NT2RP3000836  
 C-NT2RP3000841  
 C-NT2RP3000850  
 C-NT2RP3000852  
 30 C-NT2RP3000859  
 C-NT2RP3000868//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete  
 cds.//6.9E-69//1611bp//61%//U53445  
 C-NT2RP3000869  
 C-NT2RP3000901  
 35 C-NT2RP3000917//Homo sapiens Dhm1-like protein mRNA, complete cds.//0//3199bp//99%//AF064257  
 C-NT2RP3000919//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds.//  
 2.7E-185//585bp//88%//AF015264  
 C-NT2RP3000980  
 C-NT2RP3000994//MATERNAL EFFECT PROTEIN  
 40 STAUFEN.//0.00000006//78aa//48%//P25159  
 C-NT2RP3001004  
 C-NT2RP3001081  
 C-NT2RP3001084  
 C-NT2RP3001096//Rattus norvegicus leprecan (lepre1) mRNA, complete cds.//1.7E-94//787bp//66%//AF087433  
 45 C-NT2RP3001107//PEREGRIN (BR140 PROTEIN).//3E-44//260aa//40%//P55201  
 C-NT2RP3001109  
 C-NT2RP3001116  
 C-NT2RP3001119  
 C-NT2RP3001133  
 50 C-NT2RP3001140//Homo sapiens mRNA for KIAA0762 protein, partial cds.//0//2802bp//99%//AB018305  
 C-NT2RP3001155//Homo sapiens mRNA for AND-1 protein.//0//2732bp//99%//AJ006266  
 C-NT2RP3001176//HYPOTHETICAL 65.3 KD PROTEIN IN MAD1-SCY1 INTERGENIC REGION.//1.7E-10//  
 196aa//27%//P53154  
 C-NT2RP3001214  
 55 C-NT2RP3001216//CYLICIN I (MULTIPLE-BAND POLYPEPTIDE I) (FRAGMENT).//0.0000023//137aa//33%//  
 P35663  
 C-NT2RP3001221//GAMMA-BUTYROBETAINE,2-OXOGLUTARATE DIOXYGENASE (EC 1.14.11.1) (GAMMA-  
 BUTYROBETAINE HYDROXYLASE).//1.9E-31//353aa//30%//P80193

C-NT2RP3001236  
 C-NT2RP3001239//MICROTUBULE-ASSOCIATED PROTEIN 1B (MAP1.2) (MAP1(X)) [CONTAINS: LIGHT CHAIN LC1].//1.2E-166//395aa/51%//P14873  
 C-NT2RP3001260//Homo sapiens mRNA for KIAA0911 protein, complete cds.//0//2497bp//99%//AB020718  
 5 C-NT2RP3001307  
 C-NT2RP3001325  
 C-NT2RP3001384//Homo sapiens NAKAP95 mRNA for neighbor of A-kinase anchoring protein 95, complete cds.//0//1213bp//99%//AB025905  
 C-NT2RP3001392  
 10 C-NT2RP3001396  
 C-NT2RP3001398//TRANSCRIPTIONAL REPRESSOR CTCF.//1.3E-61//374aa/36%//P49711  
 C-NT2RP3001407//SCY1 PROTEIN.//0.00000033//143aa/25%//P53009  
 C-NT2RP3001420  
 C-NT2RP3001426//DNAJ PROTEIN (FRAGMENT).//1E-16//77aa/46%//O33529  
 15 C-NT2RP3001427//WERNER SYNDROME HELICASE HOMOLOG.//2.7E-10//159aa/33%//O09053  
 C-NT2RP3001457  
 C-NT2RP3001472//NONHISTONE CHROMOSOMAL PROTEIN 6A.//9.1E-13//87aa/43%//P11632  
 C-NT2RP3001495//Human oxidoreductase (HHCMA56) mRNA, complete cds.//0//1475bp//99%//U13395  
 C-NT2RP3001497//Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA, complete cds.//  
 20 0//2295bp//99%//AF064801  
 C-NT2RP3001529//SPOOB-ASSOCIATED GTP-BINDING PROTEIN.//1E-61//345aa/42%//P20964  
 C-NT2RP3001621  
 C-NT2RP3001629  
 C-NT2RP3001642//HYPOTHETICAL PROTEIN KIAA0210.//6.8E-18//91aa/38%//Q92609  
 25 C-NT2RP3001646//WD-40 REPEAT PROTEIN MSI2.//8.8E-09//132aa/31%//O22468  
 C-NT2RP3001676  
 C-NT2RP3001679  
 C-NT2RP3001799//MYOSIN HEAVY CHAIN, STRIATED MUSCLE.//1.6E-11//348aa/27%//P24733  
 C-NT2RP3001819//RING CANAL PROTEIN (KELCH PROTEIN).//7.4E-18//249aa/30%//Q04652  
 30 C-NT2RP3001896  
 C-NT2RP3001915  
 C-NT2RP3001929  
 C-NT2RP3003193//ZINC FINGER PROTEIN 135.//7.3E-98//269aa/62%//P52742  
 C-NT2RP3004466  
 35 C-NT2RP3004480//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS35.//3.3E-113//466aa/42%//P34110  
 C-NT2RP3004539//Homo sapiens mRNA for KIAA0632 protein, partial cds.//0//1520bp//99%//AB014532  
 C-NT2RP3004544//Homo sapiens mRNA for KIAA0554 protein, partial cds.//0//974bp//95%//AB011126  
 C-NT2RP3004569//ANKYRIN, BRAIN VARIANT 1 (ANKYRIN B) (ANKYRIN, NONERYTHROID).//0.000000038//  
 40 150aa/28%//Q01484  
 C-NT2RP3004572//Homo sapiens cofactor of initiator function (CIF150) mRNA, complete cds.//0//1770bp//99%//AF026445  
 C-NT2RP3004578//Homo sapiens mRNA for KIAA0477 protein, complete cds.//0//1639bp//99%//AB007946  
 C-NT2RP3004594//Homo sapiens mRNA for AND-1 protein.//0//1807bp//99%//AJ006266  
 45 C-NT2RP3004617//ZINC-BINDING PROTEIN A33.//7.2E-75//464aa/35%//Q02084  
 C-NT2RP3004618//Homo sapiens putative RNA-binding protein Q99 mRNA, complete cds.//0//3972bp//98%//AF093097  
 C-NT2RP3004669//ETHANOLAMINE KINASE (EC 2.7.1.82) (EASILY SHOCKED PROTEIN).//1.7E-72//254aa/  
 45%//P54352  
 50 C-NT2RP4000008//CHLORINE CHANNEL PROTEIN P64.//2.6E-98//239aa/64%//P35526  
 C-NT2RP4000051//SYNAPTONEMAL COMPLEX-PROTEIN SC65.//4.9E-51//335aa/37%//Q64375  
 C-NT2RP4000078//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//3013bp//99%//AB020657  
 C-NT2RP4000109//Homo sapiens mRNA for MEGF5, partial cds.//0//2161bp//99%//AB011538  
 C-NT2RP4000111//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100  
 55 KD SUBUNIT).//0//728aa/99%//Q10568  
 C-NT2RP4000129  
 C-NT2RP4000147//Drosophila melanogaster putative ARF1 GTPase activating protein (ARF1-GAP) mRNA, com-  
 plete cds.//3.8E-28//528bp//67%//AF011427

C-NT2RP4000150  
 C-NT2RP4000151  
 C-NT2RP4000159  
 C-NT2RP4000185  
 5 C-NT2RP4000210//Homo sapiens mRNA for KIAA0700 protein, partial cds./0//4149bp//99%//AB014600  
 C-NT2RP4000212//atrial gland-specific antigen precursor (AGSA).//5.9E-15//104aa//40%//P15287  
 C-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP).//0//1932bp//99%//AJ006470  
 C-NT2RP4000246//NPC DERIVED PROLINE RICH PROTEIN 1 (NDPP-1).//2.7E-84//208aa//76%//Q03173  
 10 C-NT2RP4000259//GLUTATHIONE PEROXIDASE 2 (EC 1.11.1.9).//5.5E-29//153aa//43%//O23968  
 C-NT2RP4000290//HYPOTHETICAL 116.5 KD PROTEIN C20G8.09C IN CHROMOSOME I.//3.5E-297//1024aa//55%//P87115  
 C-NT2RP4000312//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE).//1.5E-26//237aa//28%//Q01631  
 15 C-NT2RP4000323//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN).//0.0000003//101aa//32%//P26372  
 C-NT2RP4000355  
 C-NT2RP4000360//Homo sapiens mRNA for KIAA0738 protein, complete cds./0//4074bp//99%//AB018281  
 C-NT2RP4000367//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds./0//  
 20 4782bp//99%//AF044195  
 C-NT2RP4000370//MITOCHONDRIAL PEPTIDE CHAIN RELEASE FACTOR 1 PRECURSOR (MRF-1).//2.6E-77//262aa//54%//O75570  
 C-NT2RP4000376//Homo sapiens mRNA for phospholipase A2 activating protein.//0//2412bp//99%//AJ238243  
 C-NT2RP4000381  
 25 C-NT2RP4000398//ZINC FINGER PROTEIN 140.//2.9E-110//435aa//50%//P52738  
 C-NT2RP4000415  
 C-NT2RP4000417//MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE (EC 3.2.1.113)(MAN(9)-ALPHA-MANNOSIDASE) (FRAGMENT).//2.6E-51//438aa//33%//P45701  
 C-NT2RP4000448//Homo sapiens mRNA; cDNA DKFZp566G0746 (from clone DKFZp566G0746).//0//3991bp//  
 30 99%//AL050078  
 C-NT2RP4000449  
 C-NT2RP4000455//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0.//0.0000003//175aa//27%//P09309  
 C-NT2RP4000457//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 15 (EC 3.1.2.15) (UBIQUITIN THIOESTERASE 15) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 15)(DEUBIQUITINATING ENZYME 15).//  
 35 2.5E-37//291aa//38%//P50101  
 C-NT2RP4000480  
 C-NT2RP4000481//ATP-DEPENDENT RNA HELICASE DOB1 (mRNA TRANSPORT REGULATOR MTR4).//1.9E-67//721aa//29%//Q09475  
 C-NT2RP4000498//MOB1 PROTEIN (MPS1 BINDER 1).//8.8E-50//214aa//50%//P40484  
 40 C-NT2RP4000500  
 C-NT2RP4000518//ATP-DEPENDENT RNA HELICASE ROK1.//1.5E-106//495aa//45%//P45818  
 C-NT2RP4000524  
 C-NT2RP4000541  
 C-NT2RP4000556//SUR4 PROTEIN (SRE1 PROTEIN).//7.4E-14//233aa//31%//P40319  
 45 C-NT2RP4000560  
 C-NT2RP4000588  
 C-NT2RP4000614//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds./2.9E-188//863bp//99%//AF067730  
 C-NT2RP4000638  
 50 C-NT2RP4000648//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0.//0.00000037//175aa//27%//P09309  
 C-NT2RP4000657//SPORE COAT POLYSACCHARIDE BIOSYNTHESIS PROTEIN SPSE.//1.1E-32//350aa//30%//P39625  
 C-NT2RP4000704  
 C-NT2RP4000713//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//1.1E-13//295aa//27%//Q11073  
 C-NT2RP4000724//RETROVIRUS-RELATED ENV POLYPROTEIN.//3.2E-191//199aa//78%//P10267  
 C-NT2RP4000728//Homo sapiens mRNA for KIAA0931 protein, partial cds./0//3392bp//95%//AB023148  
 C-NT2RP4000737

C-NT2RP4000739//Homo sapiens mRNA for KIAA1012 protein, complete cds.//0//3574bp//99%//AB023229  
 C-NT2RP4000781//HYPOTHETICAL 27.7 KD PROTEIN IN CPT1-SPC98 INTERGENIC REGION.//  
 0.00000032//67aa//31%//P53915  
 C-NT2RP4000817//Homo sapiens mRNA for KIAA0470 protein, complete cds.//0//1927bp//99%//AB007939  
 5 C-NT2RP4000833  
 C-NT2RP4000837//Homo sapiens mRNA for zinc finger protein SALL1.//4.3E-94//810bp//65%//Y18265  
 C-NT2RP4000839//VEGETABLE INCOMPATIBILITY PROTEIN HET-E-1.//8.5E-21//271 aa//28%//Q00808  
 C-NT2RP4000855//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE)(ARGININE AMI-  
 10 NOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV)(AP-B).//5.7E-82//324aa//48%//O09175  
 C-NT2RP4000865//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//4.1E-85//174aa//55%//P16415  
 C-NT2RP4000878//MYELOID UPREGULATED PROTEIN.//6.2E-91//173aa//87%//O35682  
 C-NT2RP4000879//UBIQUITIN-ACTIVATING ENZYME E1 (A1S9 PROTEIN).//9.6E-96//513aa//42%//P22314  
 C-NT2RP4000925//FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN).//2.6E-26//  
 227aa//36%//Q06828  
 15 C-NT2RP4000927//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THI-  
 OLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING EN-  
 ZYME 1).//1.5E-76//346aa//43%//Q61068  
 C-NT2RP4000928//Homo sapiens mRNA for CDS2 protein.//0//2487bp//99%//Y16521  
 C-NT2RP4000929//PUTATIVE ATP-DEPENDENT RNA HELICASE MJ1505.//0.00000014//185aa//25%//Q58900  
 20 C-NT2RP4000955  
 C-NT2RP4000973//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//1.4E-26//  
 90aa//42%//P38660  
 C-NT2RP4000975  
 C-NT2RP4000979  
 25 C-NT2RP4000984  
 C-NT2RP4000989//UNC-47 PROTEIN.//0.0000082//173aa//25%//P34579  
 C-NT2RP4000997//DNA-DIRECTED RNA POLYMERASE 1135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA  
 POLYMERASE I SUBUNIT 2) (RPA135).//0//838aa//87%//P70700  
 C-NT2RP4001004//VACUOLAR PROTEIN 8.//3.7E-16//401aa//26%//P39968  
 30 C-NT2RP4001006  
 C-NT2RP4001010//Homo sapiens mRNA for KIAA0964 protein, complete cds.//0//2482bp//99%//AB023181  
 C-NT2RP4001041//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE-TRNA LIGASE).//1.5E-  
 92//443aa//44%//Q09996  
 C-NT2RP4001057  
 35 C-NT2RP4001064//SYNAPTONEMAL COMPLEX PROTEIN SC65.//6.7E-51//335aa//37%//Q64375  
 C-NT2RP4001079//CALCIUM-TRANSPORTING ATPASE 1 (EC 3.6.1.38) (GOLGI CA2<sup>+</sup>-ATPASE).//1.3E-123//  
 563aa//46%//P13586  
 C-NT2RP4001080//Homo sapiens mRNA for Rodi, complete cds.//0//1439bp//99%//AB023967  
 C-NT2RP4001086  
 40 C-NT2RP4001095//DOUBLE-STRANDED RNA-SPECIFIC EDITASE 1 (EC 3.5.-.) (DSRNA ADENOSINE DEAM-  
 INASE) (RNA EDITING ENZYME 1).//2.6E-17//121aa//36%//P51400  
 C-NT2RP4001100  
 C-NT2RP4001117//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//1.9E-115//224aa//100%//  
 P38378  
 45 C-NT2RP4001122//TIPD PROTEIN.//1.4E-65//253aa//41%//O15736  
 C-NT2RP4001126//TRICHOHYALIN.//2.9E-18//380aa//26%//Q07283  
 C-NT2RP4001138  
 C-NT2RP4001143//SUCCINYL-DIAMINOPIMELATE DESUCCINYLASE (EC 3.5.1.18) (SDAP).//0.00000021//  
 93aa//33%//P44514  
 50 C-NT2RP4001148//SOF1 PROTEIN.//1.3E-104//236aa//52%//P33750  
 C-NT2RP4001149  
 C-NT2RP4001150//NG-CAM RELATED CELL ADHESION MOLECULE PRECURSOR (NR-CAM) (BRAVO).//  
 3.4E-29//385aa//29%//P35331  
 C-NT2RP4001174//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT).//  
 4.7E-29//227aa//35%//P52178  
 55 C-NT2RP4001206//Drosophila melanogaster strawberry notch (sno) mRNA, complete cds.//4.4E-104//1460bp//  
 65 %//U95760  
 C-NT2RP4001207

C-NT2RP4001210  
C-NT2RP4001219//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//6.2E-27//  
90aa//42%//P38660  
C-NT2RP4001228//RING CANAL PROTEIN (KELCH PROTEIN).//1.8E-103//508aa//43%//Q04652

5 C-NT2RP4001235  
C-NT2RP4001256  
C-NT2RP4001260//Homo sapiens mRNA for KIAA0875 protein, partial cds.//0//2876bp//99%//AB020682  
C-NT2RP4001274//Human transporter protein (g17) mRNA, complete cds.//4.4E-58//1196bp//61%//U49082  
C-NT2RP4001276//TRICHOHYALIN.//7.9E-09//126aa//32%//Q07283

10 C-NT2RP4001313//MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT TOM40 (MOM38 PROTEIN) (TRANSLOCASE OF OUTER MEMBRANE 40 KD SUBUNIT).//5.9E-17//296aa//29%//P24391  
C-NT2RP4001315//Bos taurus mRNA for Rab5 GDP/GTP exchange factor, Rabex5.//8.5E-213//1129bp//92%//AJ001119  
C-NT2RP4001339//Homo sapiens mRNA for AMMERC1 protein.//9.2E-160//736bp//99%//AJ007014

15 C-NT2RP4001343  
C-NT2RP4001345//Homo sapiens mRNA for LCAT-like lysophospholipase (LLPL), complete cds.//2.7e-310//1400bp//100%//AB017494  
C-NT2RP4001351//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds.//1.4E-58//2425bp//59%//U53445

20 C-NT2RP4001353  
C-NT2RP4001372//IRREGULAR CHIASM C-ROUGHEST PROTEIN PRECURSOR (IRREC PROTEIN).//1.6E-19//222aa//30%//Q08180  
C-NT2RP4001373  
C-NT2RP4001375//NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE 1).//9.2E-17//146aa//35%//P18160

25 C-NT2RP4001379//HYPOTHETICAL 49.1 KD PROTEIN C11D3.06 IN CHROMOSOME I.//2E-53//436aa//30%//Q10085  
C-NT2RP4001407//Homo sapiens mRNA for KIAA0923 protein, complete cds.//0//2716bp//99%//AB023140  
C-NT2RP4001414//SEPTIN 2 HOMOLOG (FRAGMENT).//7.7E-190//422aa//82%//Q14141

30 C-NT2RP4001433//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.2E-138//419aa//54%//Q99676  
C-NT2RP4001474//Xenopus laevis putative Zic3 binding protein mRNA, complete cds.//2.7E-66//738bp//71%//AF129131  
C-NT2RP4001483//2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT PRECURSOR (EC 1.2.4.2) (ALPHA-KETOGLUTARATE DEHYDROGENASE).//0//962aa//78%//Q02218

35 C-NT2RP4001498//ANKYRIN REPEAT-CONTAINING PROTEIN AKR1.//1E-27//374aa//29%//P39010  
C-NT2RP4001502  
C-NT2RP4001507  
C-NT2RP4001524  
C-NT2RP4001547//HYPOTHETICAL 45.0 KD PROTEIN IN NOT1/CDC39-HMR INTERGENIC REGION.//5.7E-54//242aa//3 8%//P25656

40 C-NT2RP4001551//Homo sapiens chromatin-specific transcription elongation factor FACT 140 kDa subunit mRNA, complete cds.//0//3202bp//99%//AF152961  
C-NT2RP4001555//PUTATIVE ENDONUCLEASE VIII (EC 3.2.-.-).//4.7E-09//216aa//24%//P96902  
C-NT2RP4001567//ARMADILLO SEGMENT POLARITY PROTEIN.//0.00000054//213aa//26.%//Q02453

45 C-NT2RP4001568//ZINC FINGER PROTEIN GCS1.//1.8E-10//109aa//36%//P35197  
C-NT2RP4001571  
C-NT2RP4001574//Homo sapiens coat protein gamma-cop mRNA, complete cds.//0//3046bp//99%//AF100756  
C-NT2RP4001575//Rattus norvegicus mRNA for ARE1 protein.//0//1087bp//87%//AJ223830  
C-NT2RP4001592//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE-TRNA LIGASE) (ILERS).//1.7E-141//373aa//47%//P73505

50 C-NT2RP4001610//Homo sapiens mRNA for KIAA0869 protein, partial cds.//0//1897bp//99%//AB020676  
C-NT2RP4001614  
C-NT2RP4001634  
C-NT2RP4001638//DNA REPAIR/TRANSCRIPTION PROTEIN MET18/MMS19.//5.1E-46//234aa//32%//P40469

55 C-NT2RP4001644//MYOSIN LIGHT CHAIN KINASE (EC 2.7.1.117) (MLCK).//6.4E-19//111aa//45%//P25323  
C-NT2RP4001677  
C-NT2RP4001679  
C-NT2RP4001696//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF

100 KD SUBUNIT).//4E-10//243aa//25%//Q10568  
 C-NT2RP4001725//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT//3E-10//128aa//32%//  
 Q10282  
 C-NT2RP4001730//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-)  
 5 (DUGT).//6.4E-170//1168aa//33%//Q09332  
 C-NT2RP4001739  
 C-NT2RP4001753//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3.9E-236//665aa//58%//  
 P51523  
 C-NT2RP4001760//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FA-  
 10 CIOGENITAL DYSPLASIA PROTEIN).//4.1E-16//263aa//27%//P98174  
 C-NT2RP4001790//Homo sapiens mRNA for KIAA1015 protein, complete cds.//0//3144bp//99%//AB023232  
 C-NT2RP4001803  
 C-NT2RP4001822//PLATELET-ENDOTHELIAL TETRASPAAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYC-  
 15 OPROTEIN SFA-1) (CD151 ANTIGEN).//1.2E-30//241aa//30%//O35566  
 C-NT2RP4001823//MICROFIBRIL-ASSOCIATED GLYCOPROTEIN 4.//1.1E-19//77aa//54%//P55083  
 C-NT2RP4001828  
 C-NT2RP4001838//Homo sapiens CoREST protein (COREST) mRNA, complete cds.//6.3E-99//555.bp//73%//  
 AF155595  
 C-NT2RP4001861//TRICHOHYALEN.//1E-35//307aa//34%//P37709  
 20 C-NT2RP4001893//Homo sapiens mRNA; cDNA DKFzP5640043 (from clone DKFzP5640043).//0//1306bp//98%//  
 AL050390  
 C-NT2RP4001896//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E1.//0.000000014//345aa//25%//Q00808  
 C-NT2RP4001901  
 C-NT2RP4001927//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//1.3E-38//258aa//32%//Q12024  
 25 C-NT2RP4001938//TRANSCRIPTIONAL REPRESSOR CTCF.//9.8E-60//303aa//38%//P49711  
 C-NT2RP4001946//PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (EC 2.1.1.77) (PROTEIN- BETA-  
 ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L-ISO-  
 ASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE).//1.5E-13//211aa//28%//Q43209  
 C-NT2RP4001950//GLUTAMIC ACID-RICH PROTEIN PRECURSOR.//1.2E-13//356aa//27%//P13816  
 30 C-NT2RP4001953  
 C-NT2RP4001966  
 C-NT2RP4001975  
 C-NT2RP4002018//RING CANAL PROTEIN (KELCH PROTEIN).//6.9E-24//370aa//27%//Q04652  
 C-NT2RP4002052  
 35 C-NT2RP4002058//PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE (DEAH BOX PROTEIN 13).//1E-  
 137//679aa//40%//O43143  
 C-NT2RP4002071  
 C-NT2RP4002078//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//3E-150//722aa//  
 39%//Q05481  
 40 C-NT2RP4002081//TRANSCRIPTION INITIATION FACTOR IIA ALPHA AND BETA CHAINS (TFIILA P35 AND P19  
 SUBUNITS) (TFIILA-42) (TFIIAL).//0.0000067//250aa//31%//P52655  
 C-NT2RP4002298  
 C-NT2RP4002408//PROTEIN KINASE CEK1 (EC 2.7.1.-).//1.5E-63//159aa//53%//P38938  
 C-NT2RP4002791  
 45 C-NT2RP4002888//Homo sapiens mRNA; cDNA DKFzP434F172 (from clone DKFzP434F172).//0//2557bp//99%//  
 AL080202  
 C-NT2RP4002905  
 C-NT2RP5003461//RLR1 PROTEIN.//9.7E-22//177aa//27%//P53552  
 50 C-NT2RP5003477//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//5.5E-15//280aa//27%//Q00808  
 C-NT2RP5003492  
 C-NT2RP5003500  
 C-NT2RP5003506  
 C-NT2RP5003522//NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR).//3.3E-23//219aa//40%//  
 P37116  
 55 C-NT2RP5003524  
 C-NT2RP5003534  
 C-OVARC1000006//HISTONE H2A.1.//1.1E-55//117aa//99%//P02262  
 C-OVARC1000013//APOPTOTIC PROTEASE ACTIVATING FACTOR 1 (APAF-1).//0.0000042//102aa//32%//

O14727  
 C-OVARC1000014//Homo sapiens GLE1 (GLE1) mRNA, complete cds.//2.6E-295//1393bp//97%//AF058922  
 C-OVARC1000035  
 C-OVARC1000060//EXTRACELLULAR RIBONUCLEASE LE PRECURSOR (EC 3.1.27.1) (RNASE LE).//  
 5 0.00000032//60aa//45 %//P80022  
 C-OVARC1000087//HISTONE MACRO-H2A.1.//1.6E-12//174aa//26%//Q02874  
 C-OVARC1000091//HOST CELL FACTOR C1 (HCF) (VP16 ACCESSORY PROTEIN) (HFC1) (VCAF) (CFF).//  
 8.4E-14//259aa//30%//P51610  
 C-OVARC1000113  
 10 C-OVARC1000139//Homo sapiens CGI-21 protein mRNA, complete cds.//0//1562bp//99%//AF132955  
 C-OVARC1000148  
 C-OVARC1000151//Homo sapiens partial mRNA for putative protein p38 interacting with transcription factor Sp1.//  
 2.5E-95//461bp//98%//AJ242975  
 C-OVARC1000168  
 15 C-OVARC1000209//Oryza sativa submergence induced protein 2A mRNA, complete cds.//1.8E-32//511bp//65%//  
 AF068332  
 C-OVARC1000212  
 C-OVARC1000241//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN)  
 (MEMBER OF PAS PROTEIN 1) (MOP1) (HIF1 ALPHA).//8.2E-120//351aa//54%//Q16665  
 20 C-OVARC1000288//VACUOLAR AMINOPEPTIDASE I PRECURSOR (EC 3.4.11.22) (POLYPEPTIDASE)(LEU-  
 CINE AMINOPEPTIDASE IV) (LAPIV) (AMINOPEPTIDASE III)(AMINOPEPTIDASE YSCI).//5.4E-53//384aa//  
 30%//P14904  
 C-OVARC1000304//PROTEIN MOV-10.//1.1E-249//519aa//87%//P23249  
 C-OVARC1000309//THREONINE SYNTHASE (EC 4.2.99.2).//2.7E-40//154aa//38%//P29363  
 25 C-OVARC1000321  
 C-OVARC1000326  
 C-OVARC1000335//HYPOTHETICAL 39.3 KD PROTEIN IN GCN4-WBP1 INTERGENIC REGION.//5.9E-14//  
 200aa//27%//P40004  
 C-OVARC1000347  
 30 C-OVARC1000384  
 C-OVARC1000411  
 C-OVARC1000420  
 C-OVARC1000437//TENSIN.//7.9E-181//340aa//84%//Q04205  
 C-OVARC1000443//Homo sapiens mRNA; cDNA DKFZp434A073 (from clone DKFZp434A073).//0//1216bp//  
 35 99%//AL080126  
 C-OVARC1000461  
 C-OVARC1000465//PROTEIN TRANSPORT PROTEIN SEC7.//1.2E-25//227aa//25%//P11075  
 C-OVARC1000466  
 C-OVARC1000473//DUAL SPECIFICITY PROTEIN PHOSPHATASE 3 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPE-  
 40 CIFICITY PROTEIN PHOSPHATASE VHR).//3.1E-10//125aa//35%//P51452  
 C-OVARC1000479//Homo sapiens mRNA for KIAA0829 protein, partial cds.//0//1919bp//99%//AB020636  
 C-OVARC1000520//Homo sapiens supervillin mRNA, complete cds.//2.2E-157//892bp//91 %//AF051850  
 C-OVARC1000564  
 C-OVARC1000576  
 45 C-OVARC1000588  
 C-OVARC1000605  
 C-OVARC1000640  
 C-OVARC1000649//Human squamous cell carcinoma of esophagus mRNA for GRB-7 SH2 domain protein, com-  
 plete cds.//0//1812bp//98%//D43772  
 50 C-OVARC1000661  
 C-OVARC1000711//RAS-RELATED PROTEIN RAB-2.//1.1E-46//121aa//79%//P08886  
 C-OVARC1000959//HYPOTHETICAL PROTEIN MJ0933.//1.2E-17//127aa//33%//Q58343  
 C-OVARC1001034//Mus musculus Fn54 mRNA, partial cds.//1.5E-178//1113bp//86%//AF001533  
 C-OVARC1001038//Homo sapiens mRNA for Ariadne-2 protein.//0//1172bp//97%//AJ130978  
 55 C-OVARC1001065//Homo sapiens CGI-12 protein mRNA, complete cds.//1E-215//1027bp//98%//AF132946  
 C-OVARC1001162  
 C-OVARC1001243  
 C-OVARC1001296

C-OVARC1001360  
C-OVARC1001381//Homo sapiens mRNA for candidate tumor suppressor involved in B-CLL//6E-148//683bp//  
99%//AJ224819  
C-OVARC1001425  
5 C-PLACE1000005  
C-PLACE1000066//SSU72 PROTEIN././/1.1E-39//206aa//43%//P53538  
C-PLACE1000142//3-HYDROXYBUTYRYL-COA DEHYDRATASE (EC 4.2.1.55) (CROTONASE).//2.8E-29//  
134aa//43%//P52046  
C-PLACE1000184//Homo sapiens mRNA for KIAA0832 protein, complete cds.//5.5e-312//1411bp//99%//  
10 AB020639  
C-PLACE1000185  
C-PLACE1000213//Homo sapiens mRNA for KIAA0977 protein, complete cds.//0//1904bp//99%//AB023194  
C-PLACE1000347  
C-PLACE1000374  
15 C-PLACE1000380//Homo sapiens mRNA for KIAA0853 protein, partial cds.//0//2208bp//99%//AB020660  
C-PLACE1000383//Homo sapiens mRNA for MTMR1 protein.//0//753bp//99%//AJ224979  
C-PLACE1000401//POLIOVIRUS RECEPTOR PRECURSOR (CD155 ANTIGEN).//2.7E-30//352aa//31%//  
P15151  
C-PLACE1000406//PTB-ASSOCIATED SPLICING FACTOR (PSF).//1.2E-132//334aa//72%//P23246  
20 C-PLACE1000420//7.8-DIHYDRO-8-OXOGUANINE TRIPHOSPHATASE (EC 3.1.6.-) (8-OXO-DGTPASE).//  
0.0000028//134aa//29%//P53368  
C-PLACE1000435  
C-PLACE1000444  
C-PLACE1000562  
25 C-PLACE1000564  
C-PLACE1000588//INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1 (GUANINE NUCLEOTIDE-  
BINDING PROTEIN 1).//1.6E-270//437aa//86%//P32455  
C-PLACE1000596//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//2393bp//99%//AB020657  
C-PLACE1000611//Rattus norvegicus neural membrane protein 35 mRNA, complete cds.//2E-55//779bp//67%//  
30 AF044201  
C-PLACE1000636//MALE STERILITY PROTEIN 2.//1.2E-39//261aa//27%//Q08891  
C-PLACE1000716  
C-PLACE1000748  
35 C-PLACE1000755//Homo sapiens mRNA for Helicase-MOI, complete-cds.//4.6E-250//1189bp//97%//AB028449  
C-PLACE1000785//Homo sapiens mRNA for KIAA0648 protein, partial cds.//0//2002bp//99%//AB014548  
C-PLACE1000798  
C-PLACE1000863//PUTATIVE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN  
YHR148W.//2.5E-49//181aa//54%//P32899  
C-PLACE1000909//ANKYRIN REPEAT-CONTAINING PROTEIN AKR1.//2.6E-19//404aa//26%//P39010  
40 C-PLACE1000948  
C-PLACE1000972  
C-PLACE1000977//BETA-CHIMAERIN (BETA-CHIMERIN).//4.4E-22//129aa//35%//Q03070  
C-PLACE1001000  
C-PLACE1001092//Homo sapiens sorting nexin 4 mRNA, complete cds.//0//1500bp//99%//AF065485  
45 C-PLACE1001257//RING CANAL PROTEIN (KELCH PROTEIN).//4.3E-54//257aa//46%//Q04652  
C-PLACE1001383//ZINC-FINGER PROTEIN UBI-D4 (APOPTOSIS RESPONSE ZINC FINGER PROTEIN REQ-  
UIEM).//3E-33//138aa//42%//Q61103  
C-PLACE1001387//EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8.//2.3E-61//  
132aa//46%//Q12929  
50 C-PLACE1001399//Homo sapiens chromosome 17, clone hRPK.22\_N\_12, complete sequence.//0//2118bp//  
99%//AC005412  
C-PLACE1001412  
C-PLACE1001484//Homo sapiens chromosome 20 clone 387E22, WORKING DRAFT SEQUENCE, in unordered  
pieces.//0//1440bp//99%//AL031660  
55 C-PLACE1001503  
C-PLACE1001570  
C-PLACE1001610  
C-PLACE1001692//S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN (EC 3.1.2.14)

(THIOESTERASE n).//4E-81//263aa//56%//P08635  
 C-PLACE1001729  
 C-PLACE1001739//PUTATIVE ATP-DEPENDENT RNA HEUCASE PL10.//3.5E-75//439aa//41%//P16381  
 C-PLACE1001781//PROBABLE PHOSPHOMANNOMUTASE (EC 5.4.2.8) (PMM).//5.4E-63//427aa//35%//  
 5 Q57290  
 C-PLACE1001810  
 C-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds.//0//1995bp//99%//AF058953  
 C-PLACE1001869//L-RIBULOKINASE (EC 2.7.1.16).//2E-27//270aa//31%//P94524  
 10 C-PLACE1001912//Homo sapiens clone 24963 mRNA sequence, complete cds.//0//1196bp//99%//AF131737  
 C-PLACE1001920//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds.//0//1729bp//99%//AF099935  
 C-PLACE1001928  
 C-PLACE1001989//PUTATIVE AMIDASE (EC 3.5.1.4).//1.4E-78//496aa//37%//Q49091  
 C-PLACE1002046//LIGATIN (FRAGMENT).//1.7E-240//560aa//80%//Q61211  
 15 C-PLACE1002072  
 C-PLACE1002073//ADENYLATE CYCLASE (EC 4.6.1.1)(ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE).//0.00000053//188aa//29%//P49606  
 C-PLACE1002140  
 C-PLACE1002163  
 20 C-PLACE1002170  
 C-PLACE1002433  
 C-PLACE1002438//ZINC FINGER PROTEIN 151 (MIZ-1 PROTEIN).//0.0000042//133aa//29%//Q13105  
 C-PLACE1002465  
 C-PLACE1002529//Homo sapiens mRNA for KIAA0713 protein, partial cds.//6.7E-214//956bp//94%//AB018256  
 25 C-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds.//0//1750bp//99%//AF068180  
 C-PLACE1002722//PROBABLE G PROTEIN-COUPLED RECEPTOR KIAA0001.//9E-45//305aa//33%//Q15391  
 C-PLACE1002794  
 C-PLACE1002815  
 30 C-PLACE1002839  
 C-PLACE1002851  
 C-PLACE1002941  
 C-PLACE1002996  
 C-PLACE1003045  
 35 C-PLACE1003092  
 C-PLACE1003100//HEP27 PROTEIN (PROTEIN D).//2.6E-79//253aa//60%//Q13268  
 C-PLACE1003108  
 C-PLACE1003145  
 C-PLACE1003174//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN  
 40 LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42).//3.8E-37//143aa//51%//P42743  
 C-PLACE1003190//SOF1 PROTEIN.//1.9E-110//325aa//48%//P33750  
 C-PLACE1003200  
 C-PLACE1003296//Homo sapiens mRNA; cDNA DKFZp434G173 (from clone DKFZp434G173).//0//1706bp//  
 99%//AL080133  
 45 C-PLACE1003302//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//6.9E-206//396aa//86%//  
 P51522  
 C-PLACE1003334  
 C-PLACE1003342  
 C-PLACE1003353//Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3) mRNA, complete  
 50 cds.//0//2435bp//99%//U92715  
 C-PLACE1003369  
 C-PLACE1003602//Homo sapiens mRNA expressed in placenta.//5.9E-278//1275bp//99%//D83200  
 C-PLACE1003611  
 C-PLACE1003625//ARMADILLO SEGMENT POLARITY PROTEIN.//3.2E-10//380aa//25%//P18824  
 55 C-PLACE1003704//SPLICING FACTOR, ARGinine/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR  
 SRP75).//8E-19//209aa//34%//Q08170  
 C-PLACE1003711  
 C-PLACE1003723

C-PLACE1003762  
 C-PLACE1003771  
 C-PLACE1003784  
 C-PLACE1003923  
 5 C-PLACE1003936  
 C-PLACE1003968//5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK GAMMA-1 CHAIN).//  
 2.4E-124//326aa/73%//P80385  
 C-PLACE1004104  
 C-PLACE1004114  
 10 C-PLACE1004128//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT 4 (TRANSDUCIN BETA  
 CHAIN 4).//6.1E-181//340aa/96%//P29387  
 C-PLACE1004149  
 C-PLACE1004156  
 C-PLACE1004161  
 15 C-PLACE1004183//Homo sapiens for TOM1-like protein.//0//1279bp/97%//AJ010071  
 C-PLACE1004197//BUTYROPHILIN PRECURSOR (BT).//4.5E-10//208aa/27%//Q62556  
 C-PLACE1004203//Homo sapiens GPI-anchored membrane protein CDw108 precursor, mRNA, complete cds.//  
 0//1882bp/99%//AF069493  
 C-PLACE1004258  
 20 C-PLACE1004270//TRANSMEMBRANE PROTEASE, SERINE 2 (EC 3.4.21.-).//9.7E-36//389aa/31%//O15393  
 C-PLACE1004277//Homo sapiens two pore domain K<sup>+</sup> channel (TASK-2) mRNA, complete cds.//0//1498bp/99%//  
 AF084830  
 C-PLACE1004289  
 C-PLACE1004302//SOF1 PROTEIN.//1.9E-110//325aa/48%//P33750  
 25 C-PLACE1004316//H.sapiens mRNA for apoptosis specific protein.//0//1767bp/99%//Y11588  
 C-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1 mRNA, complete cds.//0//  
 2512bp/99%//AF100153  
 C-PLACE1004376  
 C-PLACE1004388  
 30 C-PLACE1004405  
 C-PLACE1004428//PRISTANOYL-COA OXIDASE (EC 1.3.3.-).//1.2E-39//385aa/33%//Q63448  
 C-PLACE1004437//Human NAD<sup>+</sup>-specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene  
 encoding mitochondrial protein, complete cds.//0//985bp/99%//U49283  
 C-PLACE1004451  
 35 C-PLACE1004460//MATERNAL TUDOR PROTEIN.//0.0000002//218aa/23%//P25823  
 C-PLACE1004473  
 C-PLACE1004510//Homo sapiens cofactor of initiator function (CIF150) mRNA, complete//1.3E-209//954bp//  
 99%//AF026445  
 C-PLACE1004516  
 40 C-PLACE1004548  
 C-PLACE1004564//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100  
 KD SUBUNIT (CPSF 100 KD SUBUNIT).//0//525aa/99%//Q10568  
 C-PLACE1004629//PROTEIN OS-9 PRECURSOR.//7.7E-18//264aa/32%//Q13438  
 C-PLACE1004645  
 45 C-PLACE1004646//B.taurus mRNA for retinal pigment epithelial membrane receptor p63.//4.4E-42//985bp/59%//  
 X66277  
 C-PLACE1004664  
 C-PLACE1004672  
 C-PLACE1004674//PROBABLE CALCIUM-BINDING PROTEIN ALG-2 (PMP41) (ALG-257).//1.6E-95//191aa/  
 50 96%//P12815  
 C-PLACE1004691  
 C-PLACE1004722  
 C-PLACE1004736  
 C-PLACE1004740  
 55 C-PLACE1004743//PROBABLE N-END-RECOGNIZING PROTEIN (UBIQUITIN-PROTEIN LIGASE E3 COMPO-  
 NENT) (N- RECOGNIN).//4.4E-35//578aa/27%//O60152  
 C-PLACE1004751//Homo sapiens mRNA for alpha2,3-sialyltransferase ST3Gal VI, complete cds.//7.1E-224//  
 790bp/98%//AB022918

C-PLACE1004777//N-CHIMAERIN (NC) (N-CHIMERIN) (ALPHA CHIMERIN) (A-CHIMAERIN).//1.9E-32//259aa//32%//P30337  
 C-PLACE1004804//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE).//4.7E-65//695aa//29%//Q01631  
 5 C-PLACE1004814//SPLICING FACTOR, ARGinine/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//5.9E-19//196aa//36%//Q08170  
 C-PLACE1004824  
 C-PLACE1004868//MALE STERILITY PROTEIN 2.//3.9E-39//261aa//27%//Q08891  
 C-PLACE1004885  
 10 C-PLACE1004902//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C.//9.3E-11//94aa//47%//O42643  
 C-PLACE1004918//L-LACTATE DEHYDROGENASE M CHAIN (EC 1.1.1.27) (LDHA).//4.9E-48//198aa//44%//P06151  
 15 C-PLACE1004930//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds//0//1853bp//98%//AF099936  
 C-PLACE1004934  
 C-PLACE1004937//SEL-10 PROTEIN.//6.3E-125//357aa//58%//Q93794  
 C-PLACE1004969//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//2E-14//205aa//26%//Q11073  
 C-PLACE1004982  
 20 C-PLACE1005026  
 C-PLACE1005027  
 C-PLACE1005046  
 C-PLACE1005077  
 C-PLACE1005101//Homo sapiens (clone zap128) mRNA, 3' end of cds.//1E-209//1031bp//96%//L40401  
 25 C-PLACE1005102//RING CANAL PROTEIN (KELCH PROTEIN).//2.6E-56//565aa//30%//Q04652  
 C-PLACE1005111  
 C-PLACE1005181  
 C-PLACE1005187//APAG PROTEIN.//3.8E-13//122aa//36%//P05636  
 C-PLACE1005206  
 30 C-PLACE1005232  
 C-PLACE1005243//SERINE/THREONINE PROTEIN KINASE PKPA (EC 2.7.1.-).//1.3E-27//349aa//32%//Q01577  
 C-PLACE1005261  
 C-PLACE1005266  
 C-PLACE1005277//Homo sapiens mRNA for KIAA0610 protein, partial cds.//3.2E-297//1341bp//100%//AB011182  
 35 C-PLACE1005287//INNER CENTROMERE PROTEIN (INCENP).//2.3E-13//269aa//28%//P53352  
 C-PLACE1005305//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//2E-111//226aa//92%//P08760  
 C-PLACE1005308  
 C-PLACE1005313  
 40 C-PLACE1005327  
 C-PLACE1005335  
 C-PLACE1005373//TRNA PSEUDOURIDINE SYNTHASE B (EC 4.2.1.70) (TRNA PSEUDOURIDINE 55 SYNTHASE) (PSI55 SYNTHASE) (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE).//8.6E-09//194aa//27%//O33335  
 C-PLACE1005374  
 45 C-PLACE1005480  
 C-PLACE1005481  
 C-PLACE1005494//Homo sapiens mRNA for transient receptor potential protein TRP6.//0//1649bp//99%//AJ006276  
 C-PLACE1005530//HYPOTHETICAL 47.6 KD PROTEIN C16C10.5 IN CHROMOSOME III.//5.6E-52//173aa//57%//Q09251  
 C-PLACE1005550  
 C-PLACE1005554  
 C-PLACE1005623  
 55 C-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete cds.//0//2130bp//99%//AF083255  
 C-PLACE1005656//RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M2 CHAIN (EC 1.17.4.1) (RIBONUCLEOTIDE REDUCTASE).//2.1E-148//321aa//83%//P31350

C-PLACE1005730  
 C-PLACE1005755  
 C-PLACE1005763//S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN (EC 3.1.2.14)  
 (THIOESTERASE II).//2.5E-79//209aa//53%//P08635  
 5 C-PLACE1005803  
 C-PLACE1005804//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds.//1.1E-217//994bp//99%//  
 AF027156  
 C-PLACE1005851  
 C-PLACE1005921//AIG1 PROTEIN.//3E-31//284aa//31%//P54120  
 10 C-PLACE1005923  
 C-PLACE1005925  
 C-PLACE1005934  
 C-PLACE1005936  
 C-PLACE1005951  
 15 C-PLACE1005953//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//6.7E-30//198aa//37%//P43636  
 C-PLACE1005955//VACUOLAR AMINOPEPTIDASE I PRECURSOR (EC 3.4.11.22) (POLYPEPTIDASE)//5.4E-  
 54//455aa//32%//P14904  
 C-PLACE1005966//TRANSCRIPTION INITIATION FACTOR TFIID 90 KD SUBUNIT (TAFII-90).//0.00000014//  
 20 254aa//25%//P38129  
 C-PLACE1005990  
 C-PLACE1006011//Homo sapiens mRNA for poly(ADP-ribose) polymerase-2.//0//1564bp//99%//AJ236876  
 C-PLACE1006040//Homo sapiens mRNA for alpha endosulfine.//4.7E-161//744bp//99%//X99906  
 C-PLACE1006119//Homo sapiens Ran-GTP binding protein mRNA, partial cds.//1.5E-148//681bp//99%//  
 AF039023  
 25 C-PLACE1006139  
 C-PLACE1006159  
 C-PLACE1006167  
 C-PLACE1006170//Homo sapiens mRNA for KIAA0899 protein, partial cds.//4.5E-293//953bp//99%//AB020706  
 C-PLACE1006195  
 30 C-PLACE1006196//PUTATIVE ATP-DEPENDENT RNA HELICASE C12C2.06.//2.7E-116//496aa//48%//Q09747  
 C-PLACE1006225  
 C-PLACE1006236  
 C-PLACE1006239//BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN).//2E-16//244aa//31%//  
 P28675  
 35 C-PLACE1006246  
 C-PLACE1006325//Homo sapiens mRNA; cDNA DKFZp564J142 (from clone DKFZp564J142).//3.8E-278//  
 1271-bp//99%//AL080066  
 C-PLACE1006335  
 C-PLACE1006357  
 40 C-PLACE1006385//Homo sapiens epsin 2a mRNA, complete cds.//0//1168bp//99%//AF062085  
 C-PLACE1006412  
 C-PLACE1006414  
 C-PLACE1006438//ZINC FINGER PROTEIN 165.//2.5E-45//122aa//43%//P49910  
 C-PLACE1006445  
 45 C-PLACE1006470  
 C-PLACE1006482//TRANSCRIPTION FACTOR MAFF.//7.7E-55//142aa//85%//Q90595  
 C-PLACE1006488//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//1.1E-229//367aa//96%//  
 Q00004  
 C-PLACE1006492  
 50 C-PLACE1006531  
 C-PLACE1006552  
 C-PLACE1006598//Homo sapiens clone NH0310K15, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0//  
 2182bp//99%//AC007383  
 C-PLACE1006615  
 55 C-PLACE1006626//Homo sapiens mRNA for KIAA0928 protein, partial cds.//0//1760bp//99%//AB023145  
 C-PLACE1006673  
 C-PLACE1006678//Homo sapiens mRNA for type II membrane protein, complete cds, clone:HP10328.//5.8E-24//  
 734bp//62%//AB015630

C-PLACE1006704  
C-PLACE1006731//RIBOFLAVIN KINASE (EC 2.7.1.26) (FLAVOKINASE) / FMN ADENYLYLTRANSFERASE (EC 2.7.7.2) (FAD PYROPHOSPHORYLASE) (FAD SYNTHETASE).//6.9E-13//177aa//33%//Q59263  
C-PLACE1006782  
5 C-PLACE1006819//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//9.8E-213//232aa//80%//P08547  
C-PLACE1006829//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THIOESTERASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME 4) (UBIQUITOUS NUCLEAR PROTEIN).//2E-15//188aa//29%//P35123  
C-PLACE1006883  
10 C-PLACE1006901  
C-PLACE1006917//HSH49 PROTEIN.//5.5E-12//97aa//35%//Q99181  
C-PLACE1006932  
C-PLACE1006935//HYPOTHETICAL 95.2 KD PROTEIN R144.6 IN CHROMOSOME III.//6.7E-48//278aa//41%//Q10000  
15 C-PLACE1006956//ATP-DEPENDENT PERMEASE MDL1.//1.3E-86//522aa//36%//P97998  
C-PLACE1006958//Homo sapiens mRNA for heat shock protein *apg-1*, complete cds.//0//1770bp//99%//AB023421  
C-PLACE1006961  
C-PLACE1006962  
20 C-PLACE1006966  
C-PLACE1007014//36 KD NUCLEOLAR PROTEIN HNP36 (DELAYED-EARLY RESPONSE PROTEIN 12) (DER12).//3.2E-35//180aa//33%//Q14542  
C-PLACE1007021  
C-PLACE1007105  
25 C-PLACE1007178  
C-PLACE1007226//PROBABLE OXYGEN-INDEPENDENT COPROPORPHYRINOGEN III OXIDASE (EC 1.---) (COPROPORPHYRINOGENASE) (COPROGEN OXIDASE).//1E-42//370aa//31%//P54304  
C-PLACE1007238  
C-PLACE1007239//Homo sapiens mRNA for transcription elongation factor S-II, hS-II-T1, complete cds.//6.5E-  
30 216//1068bp//96%//D50495  
C-PLACE1007242  
C-PLACE1007243//UNC-47 PROTEIN.//0.00000017//211aa//27%//P34579  
C-PLACE1007257//Homo sapiens mRNA for dia-12c protein.//0//2052bp//99%//Y15908  
C-PLACE1007274  
35 C-PLACE1007282  
C-PLACE1007301  
C-PLACE1007317//*Drosophila melanogaster* *Adrift* (*adrift*) mRNA, complete cds.//4.1E-17//1037bp//56%//AF117649  
C-PLACE1007342  
40 C-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EBBP) mRNA, complete cds.//0//2366bp//99%//AF096870  
C-PLACE1007367  
C-PLACE1007375//PHORBOL ESTER/DIACYLGLYCEROL-BINDING PROTEIN UNC-13.//0.00000044//127aa//30%//P27715  
45 C-PLACE1007386  
C-PLACE1007402  
C-PLACE1007409//WHITE PROTEIN.//1.1E-64//428aa//32%//Q17320  
C-PLACE1007416//DIPEPTIDYL PEPTIDASE IV (EC 3.4.14.5) (DPP IV) (T-CELL ACTIVATION ANTIGEN CD26) (TP103) (ADENOSINE DEAMINASE COMPLEXING PROTEIN-2) (ADABP).//8.8E-25//140aa//35%//P27487  
50 C-PLACE1007450  
C-PLACE1007452  
C-PLACE1007460  
C-PLACE1007484  
C-PLACE1007488//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FA-  
55 CIOGENITAL DYSPLASIA PROTEIN HOMOLOG).//5.4E-53//426aa//33%//P52734  
C-PLACE1007507  
C-PLACE1007511//KERATIN, TYPE I CYTOSKELETAL 19 (CYTOKERATIN 19) (K19) (CK 19).//1.4E-85//385aa//45%//P08728

C-PLACE1007524  
C-PLACE1007537//Homo sapiens ankyrin repeat-containing protein ASB-2 mRNA, complete cds.//8.9e-316//  
1485bp//98%//AF159164  
C-PLACE1007544  
5 C-PLACE1007547//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME III.//1E-49//361aa//36%//  
P34537  
C-PLACE1007583  
C-PLACE1007598//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.6E-143//666aa//44%//Q99676  
C-PLACE1007618//Homo sapiens mRNA for KIAA0977 protein, complete cds.//0//713bp//99%//AB023194  
10 C-PLACE1007621  
C-PLACE1007632//POLIOVIRUS RECEPTOR PRECURSOR.//0.0000001//228aa//31%//P32506  
C-PLACE1007645  
C-PLACE1007649//Homo sapiens mRNA for KIAA0977 protein, complete cds.//0//1952-bp//99%//AB023194  
C-PLACE1007688//LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG).//  
15 8.7E-09//279aa//28%//Q26457  
C-PLACE1007690  
C-PLACE1007697//GCN20 PROTEIN.//7.6E-119//717aa//38%//P43535  
C-PLACE1007706//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//0//3431bp//99%//AF061243  
C-PLACE1007725  
20 C-PLACE1007729//RETROVIRUS-RELATED PROTEASE (EC 3.4.23.-).//1.5E-44//231aa//42%//P10265  
C-PLACE1007730//Homo sapiens mRNA for KIAA0685 protein, complete cds.//9.2E-294//1504bp//94%//  
AB014585  
C-PLACE1007746  
C-PLACE1007791//Homo sapiens IDN3-B mRNA, complete cds.//0//1836bp//99%//AB019602  
25 C-PLACE1007810  
C-PLACE1007843  
C-PLACE1007846//Homo sapiens genomic DNA of 21q22.2 Down Syndrome region, segment 3/13.//0//1751bp//  
99%//AP000010  
C-PLACE1007858//Homo sapiens mRNA for KIAA0766 protein, complete cds.//0//3112bp//99%//AB018309  
30 C-PLACE1007897  
C-PLACE1007946//MYOSIN HEAVY CHAIN, NON-MUSCLE (ZIPPER PROTEIN) (MYOSIN II).//2.6E-14//370aa//  
25%//Q99323  
C-PLACE1007954  
C-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds.//0//2252bp//99%//  
AF084530  
C-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds.//0//2300bp//  
99%//AF079529  
C-PLACE1007969//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN M (HNRNP M).//1.1E-36//202aa//  
48%//P52272  
40 C-PLACE1007990  
C-PLACE1008000//CHANNEL ASSOCIATED PROTEIN OF SYNAPSE-110 (CHAPSYN-110) (SYNAPTIC DEN-  
SITY PROTEIN PSD-93).//6.1E-14//128aa//39%//Q63622  
C-PLACE1008002//Homo sapiens clone DJ0613C23, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0//  
1833bp//99%//AC005628  
45 C-PLACE1008044//NUCLEAR PORE COMPLEX PROTEIN NUP107 (NUCLEOPORIN NUP107) (107 KD NU-  
CLEOPORIN) (P105).//4.6e-318//613aa//94%//P52590  
C-PLACE1008095  
C-PLACE1008122  
C-PLACE1008129  
50 C-PLACE1008132//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOME III.//1.3E-24//395aa//  
31%//Q09531  
C-PLACE1008177//TRICHOHYALIN.//2.3E-29//487aa//26%//P37709  
C-PLACE1008209  
C-PLACE1008273//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP).//1.3E-283//  
55 671aa//77%//P53620  
C-PLACE1008275//DNA REPAIR PROTEIN REV1 (EC 2.7.7.-).//2.3E-18//162aa//37%//P12689  
C-PLACE1008280  
C-PLACE1008309

C-PLACE1008329  
C-PLACE1008356//Homo sapiens mRNA for KIAA0679 protein, partial cds./0//1853bp//100%//AB014579  
C-PLACE1008398//GENE 33 POLYPEPTIDE./7.3E-114//243aa//87%//P05432  
C-PLACE1008401  
5 C-PLACE1008402//GENERAL VESICULAR TRANSPORT FACTOR P115 (TRANSCYTOSIS ASSOCIATED PROTEIN) (TAP).//0//698aa//95%//P41541  
C-PLACE1008429//ANKYRIN HOMOLOG PRECURSOR./3.1E-11//189aa//32%//Q06527  
C-PLACE1008457  
C-PLACE1008465  
10 C-PLACE1008488  
C-PLACE1008524//Human DNA sequence from clone 34B21 on chromosome 6p12.1-21.1. Contains part of a gene for a novel protein with ZU5 domain similar to part of Tight Junction Protein ZO1 (TJP1) and UNC5 Homologs, the gene for a novel BZRP (peripheral benzodiazepine receptor).//0//1980bp//99%//AL031778  
C-PLACE1008531  
15 C-PLACE1008532  
C-PLACE1008533//101 KD MALARIA ANTIGEN (P101) (ACIDIC BASIC REPEAT ANTIGEN).//1.1E-09//62aa//48%//P22620  
C-PLACE1008568  
C-PLACE1008603//NUCLEAR PORE COMPLEX PROTEIN NUP155 (NUCLEOPORIN NUP155) (155 KD NUCLEOPORIN) (P140).//7.8E-236//453aa//96%//P37199  
20 C-PLACE1008621  
C-PLACE1008626  
C-PLACE1008627//Homo sapiens mRNA for cysteine-rich protein.//0//1850bp//99%//AJ006591  
C-PLACE1008629  
25 C-PLACE1008650//Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA, complete cds./0//1548bp//100%//AF044333  
C-PLACE1008693  
C-PLACE1008696//Homo sapiens NADH dehydrogenase-ubiquinone Fe-S protein 8 23 kDa subunit (NDUFS8) gene, nuclear gene encoding mitochondrial protein, complete cds./0//3002bp//99%//AF038406  
30 C-PLACE1008790//IMPORTIN ALPHA-6 SUBUNIT (KARYOPHERIN ALPHA-6 SUBUNIT) (IMPORTIN ALPHA S2).//3.1E-280//533aa//98%//O35345  
C-PLACE1008808//Homo sapiens mRNA for cell cycle checkpoint protein rad1A.//2.3E-269//1225bp//99%//AJ004974  
C-PLACE1008813  
35 C-PLACE1008854  
C-PLACE1008867  
C-PLACE1008887  
C-PLACE1008902  
C-PLACE1008925  
40 C-PLACE1009020//NIFS PROTEIN./3.9E-55//279aa//41%//P12623  
C-PLACE1009027//Homo sapiens mRNA for doublecortin.//0//1919bp//99%//AJ003112  
C-PLACE1009045  
C-PLACE1009060//BRO1 PROTEIN./6.7E-19//567aa//24%//P48582  
C-PLACE1009090  
45 C-PLACE1009091  
C-PLACE1009094//FURIN-LIKE PROTEASE 2 PRECURSOR (EC 3.4.21.75) (FURIN 2).//1.9E-44//480aa//30%//P30432  
C-PLACE1009099//ZINC FINGER PROTEIN 41 (FRAGMENT).//1.1E-179//452aa//67%//P51814  
C-PLACE1009110  
50 C-PLACE1009111  
C-PLACE1009130//UBIQUITIN-PROTEIN LIGASE E3A (EC 6.3.2.-) (ONCOGENIC PROTEIN-ASSOCIATED PROTEIN E6-AP).//2E-68//181aa//43%//Q05086  
C-PLACE1009158  
C-PLACE1009166  
55 C-PLACE1009174  
C-PLACE1009186  
C-PLACE1009190  
C-PLACE1009230

C-PLACE1009319//Rattus norvegicus outer membrane protein (OMP25) mRNA, complete cds; nuclear gene for mitochondrial product.//2.1E-132//1229bp//75%//AF107295  
 C-PLACE1009328  
 C-PLACE1009335  
 5 C-PLACE1009338  
 C-PLACE1009368//METAL HOMEOSTASIS FACTOR ATX2.//2.5E-10//151aa//29%//Q12067  
 C-PLACE1009375  
 C-PLACE1009388  
 10 C-PLACE1009404//HYPOTHETICAL 105.6 KD PROTEIN C16C9.06C IN CHROMOSOME I.//0.000000047//  
 165aa//33%//Q09820  
 C-PLACE1009434  
 C-PLACE1009443  
 C-PLACE1009444//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA (EC 2.7.1.67) (PI4-KINASE) (PTDINS-4-KI-  
 15 NASE) (PI4K-ALPHA).//7.8E-71//82aa//89%//P42356  
 C-PLACE1009459  
 C-PLACE1009468//PHOSPHOLIPASE A-2-ACTIVATING PROTEIN (PLAP).//3.1E-289//550aa//93%//P54319  
 C-PLACE1009476//PUTATIVE ATP-DEPENDENT RNA HELICASE T26G10.1 IN CHROMOSOME III.//3.9E-40//  
 179aa//37%//P34580  
 C-PLACE1009524//ARF NUCLEOTIDE-BINDING SITE OPENER (ARNO PROTEIN) (ARF EXCHANGE FAC-  
 20 TOR).//8.1E-99//228aa//75%//Q99418  
 C-PLACE1009542  
 C-PLACE1009571  
 C-PLACE1009581  
 25 C-PLACE1009596//VEGETATILE INCOMPATIBILITY PROTEIN HET-E-1.//5.1E-54//291aa//40%//Q00808  
 C-PLACE1009607  
 C-PLACE1009621  
 C-PLACE1009622//MATERNAL EFFECT PROTEIN STAUFEN.//1.3E-60//209aa//41%//P25159  
 C-PLACE1009659//MEMBRANE-ASSOCIATED PROTEIN HEM-2 (NAPI PROTEIN).//1.5E-285//538aa//99%//  
 P55161  
 30 C-PLACE1009665  
 C-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds.//0//1854bp//100%//AF062534  
 C-PLACE1009708//HYPOTHETICAL 143.3 KD TRP-ASP REPEATS CONTAINING PROTEIN C12G12.13C IN  
 CHROMOSOME I.//7E-33//166aa//43%//Q09876  
 C-PLACE1009721//MSF1 PROTEIN.//1.7E-22//176aa//33%//P35200  
 35 C-PLACE1009731//AIG1 PROTEIN.//1.6E-22//274aa//28%//P54120  
 C-PLACE1009763//Homo sapiens mRNA for Nedd8-activating enzyme hUba3, complete cds.//4.3E-294//1329bp//  
 100%//AB012190  
 C-PLACE1009794  
 C-PLACE1009845//Homo sapiens mRNA for KIAA0905 protein, complete cds.//0//2685bp//99%//AB020712  
 40 C-PLACE1009886  
 C-PLACE1009908//HYPOTHETICAL GTP-BINDING PROTEIN IN SEH1-PRP20 INTERGENIC REGION.//1.9E-  
 108//277aa//43%//P53145  
 C-PLACE1009971  
 C-PLACE1009992//LIMULUS CLOTTING FACTOR C PRECURSOR (EC 3.4.21.84).//4.6E-59//450aa//34%//  
 45 P28175  
 C-PLACE1009995//Homo sapiens mRNA; cDNA DKFZp5640123 (from clone DKFZp5640123).//0//1962bp//99%//  
 AL080122  
 C-PLACE1009997//Rattus norvegicus A-kinase anchoring protein AKAP 220 mRNA, complete cds.//5.2E-70//  
 736bp//73%//U48288  
 50 C-PLACE1010023  
 C-PLACE1010031  
 C-PLACE1010053//M.musculus Spnr mRNA for RNA binding protein.//6E-279//1402bp//94%//X84692  
 C-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.//0//2019bp//99%//AF065482  
 C-PLACE1010076  
 55 C-PLACE1010096//100 KD PROTEIN (EC 6.3.2.-).//1.4E-268//506aa//98%//Q62671  
 C-PLACE1010102  
 C-PLACE1010105//RING CANAL PROTEIN (KELCH PROTEIN).//7.3E-114//537aa//44%//O04652  
 C-PLACE1010106//Homo sapiens mRNA; cDNA DKFZp586M1418 (from clone DKFZp586M1418).//0//1974bp//

99%//AL049385  
C-PLACE1010134//TRANSCRIPTION REGULATORY PROTEIN SNF2 (SWI/SNF COMPLEX COMPONENT SNF2) (REGULATORY PROTEIN SWI2) (REGULATORY PROTEIN GAM1) (TRANSCRIPTION FACTOR TYE3).//1.7E-20//156aa//42%//P22082  
5 C-PLACE1010148//CYLICIN I (MULTIPLE-BAND POLYPEPTIDE I).//0.00000046//431aa//23%//P35662  
C-PLACE1010194//SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35) (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN).//9.8E-11//95aa//49%//Q01130  
C-PLACE1010202  
C-PLACE1010261//SEGREGATION DISTORTER PROTEIN.//1.6E-77//214aa//62%//P25722  
10 C-PLACE1010274//Homo sapiens mRNA; cDNA DKFZp5640123 (from clone DKFZp5640123).//0//1964bp//99%//  
AL080122  
C-PLACE1010293  
C-PLACE1010321//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT).//  
15 1.1E-09//350aa//22%//P52178  
C-PLACE1010324  
C-PLACE1010329  
C-PLACE1010362//1-PHOSPHATIDYLINOSITOL PHOSPHODIESTERASE PRECURSOR (EC 3.1.4.10)  
(PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE C) (PI-PLC).//0.00000002//126aa//29%//P34024  
C-PLACE1010364  
20 C-PLACE1010383  
C-PLACE1010481//Homo sapiens mRNA for KIAA0836 protein, partial cds.//0//2121bp//99%//AB020643  
C-PLACE1010491  
C-PLACE1010492  
C-PLACE1010522//Homo sapiens mRNA for DEPP (decidual protein induced by progesterone), complete cds.//  
25 0//1981bp//99%//AB022718  
C-PLACE1010529  
C-PLACE1010547//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//0.00000012//616aa//24%//  
P253 86  
C-PLACE1010599//Homo sapiens Pex14 mRNA for peroxisomal membrane anchor protein, complete cds.//0//  
30 1904bp//99%//AB017546  
C-PLACE1010616  
C-PLACE1010622//TROPONIN T, CARDIAC MUSCLE ISOFORMS (TNTC).//0.00000016//120aa//28%//P02642  
C-PLACE1010629  
C-PLACE1010630  
35 C-PLACE1010661//TESTIS-SPECIFIC PROTEIN PBS13.//5.7E-75//423aa//39%//Q01755  
C-PLACE1010714  
C-PLACE1010720//Homo sapiens mRNA for chromosome-associated polypeptide-C, complete cds.//4E-299//  
1091bp//99%//AB019987  
C-PLACE1010743//Homo sapiens myosin-IXb splice variant (Myo9b) mRNA, partial cds.//8.9E-91//668bp//82%//  
40 AF020267  
C-PLACE1010771//M.musculus HCNGP mRNA.//7.4E-168//966bp//89%//X68061  
C-PLACE1010786  
C-PLACE1010800  
C-PLACE1010811  
45 C-PLACE1010870//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.3E-143//407aa//  
58%//Q05481  
C-PLACE1010877//Homo sapiens mRNA for KIAA0610 protein, partial cds.//0//1885bp//99%//AB011182  
C-PLACE1010900  
C-PLACE2000050  
50 C-PLACE4000522//NEUROGENIC LOCUS NOTCH PROTEIN HOMOLOG PRECURSOR (XOTCH PROTEIN)-//  
2.4E-191//828aa//48%//P21783  
C-PLACE4000590  
C-PLACE4000638  
C-PLACE4000650//TUBERIN (TUBEROUS SCLEROSIS 2 HOMOLOG PROTEIN).//7.9E-17//201aa//34%//  
55 P49816  
C-Y79AA1001647

## Homology Search Result Data 7.

[0315] The result of the homology search of the SwissProt using the 5'-end sequence (54 clones selected in EXAM-  
PLE 16).

## 5 [0316] Data include

the name of clone,  
definition of the top hit data,  
the P-value: the length of the compared sequence: identity (%), and  
10 the organism and the Accession No. of the top hit data, as in the order separated by //.

[0317] Data are not shown for the clones in which the P-value was higher than 1.

F-HEMBA1000497//METALLOTHIONEIN-LIKE PROTEIN 2A (MT-2A) (MT-K) (MT-1G).//0.13//52//38//P25860  
 15 F-HEMBA1001750//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 64E (EC 3.1.2.15) (UBIQUITIN THI-  
OLESTERASE 64E) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 64E) (DEUBIQUITINATING ENZYME  
64E).//2.2e-28//104//59//Q24574  
 F-HEMBA1003854//VERPROLIN.//0.012//138//31//P37370  
 F-HEMBA1004193//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3) (FRAGMENT).//0.93//39//  
 20 33//Q37131  
 F-HEMBA1004860//HIGH POTENTIAL IRON-SULFUR PROTEIN, ISOZYME 2 (HIP1P 2).//0.90//20//50//P38524  
 F-HEMBA1005572//ZINC FINGER PROTEIN 124 (HZF-16).//7.6e-46//141//58//Q15973  
 F-HEMBA1006038//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENT).//0.0033//32//46//P70560  
 F-HEMBA1006092//VERPROLIN.//1.0//62//35//P37370  
 25 F-HEMBA1006406//MATING PHEROMONE ER-10 PRECURSOR (EUPLOMONE R10).//0.30//41//36//P12350  
 F-HEMBA1006650//MATING-TYPE PHEROMONE BAP1(2) PRECURSOR.//0.089//21//52//Q02593  
 F-HEMBA1006812//HEAT SHOCK PROTEIN HTGA (HEAT SHOCK PROTEIN HTPY).//0.38//156//30//P28697  
 F-HEMBB1000672  
 F-HEMBB1001197//DNA-BINDING PROTEIN 65 (PROTEIN GP65).//1.0//30//36//P16012  
 30 F-HEMBB1001871//BONE/CARTILAGE PROTEOGLYCAN I PRECURSOR (BIGLYCAN) (PG-S1).//3.7e-54//  
241//47//P47853  
 F-MAMMA1001252//HYPOTHETICAL 9.1 KD PROTEIN IN NIRQ 3'REGION (ORF3).//0.59//48//39//Q51483  
 F-MAMMA1002094  
 F-NT2RM4000634//T-CELL RECEPTOR BETA CHAIN PRECURSOR (ANA 11).//0.26//58//27//P06333  
 35 F-NT2RM4000657//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC  
3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III) (FRAGMENT).//8.9e-20//83//48//P10895  
 F-NT2RM4000783//ZINC FINGER PROTEIN (FRAGMENT).//1.0//42//40//P19326  
 F-NT2RM4000857//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COMPLEX ACID LABILE CHAIN  
 PRECURSOR (ALS).//6.0e-23//207//32//Q02833  
 40 F-NT2RM4001178//HOMEobox PROTEIN OTX3 (ZOTX3).//0.012//156//28//Q90267  
 F-NT2RM4002420//GLUTAMIC ACID-RICH PROTEIN PRECURSOR.//0.0012//81//37//P13816  
 F-NT2RP2000198//CREB-BINDING PROTEIN.//0.29//98//37//Q92793  
 F-NT2RP2000551//PROTEIN Q300.//0.00017//23//60//Q02722  
 F-NT2RP2000660//HYPOTHETICAL PROTEIN MJ0401.//1.0//41//29//Q57844  
 45 F-NT2RP2001214//MALE SPECIFIC SPERM PROTEIN MST84DC.//0.27//13//61//Q01644  
 F-NT2RP2001460//PROTEIN KINASE C-LIKE (EC 2.7.1.-).//0.089//99//29//Q99014  
 F-NT2RP2001756//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAGMENT)-//4.0e-13//177//  
28//P16372  
 F-NT2RP2002056//HYPOTHETICAL 6.0 KD PROTEIN IN THI12 5'REGION.//0.37//12//75//P53820  
 50 F-NT2RP2002677//NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3).//0.99//61//32//Q42616  
 F-NT2RP2002755//OCTAPEPTIDE-REPEAT PROTEIN T2.//3.3e-10//90//35//Q06666  
 F-NT2RP2002843//CYTOCHROME B.//0.78//103//26//P48884  
 F-NT2RP2003101//ATPASE INHIBITOR, MITOCHONDRIAL HOMOLOG.//0.40//28//46//P37209  
 F-NT2RP2003799//HYPOTHETICAL PROTEIN MJ0116.1.//0.80//55//32//P81303  
 55 F-NT2RP2004095  
 F-NT2RP2004732  
 F-NT2RP2004920//HISTIDINE-RICH, METAL BINDING POLYPEPTIDE.//0.18//18//55//Q48251  
 F-NT2RP2005454

F-NT2RP2005776//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANSFERASE) (FRAGMENT).//7.4e-38//136//41//P51003  
 F-NT2RP2005806//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//4.0e-08//180//28//P32323  
 F-NT2RP2005882  
 5 F-NT2RP3001282//METHYL-ACCEPTING CHEMOTAXIS PROTEIN TLPB.//0.0022//69//39//P39217  
 F-NT2RP3001723//TRANSCRIPTIONAL REGULATORY PROTEIN ALGP (ALGINATE REGULATORY PROTEIN ALGR3).//0.00035//127//31//P15276  
 F-NT2RP3002099//NONHISTONE CHROMOSOMAL PROTEIN HMG-17.//0.97//71//28//P05204  
 F-NT2RP3003155//CCAAT DISPLACEMENT PROTEIN (HOMEobox PROTEIN CLOX) (CLOX-1) (FRAGMENT).//0.064//110//34//P39881  
 10 F-NT2RP3004028//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3) (FRAGMENT).//0.020//95//29//P15583  
 F-OVARC1000008//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//2.8e-05//165//29//P17437  
 15 F-OVARC1000724//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//0.035//152//30//P10162  
 F-OVARC1000751//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICPO (VMW118 PROTEIN).//0.38//124//31//P28284  
 F-OVARC1001029  
 20 F-PLACE1000814//EC PROTEIN HOMOLOG 2 (FRAGMENT).//0.45//61//24//Q42377  
 F-PLACE1003030//GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29).//0.70//121//32//P47845  
 F-PLACE1005549//RHO1 GDP-GTP EXCHANGE PROTEIN 1 (PROTEIN KINASE C SUPPRESSOR SKC1).//  
 25 3.2e-08//205//24//P53046  
 F-PLACE1007218//IG KAPPA CHAIN V-III REGION (PC 7210).//0.99//52//38//P01668

## Homology Search Result Data 8.

30 [0318] The result of the homology search of the GenBank using the clone sequence of 5'-end (54 clones selected in EXAMPLE 16.) except EST and STS.  
 [0319] Data include

35 the name of clone,  
 definition of the top hit data,  
 the P-value: the length of the compared sequence: identity (%), and  
 the Accession No. of the top hit data, as in the order separated by //.

[0320] Data are not shown for the clones in which the P-value was higher than 1.

40 F-HEMBA1000497  
 F-HEMBA1001750//Human mitochondrial genes for several tRNAs (Phe, Val, Leu) and 12S and 16S ribosomal RNAs.//6.6e-101//473//99//V00710  
 F-HEMBA1003854//Homo sapiens clone RG270D13, \*\*\* SEQUENCING IN PROGRESS \*\*\*, 18 unordered pieces.//1.7e-05//412//61//AC005081  
 F-HEMBA1004193//Human BAC clone RG343H22 from 7q31, complete sequence.//0.77//466//59//AC002386  
 F-HEMBA1004860//Human pigment epithelium-derived factor gene, complete cds.//6.7e-07//492//57//U29953  
 F-HEMBA1005572//HZF-16=Kruppel-related zinc finger gene homolog {alternatively spliced} [human, hepatoblastoma cell line, HEP-G2, mRNA, 2080 nt].//2.9e-47//341//77//S54641  
 45 F-HEMBA1006038//Human DNA sequence from clone 989H11 on chromosome 22q13.1-13.2, complete sequence.//0.28//436//59//Z83851  
 F-HEMBA1006092//Human chromosome 16p13.11 BAC clone CIT987SK-29B12 complete sequence.//0.28//309//60//U95738  
 50 F-HEMBA1006406//HS\_2268\_B2\_C07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2268 Col=14 Row=F, genomic survey sequence.//3.7e-69//340//99//AQ070566  
 F-HEMBA1006650//H.sapiens CpG island DNA genomic Mse1 fragment, clone 5h5, forward read cpg5h5.f1a.//9.4e-24//143//96//Z55730  
 F-HEMBA1006812//X.laevis xUBFalphal mRNA for upstream binding factor 2.//0.96//234//64//X59863

F-HEMBB1000672//CIT-HSP-2350H6.TF CIT-HSP Homo sapiens genomic clone 2350H6, genomic survey sequence.//1.1e-68//375//94//AQ059158  
 F-HEMBB1001197//Drosophila melanogaster strawberry notch (sno) mRNA, complete cds.//2.8e-10//229//66//U95760  
 5 F-HEMBB1001871//Equus caballus dermatan sulfate proteoglycan II mRNA, complete cds.//1.2e-27//619//62//AF038127  
 F-MAMMA1001252  
 F-MAMMA1002094//H.sapiens CpG island DNA genomic Mse1 fragment, clone 184g7, forward read cpg184g7.ft1a.//3.4e-29//167//97//Z59993  
 10 F-NT2RM4000634//Chionoecetes opilio (clone COP41) DNA microsatellite repeat regions.//1.4e-21//230//73//L49136  
 F-NT2RM4000657//Human mRNA for phospholipase C, complete cds.//0.029//245//61//D42108  
 F-NT2RM4000783//Homo sapiens chromosome 16, cosmid clone 330D11 (LANL), complete sequence.//3.7e-36//324//70//AC005199  
 15 F-NT2RM4000857//RPCI11-49P19.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-49P19, genomic survey sequence.//1.5e-62//322//97//AQ051961  
 F-NT2RM4001178//Streptomyces coelicolor cosmid 7H1.//0.0025//296//62//AL021411  
 F-NT2RM4002420//Homo sapiens chromosome 17, clone hRPK.63\_A\_1, complete sequence.//0.00013//121//76//AC005670  
 20 F-NT2RP2000198//Human platelet glycoprotein IX mRNA, 3' end.//0.016//246//62//M25827  
 F-NT2RP2000551//Rattus norvegicus microsatellite sequence clone 82G9.//2.0e-08//223//69//AJ233812  
 F-NT2RP2000660//Homo sapiens chromosome 19, cosmid R30953, complete sequence.//0.0073//209//66//AC005622  
 F-NT2RP2001214  
 25 F-NT2RP2001460//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//1.0//80//76//AC005189  
 F-NT2RP2001756//CIT-HSP-2373P1.TR CIT-HSP Homo sapiens genomic clone 2373P1, genomic survey sequence.//3.0e-38//220//94//AQ110589  
 F-NT2RP2002056//Genomic sequence from Human 17, complete sequence.//1.2e-80//317//91//AC002094  
 30 F-NT2RP2002677//Homo sapiens chromosome 10 clone CIT987SK-1031G15 map 10q25, \*\*\* SEQUENCING IN PROGRESS \*\*\*, 1 ordered pieces.//0.032//141//70//AC006097  
 F-NT2RP2002755//Homo sapiens genomic DNA of 21q22.2 Down Syndrome region, segment 9/13.7/1.8e-22//377//69//AP000018  
 F-NT2RP2002843//Homo sapiens BAC clone RG030L05 from 7q22, complete sequence.//6.5e-16//311//63//AC005050  
 35 F-NT2RP2003101//Human FMR1 gene, 5' end.//0.32//105//67//L19476  
 F-NT2RP2003799//Human DNA for 5' terminal region of LINE-1 transposable element clone CGL1-4.//1.6e-33//119//96//X52233  
 F-NT2RP2004095//HS\_3083\_A1\_A02\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3083 Col=3 Row=A, genomic survey sequence.//1.0e-14//154//79//AQ106698  
 40 F-NT2RP2004732//CIT-HSP-631P16.TP CIT-HSP Homo sapiens genomic clone 631P16, genomic survey sequence.//2.3e-20//120//99//B79035  
 F-NT2RP2004920//Plasmodium falciparum MAL3P4, complete sequence.//0.030//397//59//AL008970  
 F-NT2RP2005454//Plasmodium falciparum chromosome 2, section 47 of 73 of the complete sequence.//0.97//455//56//AE001410  
 F-NT2RP2005776//H.sapiens PAP mRNA.//1.0e-33//451//68//X76770  
 F-NT2RP2005806//Mus musculus musculus sex determining protein (Sry) gene, complete cds.//0.029//412//60//U70652  
 50 F-NT2RP2005882//Human DNA sequence from PAC 389A20 on chromosome X contains ESTs STS, CpG islands and polymorphic CA repeat.//9.4e-25//155//90//Z93242  
 F-NT2RP3001282//RPCI11-52L16.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-52L16, genomic survey sequence.//3.2e-21//122//100//AQ052775  
 F-NT2RP3001723//H.sapiens CpG island DNA genomic Mse1 fragment, clone 13g5, reverse read cpg13g5.rt1a.//2.2e-18//163//85//Z56771  
 55 F-NT2RP3002099//Homo sapiens chromosome 17, clone hCIT.296\_K\_1, complete sequence.//1.3e-76//351//86//AC005180  
 F-NT2RP3003155  
 F-NT2RP3004028//Sequence 1 from patent US 5618695.//3.3e-13//217//70//I40055

F-OVARC1000008///0.0040//674//57//M82836  
 F-OVARC1000724//Herpes simplex virus type I immediate early (IE) gene 3 for transcriptional activator IE175 (= ICP 4).//1.1e-07//519//59//X06461  
 F-OVARC1000751//Homo sapiens DNA from chromosome 19, cosmid R29144, complete sequence.//7.2e-11//  
 5 509//62//AC004221  
 F-OVARC1001029//Human DNA sequence from clone 19408 on chromosome 6q24.1-25.3 Contains STS and GSSs, complete sequence.//1.1e-05//388//61//AL031769  
 F-PLACE1000814//Homo sapiens BAC clone GS011E15 from 5q31, complete sequence.//1.4e-84//717//78//  
 AC002427  
 10 F-PLACE1003030  
 F-PLACE1005549//Human guanine nucleotide regulatory protein (NET1) mRNA, complete cds.//4.9e-56//709//  
 68//U02081  
 F-PLACE1007218//Homo sapiens chromosome 20 clone RP3-387E22, \*\*\* SEQUENCING IN PROGRESS \*\*\*, in  
 15 unordered pieces.//3.1e-39//214//98//AL031660

## Homology Search Result Data 9.

[0321] The result of the homology search of the GenBank using the clone sequence of 3'-end (54 clones selected in EXAMPLE 16.) except EST and STS.

[0322] Data include

the name of clone,  
 definition of the top hit data,  
 the P-value: the length of the compared sequence: identity (%), and  
 25 the Accession No. of the top hit data, as in the order separated by //.

[0323] Blank indicates that the 3'-end sequence corresponding to the 5'-end was not determined in the clone.

[0324] Data are not shown for the clones in which the P-value was higher than 1.

30 R-HEMBA1000497///\*\*\*ALU WARNING: Human Alu-J subfamily consensus sequence.//1.4e-38//185//84//U14567  
 R-HEMBA1001750//Hansenula wingei mitochondrial DNA, complete sequence.//1.7e-07//399//59//D31785  
 R-HEMBA1003854//Human DNA sequence from clone 224A6 on chromosome 1p35.1-36.23 Contains part of a  
 gene similar to Mouse Wnt-4 protein, the gene for CDC42 (cell division cycle 42 (GTP-binding protein, 25kD)),  
 ESTs, STSs, GSSs and a CpG Island, complete sequence.//1.4e-75//309//85//AL031281  
 35 R-HEMBA1004193///\*\*\*ALU WARNING: Human Alu-J subfamily consensus sequence.//1.1e-34//188//81//U14567  
 R-HEMBA1004860//Homo sapiens 12q13.1 PAC RPCI3-197B17 (Roswell Park Cancer Institute Human PAC li-  
 brary) complete sequence.//1.3e-06//239//66//AC004241  
 R-HEMBA1005572//Homo sapiens chromosome 21 PAC RPCIP704E14135Q2, complete sequence.//3.1e-21//  
 341//67//AJ010598  
 40 R-HEMBA1006038//Homo sapiens chromosome 19, cosmid R34094, complete sequence.//1.7e-24//307//71//  
 AC004678  
 R-HEMBA1006092//H.Sapiens mRNA for alpha2-subunit of soluble guanylyl cyclase.//0.76//246//62//X63282  
 R-HEMBA1006406//Human DNA sequence from clone 113J7 on chromosome Xp11.22-11.4 Contains part of a  
 45 putative Homeobox (pseudo?) gene, ESTs and an STS, complete sequence.//1.3e-31//297//77//AL023574  
 R-HEMBA1006650//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//1.8e-15//350//  
 65//AC003071  
 R-HEMBA1006812//Homo sapiens chromosome X clone RP3-424J12, \*\*\* SEQUENCING IN PROGRESS \*\*\*, in  
 unordered pieces.//1.8e-55//430//81//Z82207  
 50 R-HEMBB1000672//Homo sapiens clone UWGC:y54c283 from 6p21, complete sequence.//9.1e-39//437//71//  
 AC006166  
 R-HEMBB1001197//Homo sapiens PAC clone DJ0964C11 from 7p14-p15, complete sequence.//1.5e-37//275//  
 85//AC004593  
 R-HEMBB1001871//Plasmodium falciparum chromosome 12 clone 3D7, \*\*\* SEQUENCING IN PROGRESS \*\*\*,  
 55 5 unordered pieces.//0.00097//410//59//AC004688  
 R-MAMMA1001252//Homo sapiens clone 201104, \*\*\* SEQUENCING IN PROGRESS \*\*\*, 4 unordered pieces.//  
 2.9e-13//364//64//AC004529  
 R-MAMMA1002094//HS\_3163\_A1\_A09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3163 Col=17 Row=A, genomic survey sequence.//5.9e-41//256//91//AQ141441

R-NT2RM4000634//Homo sapiens chromosome 19, cosmid R30783, complete sequence./.1-6e-21//283//73//  
AC005258

R-NT2RM4000657

R-NT2RM4000783

5 R-NT2RM4000857//RPCI11-63K2.TK RPCI-11 Homo sapiens genomic clone RPCI-11-63K2, genomic survey se-  
quence./.4.0e-07//62//98//AQ203073

R-NT2RM4001178

R-NT2RM4002420

10 R-NT2RP2000198//Homo sapiens Chromosome 16 BAC clone CIT987-SK37914 -complete genomic sequence,  
complete sequence./.0.58//108//67//AC002307

R-NT2RP2000551//Homo sapiens DNA, pseudoautosomal boundary-like sequence PABL2./.6.2e-72//391//87//  
D30043

R-NT2RP2000660//Homo sapiens chromosome 17, clone hRPK.640\_I\_15, complete sequence./.0.0058//166//  
69//AC005324

15 R-NT2RF2001214//Saccharomyces douglasii mitochondrial tRNA-Ser and tRNA-Phe genes, partial sequence,  
and Var1p (var1) gene, mitochondrial gene encoding mitochondrial protein, complete cds./.0.93//117//65//U49822  
R-NT2RP2001460

R-NT2RP2001756//CIT-HSP-2382021.TR CIT-HSP Homo sapiens genomic clone 2382021, genomic survey se-  
quence./.3.4e-91//507//92//AQ114228

20 R-NT2RP2002056//Homo sapiens DNA sequence from PAC 95C20 on chromosome Xp11.3-11.4. Contains STSs  
and the DDX7 locus with GT and GTG repeat polymorphisms, complete sequence./.0.00022//225//69//Z97181  
R-NT2RP2002677//CIT-HSP-2349K20.TF CIT-HSP Homo sapiens genomic clone 2349K20, genomic survey se-  
quence./.3.1e-29//178//94//AQ062168

R-NT2RP2002755//Human DNA sequence from cosmid U65A4, between markers DDX366 and DDX87 on chro-  
mosome X \*./.5.3e-39//449//72//Z81014

25 R-NT2RP2002843//Homo sapiens chromosome 17, clone hRPK.22\_N\_12, complete sequence./.0.0097//498//  
59//AC005412

R-NT2RP2003101//CIT-HSP-238301.TR CIT-HSP Homo sapiens genomic clone 238301, genomic survey se-  
quence./.1.2e-32//344//75//AQ196754

30 R-NT2RP2003799//.3.6e-05//408//60//AL010237

R-NT2RP2004095//Plasmodium falciparum chromosome 4 strain 3D7, \*\*\* SEQUENCING IN PROGRESS \*\*\*, in  
unordered pieces./.2.1e-10//455//61//AL034557

R-NT2RP2004732//Human DNA sequence from clone 703H14 on chromosome 1q23.2-24.3 Contains 3' end of a  
novel gene, ESTs, CA repeat(D1S445), STS, GSSs, complete sequence./.5.1e-51//383//74//AL031287

35 R-NT2RP2004920//Homo sapiens chromosome 5, P1 clone 878H11 (LBNL H45), complete sequence./.0.062//  
315//61//AC005219

R-NT2RP2005454//Human DNA sequence from PAC 121G13 on chromosome 6 contains flow sorted chromosome  
6 HindIII fragment ESTs. polymorphic CA repeat, CpG island, CpG island genomic fragments./.0.75//246//63//  
Z86062

40 R-NT2RP2005776//Homo sapiens PAC clone DJ1189D06 from 7p15.3-p14, complete sequence./.0.91//232//61//  
AC005232

R-NT2RP2005806//Human neurofibromatosis type 1 (NF1) gene, intron 19a, complete sequence./.1.3e-19//405//  
66//U37368

R-NT2RP2005882//Plasmodium falciparum MAL3P1, complete sequence./.1.1e-09//533//60//Z97348

45 R-NT2RP3001282//Plasmodium falciparum MAL3P8, complete sequence./.0.00026//499//58//AL034560

R-NT2RP3001723//Human BAC clone RG354L07 from 7q31, complete sequence./.0.00035//337//61//AC002466

R-NT2RP3002099//Homo sapiens chromosome 17, clone hCIT.296\_K\_1, complete sequence./.1.8e-44//307//86//  
AC005180

R-NT2RP3003155

50 R-NT2RP3004028//F14A6-Sp6 IGF Arabidopsis thaliana genomic clone F14A6, genomic survey sequence./.0.95//  
95//65//B21351

R-OVARC1000008

R-OVARC1000724//Homo sapiens BAC clone RG017K18 from 7q31, complete sequence./.0.91//83//71//  
AC005161

55 R-OVARC1000751//HS\_2222\_A2\_C09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=2222 Col=18 Row=E, genomic survey sequence./.2.8e-12//176//72//AQ033143  
R-OVARC1001029//Homo sapiens Xp22 Cosmid U151G1 (from Lawrence Livermore X library) and PAC  
RPCI1-93D11 (from Roswell Park Cancer Center) complete sequence./.1.2e-09//165//75//AC002357

R-PLACE1000814//Homo sapiens BAC clone GS465N13 from 7p15-p21, complete sequence.//6.2e-52//514//75//  
AC004744

R-PLACE1003030//Homo sapiens snRNA activating protein complex 190kD subunit (SNAP190) mRNA, complete  
cds.//9.6e-33//225//90//AF032387

5 R-PLACE10e5549//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19P17, complete se-  
quence.//0.097//323//61//AB007644

R-PLACE1007218//Homo sapiens chromosome 20 clone RP3-387E22, \*\*\* SEQUENCING IN PROGRESS \*\*\*, in  
unordered pieces.//1.1e-88//497//91//AL031660

10 Homology Search Result Data 10.

[0325] The result of the homology search of the Human Unigene using the clone sequence of 5'-end (54 clones selected in EXAMPLE 16.).

[0326] Data include

15 the name of clone,  
title of the top hit data,  
the P-value: the length of the compared sequence: identity (%), and  
the Accession No. of the top hit data, as in the order separated by //.

20 [0327] Data are not shown for the clones in which the P-value was higher than 1.

F-HEMBA1000497//ou15a11.x1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone IMAGE:1626332 3', mRNA  
sequence.//1.0//186//65//AI018130

25 F-HEMBA1001750//Human mRNA for TI-227H.//2.5e-101//473//99//D50525

F-HEMBA1003854//Homo sapiens mRNA for KIAA1031 protein, partial cds.//7.2e-06//103//80//AB028954

F-HEMBA1004193//Homo sapiens mRNA for TL132.//0.75//334//59//AJ012755

F-HEMBA1004860//ny07e01.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone IMAGE:1271064 3' similar to con-  
tains Alu repetitive element;; mRNA sequence.//3.7e-06//140//70//AA749151

30 F-HEMBA1005572//HZF-16=Kruppel-related zinc finger gene homolog {alternatively spliced} [human, hepatob-  
lastoma cell line, HEP-G2, mRNA, 2080 nt].//1.1e-48//341//77//S54641

F-HEMBA1006038//Homo sapiens gene for insulin receptor substrate-2, complete cds.//0.036//297//60//  
AB000732

F-HEMBA1006092//ab80f12.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:853295 3' sim-  
ilar to contains Alu repetitive element;; mRNA sequence.//0.65//150//63//AA663266

35 F-HEMBA1006406//ws26e11.x1 NCI\_CGAP\_GC6 Homo sapiens cDNA clone IMAGE:2498348 3' similar to TR:  
002710 002710 GAG POLYPROTEIN ; mRNA sequence.//1.4e-32//518//67//AI989639

F-HEMBA1006650//Homo sapiens Arp2/3 protein complex subunit p20-Arc (ARC20) mRNA, complete cds.//1.3e-  
19//136//90//AF006087

40 F-HEMBA1006812//zh49f01.s1 Soares\_fetal\_liver\_spleen\_1NFLS\_S1 Homo sapiens cDNA clone IMAGE:  
415417 3', mRNA sequence.//1.3e-120//579//98//W80404

F-HEMBB1000672//Homo sapiens mRNA for KIAA1040 protein, partial cds.//0.00047//706//57//AB028963

F-HEMBB1001197//tq45e03.x1 NCI\_CGAP\_Ut1 Homo sapiens cDNA clone IMAGE:2211772 3' similar to TR:  
001940 001940 STRAWBERRY NOTCH ;, mRNA sequence.//1.2e-16//117//92//AI580023

45 F-HEMBB1001871//Human chondroitin/dermatan sulfate proteoglycan (PG40) core protein mRNA, complete  
cds.//4.6e-26//527//62//M14219

F-MAMMA1001252

F-MAMMA1002094

50 F-NT2RM4000634//DKFZp434D1813\_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D1813 5',  
mRNA sequence.//9.7e-16//226//69//AL040136

F-NT2RM4000657//Homo sapiens mRNA for KIAA1069 protein, partial cds.//7.6e-179//817//99//AB028992

F-NT2RM4000783//wd82f06.x1 NCI\_CGAP\_Lu24 Homo sapiens cDNA clone IMAGE:2338115 3', mRNA se-  
quence.//1.8e-20//470//65//AI703299

F-NT2RM4000857//Homo sapiens KIAA0416 mRNA, partial cds.//1.9e-46//749//65//AB007876

55 F-NT2RM4001178//Homo sapiens protein tyrosine phosphatase (PAC-1) mRNA, complete cds.//0.0024//254//63//  
L11329

F-NT2RM4002420//wg39f11.x1 Soares\_NSF\_F8\_9W\_OT\_PA\_P\_S1 Homo sapiens cDNA clone IMAGE:  
2367501 3' similar to contains element L1 L1 repetitive element ; mRNA sequence.//1.4e-13//127//84//AI742251

F-NT2RP2000198//Human mRNA for platelet glycoprotein IX./.0.0033//241//62//X52997  
 F-NT2RP2000551//ze37d12.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361175 3', mRNA sequence./.5.0e-07//116//71//AA017066  
 5 F-NT2RP2000660//qx01g11.x1 NGI\_CGAP\_Br14 Homo sapiens cDNA clone IMAGE:1999364 3', mRNA sequence./.0.027//120//65//AI225283  
 F-NT2RP2001214  
 F-NT2RP2001460//wb50h10.x1 NCI\_CGAP\_GC6 Homo sapiens cDNA clone IMAGE:2309155 3', mRNA sequence./.0.0013//89//78//AI651878  
 10 F-NT2RP2001756//zw54e12.s1 Soares\_total\_fetus\_Nb2HF8\_9w Homo sapiens cDNA clone IMAGE:773902 3' similar to TR:G456660 G456660 ZINC FINGER PROTEIN ZFP-1 ; mRNA sequence./.2.3e-18//120//93//AA427992  
 F-NT2RP2002056//tw44g09.x1 NCI\_CGAP\_Ut1 Homo sapiens cDNA clone IMAGE:2262592 3' similar to contains Alu repetitive element; mRNA sequence./.2.4e-07//99//79//AI811687  
 F-NT2RP2002677  
 15 F-NT2RP2002755//zj83d10.s1 Soares\_fetal\_liver\_spleen\_1NFLS\_S1 Homo sapiens cDNA clone IMAGE:461491 3' similar to contains element TAR1 repetitive element ; mRNA sequence./.1.9e-19//229//76//AA705059  
 F-NT2RP2002843//wt88dl2.x1 NCI\_CGAP\_GC6 Homo sapiens cDNA clone IMAGE:2514551 3' similar to TR: P79522 P79522 MHC CLASS I REGION PROLINE RICH PROTEIN.; mRNA sequence./.8.2e-15//314//67//AI964055  
 20 F-NT2RP2003101//wi65a03.x1 NCI\_CGAP\_Kid12 Homo sapiens cDNA clone IMAGE:2398156 3', mRNA sequence./.0.38//106//68//AI763133  
 F-NT2RP2003799//Homo sapiens mRNA; cDNA DKFZp564C142 (from clone DKFZp564C142).//2.5e-29//124//91//AL049979  
 F-NT2RP2004095  
 25 F-NT2RP2004732//Homo sapiens mRNA for KIAA0884 protein, partial cds./.2.6e-109//533//96//AB020691  
 F-NT2RP2004920//wz68d10.x1 NCI\_CGAP\_Mel15 Homo sapiens cDNA clone IMAGE:2563219 3' similar to TR: 000172 000172 LINE-1 REVERSE TRANSCRIPTASE ;, mRNA sequence./.0.0020//220//61//AI969546  
 F-NT2RP2005454//Homo sapiens mRNA for KIAA0977 protein, complete cds./.0.058//143//69//AB023194  
 F-NT2RP2005776//H.sapiens PAP mRNA./.4.3e-35//451//68//X76770  
 30 F-NT2RP2005806//HSZ78328 Human fetal brain S. Meier-Ewert Homo sapiens cDNA clone 2.48 (CEPH) 3', mRNA sequence./.2.0e-05//385//62//Z78328  
 F-NT2RP2005882//Human mRNA for KIAA0364 gene, complete cds./.7.3e-23//141//94//AB002362  
 F-NT2RP3001282  
 35 F-NT2RP3001723//ws73d05.x1 NCI\_CGAP\_Co3 Homo sapiens cDNA clone IMAGE:2503593 3' similar to contains MSR1.t1 TAR1 repetitive element ; mRNA sequence./.2.6e-07//245//66//AW008782  
 F-NT2RP3002099//yg49d01.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:36239 3', mRNA sequence./.0.58//164//64//R46086  
 F-NT2RP3003155  
 40 F-NT2RP3004028//Homo sapiens mRNA for KIAA1074 protein, complete cds./.1.3e-29//488//66//AB028997  
 F-OVARC1000008//Homo sapiens mRNA for KIAA0665 protein, complete cds./.0.00032//430//59//AB014565  
 F-OVARC1000724//Homo sapiens mRNA for KIAA0641 protein, complete cds./.0.0054//426//58//AB014541  
 F-OVARC1000751//Human Tis11d gene, complete cds./.4.6e-12//527//62//U07802  
 F-OVARC1001029//qv29c05.x1 NCI\_CGAP\_Ov31 Homo sapiens cDNA clone IMAGE:1982984 3' similar to contains element L1 repetitive element ; mRNA sequence./.0.0012//145//68//AI252422  
 45 F-PLACE1000814//ak42f05.s1 Soares\_testis\_NHT Homo sapiens cDNA clone IMAGE:1408641 3', mRNA sequence./.7.1e-31//275//76//AA868469  
 F-PLACE1003030  
 F-PLACE1005549//Homo sapiens mRNA for Rho guanine nucleotide-exchange factor, splice variant NET1A./.1.2e-57//737//67//AJ010046  
 50 F-PLACE1007218//yo34a08.s1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:179798 3', mRNA sequence./.2.2e-21//216//76//H52716

## Homology Search Result Data 11.

[0328] The result of the homology search of the Human Unigene using the clone sequence of 3'-end (54 clones selected in EXAMPLE 16.).

[0329] Data include

the name of clone,

title of the top hit data,  
 the P-value: the length of the compared sequence: identity (%), and  
 the Accession No. of the top hit data, as in the order separated by //.

5 [0330] Blank indicates that the 3'-end sequence corresponding to the 5'-end was not determined in the clone.  
 [0331] Data are not shown for the clones in which the P-value was higher than 1.

R-HEMBA1000497//np09h02.s1 NCI\_CGAP\_Pr3 Homo sapiens cDNA clone IMAGE:1115859 similar to contains  
 10 Alu repetitive element;contains element MER22 repetitive element ; mRNA sequence.//6.2e-38//185//83//  
 AA614254  
 R-HEMBA1001750//yy71b10.s1 Soares\_multiple\_sclerosis\_2NbHMSP Homo sapiens cDNA clone IMAGE:  
 278971 3', mRNA sequence.//0.004511193//63//N63303  
 R-HEMBA1003854//Homo sapiens mRNA; cDNA DKFZp564F133 (from clone DKFZp564F133).//3.4e-72//310//  
 80//AL049263  
 15 R-HEMBA1004193//tr01e08.x1 NCI\_CGAP\_Ov23 Homo sapiens cDNA clone IMAGE:2217062 3' similar to con-  
 tains Alu repetitive element;contains element MER4 repetitive element ; mRNA sequence.//1.5e-33//186//81//  
 AI914747  
 R-HEMBA1004860//qh16b06.x1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone IMAGE:1844819 3', mRNA  
 20 sequence.//0.017//118//69//AI218308  
 R-HEMBA1005572//wj16h05.x1 NCI\_CGAP\_Kid12 Homo sapiens cDNA clone IMAGE:2403033 3', mRNA se-  
 quence.//4.6e-111//522//99//AI861830  
 R-HEMBA1006038//DKFZp434E1117\_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434E1117 5',  
 mRNA sequence.//1.2e-22//295//72//AL041450  
 25 R-HEMBA1006092//qt30d09.x1 Soares\_pregnant\_uterus\_NbHPU Homo sapiens cDNA clone IMAGE: 1949489  
 3' similar to contains element PTR5 repetitive element ; mRNA sequence.//1.4e-87//422//98//AI337963  
 R-HEMBA1006406//Homo sapiens mRNA for KIAA0752 protein, partial cds.//4.1e-30//291-I//76//AB018295  
 R-HEMBA1006650//H.sapiens mRNA for serine/threonine protein kinase EMK.//3.6e-09//319//62//X97630  
 R-HEMBA1006812//Human mRNA for KIAA0118 gene, partial cds.//3.1e-52//337//87//D42087  
 R-HEMBB1000672//Homo sapiens mRNA; cDNA DKFZp434M011 (from clone DKFZp434M011).//3.2e-48//276//  
 30 74//AL096734  
 R-HEMBB1001197//zt35b11.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:724317 5' similar  
 to contains Alu repetitive element; mRNA sequence.//9.9e-44//275//88//AA410788  
 R-HEMBB1001871//wg20c02.x1 Soares\_NSF\_F8\_9W\_OT\_PA\_P\_S1 Homo sapiens cDNA clone IMAGE:  
 2365634 3', mRNA sequence.//6.3e-104//501//98//AI741321  
 35 R-MAMMA1001252//aa61h04.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone IMAGE:825463 3' similar to con-  
 tains Alu repetitive element;contains element XTR repetitive element ; mRNA sequence.//9.0e-19//127//91//  
 AA504355  
 R-MAMMA1002094//wd28h12.x1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone IMAGE:2329511 3', mRNA  
 40 sequence.//2.5e-68//328//99//AI936520  
 R-NT2RM4000634//DKFZp434F2016\_s1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434F2016 3',  
 mRNA sequence.//8.2e-20//185//81//AL041146  
 R-NT2RM4000657//Homo sapiens mRNA for KIAA1069 protein, partial cds.//5.7e-62//335//94//AB028992  
 R-NT2RM4000783  
 R-NT2RM4000857//Human megakaryocyte stimulating factor mRNA, complete cds.//0.00074//360//61//U70136  
 45 R-NT2RM4001178//tk08e03.x1 NCI\_CGAP\_Lu24 Homo sapiens cDNA clone IMAGE:2150428 3', mRNA se-  
 quence.//0.77//96//62//AI457506  
 R-NT2RM4002420//wl58b04.x1 NCI\_CGAP\_Bm25 Homo sapiens cDNA clone IMAGE:2429071 3', mRNA se-  
 quence.//2.4e-85//438//94//AI857508  
 50 R-NT2RP2000198//nx19b11.s1 NCI\_CGAP\_GC3 Homo sapiens cDNA clone IMAGE:1256541 3', mRNA se-  
 quence.//1.9e-45//270//91//AA738352  
 R-NT2RP2000551//tg80h11.x1 Soares\_NhHMPu\_S1 Homo sapiens cDNA clone IMAGE:2115141 3', mRNA se-  
 quence.//3.3e-53//311//85//AI417680  
 R-NT2RP2000660//ns42a06.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone IMAGE:1186258 3', mRNA se-  
 quence.//4.3e-26//142//97//AA805691  
 55 R-NT2RP2001214//tw65g08.x1 NCI\_CGAP\_Ut3 Homo sapiens cDNA clone IMAGE:2264606 3' similar to contains  
 element MSR1 repetitive element ; mRNA sequence.//1.5e-57//289//97//AI680174  
 R-NT2RP2001460  
 R-NT2RP2001756//zw54e12.s1 Soares\_total\_fetus\_Nb2HF8\_9w Homo sapiens cDNA clone IMAGE:773902 3'

similar to TR:G456660 G456660 ZINC FINGER PROTEIN ZFP-1 ; mRNA sequence.//6.0e-13//85//96//AA427992  
 R-NT2RP2002056/yh26a12.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:130846 3', mRNA sequence.//0.0016//208//65//R22302  
 R-NT2RP2002677//Homo sapiens mRNA for KIAA0524 protein, partial cds.//3.4e-26//339//71//AB011096  
 5 R-NT2RP2002755/qd50d10.x1 Soares\_fetal\_heart\_NbHH19W Homo sapiens cDNA clone IMAGE:1732915 3', mRNA sequence.//1.5e-26//419//66//AI190698  
 R-NT2RP2002843/at31f08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2373639 3' similar to contains L1.t1 L1 repetitive element; , mRNA sequence.//1.8e-45//463//74//AI749673  
 10 R-NT2RP2003101/ty24h05.x1 NCI\_CGAP\_Ut3 Homo sapiens cDNA clone IMAGE:2280057 3', mRNA sequence.//7.5e-73//347//99//AI758824  
 R-NT2RP2003799/Homo sapiens mRNA for KIAA0751 protein, complete cds.//0.0026//247//65//AB018294  
 R-NT2RP2004095/zv08c02.s1 Soares\_NhHMPu\_S1 Homo sapiens cDNA clone IMAGE:753026 3' similar to contains element MER32 repetitive element ; mRNA sequence.//9.6e-07//188//66//AA436455  
 15 R-NT2RP2004732/tu60a07.x1 NCI\_CGAP\_Gas4 Homo sapiens cDNA clone IMAGE:2255412 3' similar to contains Alu repetitive element;contains element L1 repetitive element ; mRNA sequence.//4.3e-25//414//68//AI678956  
 R-NT2RP2004920/wd13h02.x1 NCI\_CGAP\_Co3 Homo sapiens cDNA clone IMAGE:2328051 3', mRNA sequence.//6.8e-91//483//93//AI694022  
 20 R-NT2RP2005454/yy77g09.s1 Soares\_multiple\_sclerosis\_2NbHMSP Homo sapiens cDNA clone IMAGE:279616 3', mRNA sequence.//0.0070//325//59//N48302  
 R-NT2RP2005776/qq97d06.x1 Soares\_total\_fetus\_Nb2HF8\_9w Homo sapiens cDNA clone IMAGE:1939307 3', mRNA sequence.//7.5e-08//89//82//AI338419  
 R-NT2RP2005806/wc29h01.x1 NCI\_CGAP\_Kid11 Homo sapiens cDNA clone IMAGE:2316625 3' similar to contains MER2.b3 MER2 repetitive element ; mRNA sequence.//3.2e-16//235//71//AI671398  
 25 R-NT2RP2005882/wo31f09.x1 NCI\_CGAP\_Gas4 Homo sapiens cDNA clone IMAGE:2456969 3', mRNA sequence.//0.00095//352//59//AI925528  
 R-NT2RP3001282/wg35b03.x1 Soares\_NSF\_F8\_9W\_OT\_PA\_P\_S1 Homo sapiens cDNA clone IMAGE:2367053 3', mRNA sequence.//1.7e-113//555//97//AI769199  
 R-NT2RP3001723/wo48e06.x1 NCI\_CGAP\_Gas4 Homo sapiens cDNA clone IMAGE:2458594 3', mRNA sequence.//4.2e-98//471//98//AI926617  
 30 R-NT2RP3002099//DKFZp564L227\_s1 564 (synonym: hfbr2) Homo sapiens cDNA clone DKFZp564L227 3', mRNA sequence.//9.2e-50//329//87//AL037910  
 R-NT2RP3003155/zp07a07.s1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:595668 3', mRNA sequence.//1.4e-30//159//99//AA173172  
 35 R-NT2RP3004028//Homo sapiens protein kinase C-alpha mRNA, partial 3' UTR.//0.43//66//75//AF035594  
 R-OVARC1000008/wa69e12.x1 SoaresNFL\_T\_GBC\_S1 Homo sapiens cDNA clone IMAGE:2301454 3', mRNA sequence.//1.0e-77//376//98//AI699393  
 R-OVARC1000724/tf94b10.x1 NCI\_CGAP CLL1 Homo sapiens cDNA clone IMAGE:2106907 3', mRNA sequence.//0.71//27//100//AI380236  
 40 R-OVARC1000751/og93d04.s1 NCI\_CGAP\_Kid5 Homo sapiens cDNA clone IMAGE:1455847 3', mRNA sequence.//3.5e-13//274//63//AA863306  
 R-OVARC1001029/yz96e02.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:290906 5' similar to contains Alu repetitive element;contains element PTR5 repetitive element ; mRNA sequence.//3.5e-13//175//74//N99464  
 45 R-PLACE1000814/tg49a08.x1 SoaresNFL\_T\_GBC\_S1 Homo sapiens cDNA clone IMAGE:2112086 3' similar to contains LI.t2 L1 L1 repetitive element; mRNA sequence.//2.2e-18//285//69//AI424789  
 R-PLACE1003030//Homo sapiens snRNA activating protein complex 190kD subunit (SNAP190) mRNA, complete cds.//4.0e-34//225//90//AF032387  
 R-PLACE1005549/tm26b11.x1 SoaresNFL\_T\_GBC\_S1 Homo sapiens cDNA clone IMAGE:2157693 3', mRNA sequence.//0.91//127//66//AI480253  
 50 R-PLACE1007218/yq06e01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:196152 5' similar to contains Alu repetitive element;contains LTR4 repetitive element; mRNA sequence.//2.4e-36//245//87//R92256

55 Homology Search Result Data 12.

[0332] Data obtained by the homology search for full-length nucleotide sequences and deduced amino acid sequences. Each data includes Clone name, Definition in hit data, P value, Length of sequence to be compared, Homology,

and Accession number (No.) of hit data. These items are shown in this order and separated by a double-slash mark, //.

5 C-HEMBA1000012//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--TRNA LIGASE)  
 (LEURS).//6.4E-99//457aa//45%//Q09996  
 C-HEMBA1000020//Homo sapiens beta 2 gene.//7.5E-264//1194bp//95%//X02344  
 C-HEMBA1000129//HYTOTHEICAL HELICASE C8A4.08C IN CHROMOSOME I.//3.8E-25//166aa//36%//  
 Q09884  
 C-HEMBA1000201//Homo sapiens mRNA for integrase interactor 1b protein (INI1B).//0//1612bp//99%//AJ011738  
 C-HEMBA1000216//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PRO-  
 TEIN).//1E-86//146aa//56%//Q61221  
 C-HEMBA1000231  
 C-HEMBA1000264  
 C-HEMBA1000280  
 C-HEMBA1000282  
 15 C-HEMBA1000303//"Mus musculus Plenty of SH3s (POSH) mRNA, complete cds."//7.1E-254//  
 1440bp//87%//AF030131  
 C-HEMBA1000333//"Homo sapiens mRNA for KIAA0874 protein, partial cds."//4.8E-253//1148bp//  
 99%//AB020681  
 C-HEMBA1000351  
 20 C-HEMBA1000356//Homo sapiens mRNA; cDNA DKFZp566C243 (from clone DKFZp566C243).//3.3E-287//  
 815bp//98%//AL050274  
 C-HEMBA1000396  
 C-HEMBA1000411//ANKYRIN.//5.7E-12//127aa//38%//Q02357  
 C-HEMBA1000442  
 25 C-HEMBA1000456  
 C-HEMBA1000504  
 C-HEMBA1000518//PECANEX PROTEIN.//2.1E-19//227aa//38%//P18490  
 C-HEMBA1000519  
 C-HEMBA1000523//TESTIS-SPECIFIC PROTEIN PBS13.//2.4E-44//292aa//36%//Q01755  
 30 C-HEMBA1000542//"Rattus norvegicus mRNA for dipeptidyl peptidase III, complete cds."//2.2E-194//  
 663bp//83%//D89340  
 C-HEMBA1000545  
 C-HEMBA1000557  
 35 C-HEMBA1000592//"Homo sapiens sorting nexin 6 (SNX6) mRNA, complete cds."//0//1465bp//99%//  
 AF121856  
 C-HEMBA1000594  
 C-HEMBA1000604  
 C-HEMBA1000622  
 C-HEMBA1000637  
 40 C-HEMBA1000655  
 C-HEMBA1000657//"Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA,  
 complete cds."//7.2E-156//1366bp//76%//U35776  
 C-HEMBA1000749  
 C-HEMBA1000769  
 45 C-HEMBA1000773  
 C-HEMBA1000774  
 C-HEMBA1000822  
 C-HEMBA1000843  
 C-HEMBA1000852//ARYLSULFATASE D PRECURSOR (EC 3.1.6.-) (ASD).//1E-78//119aa//87%//P51689  
 50 C-HEMBA1000870  
 C-HEMBA1000908  
 C-HEMBA1000934  
 C-HEMBA1000972  
 C-HEMBA1000986  
 55 C-HEMBA1000991  
 C-HEMBA1001008  
 C-HEMBA1001059//"Human N-acetylgalactosamine 6-sulphatase (GALNS) gene, exon 14."//4.8E-  
 169//786bp//99%//U06088

C-HEMBA1001094  
 C-HEMBA1001302//"Homo sapiens calcium binding protein precursor, mRNA, complete cds.";//9.6E-  
 258//682bp//94%//AF153686  
 C-HEMBA1001330  
 5 C-HEMBA1001497  
 C-HEMBA1001569//SYNAPTOBREVIN 2 (VESICLE ASSOCIATED MEMBRANE PROTEIN 2) (VAMP-2).//2.3E-  
 53//110aa//100%//P19065  
 C-HEMBA1001570  
 C-HEMBA1001620//MYO-INOSITOL-1-PHOSPHATE SYNTHASE (EC 5.5.1.4) (IPS).//1.6E-166//506aa//60%//  
 10 P42803  
 C-HEMBA1001640  
 C-HEMBA1001655  
 C-HEMBA1001672//"Homo sapiens methyl-CpG binding domain-containing protein MBD3 (MBD3) mRNA,  
 complete cds.";//0//1707bp//98%//AF072247  
 15 C-HEMBA1001711  
 C-HEMBA1001723//"Rattus norvegicus G beta-like protein GBL mRNA, complete cds.";//4.7E-172//  
 1240bp//81%//AF051155  
 C-HEMBA1001746//"Homo sapiens squamous cell carcinoma antigen recognized by T cell (SART-2) mRNA,  
 complete cds.";//7.6E-59//998bp//64%//AF098066  
 20 C-HEMBA1001781  
 C-HEMBA1001804//"Homo sapiens zinc finger DNA binding protein 99 (ZNF281) mRNA, complete cds.  
 &quot;;//0//1637bp//99%//AF125158  
 C-HEMBA1001822//"Mus musculus Ese2L protein mRNA, complete cds.";//1.9E-235//1329bp//89%//  
 AF132479  
 25 C-HEMBA1001824  
 C-HEMBA1001866//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-)  
 (DUGT).//5.7E-51//234aa//41%//Q09332  
 C-HEMBA1001910  
 C-HEMBA1001913//GCN20 PROTEIN.//2.3E-81//158aa//50%//P43535  
 30 C-HEMBA1001921//"Homo sapiens germinal center kinase related protein kinase mRNA, complete cds.  
 &quot;;//0//1850bp//99%//AF000145  
 C-HEMBA1001939  
 C-HEMBA1001950//"Homo sapiens mRNA for KIAA0971 protein, complete cds.";//0//1974bp//99%//  
 AB023188  
 35 C-HEMBA1001967//"Homo sapiens NY-REN-57 antigen mRNA, partial cds.";//0//1721bp//99%//  
 AF155114  
 C-HEMBA1002035//Homo sapiens mRNA; cDNA DKFZp586E0518 (from clone DKFZp586E0518).//0//2149bp//  
 99%//AL050089  
 C-HEMBA1002092//"Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-3) mRNA, complete cds.  
 &quot;;//1.3E-271//1583bp//88%//U92703  
 40 C-HEMBA1002102//ANKYRIN.//4.40E-10//106aa//35%//Q02357  
 C-HEMBA1002150  
 C-HEMBA1002151//"Rattus norvegicus p34 mRNA, complete cds.";//1.1E-153//1059bp//82%//  
 AF178669  
 45 C-HEMBA1002189  
 C-HEMBA1002215//TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)].//2.2E-199//392aa//89%//P47226  
 C-HEMBA1002229  
 C-HEMBA1002241//PROLIFERATING-CELL NUCLEOLAR ANTIGEN P120 (PROLIFERATION-ASSOCIATED  
 NUCLEOLAR PROTEIN P120).//3.70E-06//95aa//33%//P46087  
 50 C-HEMBA1002341//"Homo sapiens mRNA for KIAA0771 protein, partial cds.";//0//1514bp//99%//  
 AB018314  
 C-HEMBA1002417//"Homo sapiens chromosome 19, cosmid R28784, complete sequence.";//1.4E-  
 299//294bp//100%//AC005954  
 C-HEMBA1002547//"Homo sapiens agrin precursor mRNA, partial cds.";//0//1605bp//97%//AF016903  
 55 C-HEMBA1002703  
 C-HEMBA1002779  
 C-HEMBA1002816  
 C-HEMBA1002970

C-HEMBA1002999//"Rattus norvegicus lamina associated polypeptide 1C (LAP1C) mRNA, complete cds.  
 &quot;//1.4E-171//1552bp//75%//U20286  
 C-HEMBA1003021  
 C-HEMBA1003077//SLIT PROTEIN PRECURSOR//2.6E-15//199aa//31%//P24014  
 5 C-HEMBA1003079  
 C-HEMBA1003273  
 C-HEMBA1003304  
 C-HEMBA1003309  
 C-HEMBA1003376  
 10 C-HEMBA1003384  
 C-HEMBA1003531  
 C-HEMBA1003548  
 C-HEMBA1003556  
 C-HEMBA1003571  
 15 C-HEMBA1003579  
 C-HEMBA1003684//ZINC FINGER PROTEIN 151 (MIZ-1 PROTEIN).//2E-73//526aa//32%//Q13105  
 C-HEMBA1003692  
 C-HEMBA1003720  
 C-HEMBA1003725  
 20 C-HEMBA1003729  
 C-HEMBA1003758  
 C-HEMBA1003773//"Mus musculus signal recognition particle receptor beta subunit mRNA, complete cds.  
 &quot;//5.8E-81//511bp//86%//U17343  
 C-HEMBA1003783//"Mus musculus bromodomain-containing protein BP75 mRNA, complete cds.&quot;//  
 25 1.1E-190//1204bp//84%//AF084259  
 C-HEMBA1003799  
 C-HEMBA1003804  
 C-HEMBA1003805//"Mus musculus KH domain RNA binding protein QKI-5A mRNA, complete cds.&quot;//  
 0//988bp//95%//AF090402  
 30 C-HEMBA1003836//MOB1 PROTEIN (MPS1 BINDER 1).//8.10E-31//134aa//52%//P40484  
 C-HEMBA1003856  
 C-HEMBA1003866//"Mus musculus semaphorin Vla mRNA, complete cds.&quot;//1.2E-105//1192bp//70%//  
 AF030430  
 C-HEMBA1003879  
 35 C-HEMBA1003880  
 C-HEMBA1003893  
 C-HEMBA1003908  
 C-HEMBA1003937  
 C-HEMBA1003942  
 40 C-HEMBA1003958  
 C-HEMBA1003976  
 C-HEMBA1003978//"Homo sapiens mRNA for KIAA0840 protein, partial cds.&quot;//0//1530bp//100%//  
 AB020647  
 C-HEMBA1003985  
 45 C-HEMBA1004011  
 C-HEMBA1004024  
 C-HEMBA1004038  
 C-HEMBA1004045  
 C-HEMBA1004048  
 50 C-HEMBA1004111//"Homo sapiens mRNA for KIAA1276 protein, partial cds.&quot;//1.00E-163//751bp//  
 99%//AB033102  
 C-HEMBA1004131//SEPTIN 2 HOMOLOG (FRAGMENT).//1.6E-166//416aa//72%//Q14141  
 C-HEMBA1004138  
 C-HEMBA1004143  
 55 C-HEMBA1004150  
 C-HEMBA1004168//"Homo sapiens geminin mRNA, complete cds.&quot;//3.9E-208//951 bp//99%//  
 AF067855  
 C-HEMBA1004200

C-HEMBA1004202//RAS-RELATED PROTEIN RAB-13.//6.2E-30//208aa//37%//P51153  
 C-HEMBA1004203//NUCLEOLAR PROTEIN NOP2.//1.5E-12//258aa//29%//P40991  
 C-HEMBA1004238  
 C-HEMBA1004248//"Homo sapiens insulin induced protein 2 mRNA, complete cds."//8.20E-175//  
 5 552bp//97%//AF125392  
 C-HEMBA1004272  
 C-HEMBA1004274  
 C-HEMBA1004275//"Homo sapiens mRNA for KIAA1111 protein, partial cds."//0//1341bp//99%//  
 AB029034  
 10 C-HEMBA1004286//"Homo sapiens TGF beta receptor associated protein-1 mRNA, complete cds."//  
 0//1982bp//99%//AF022795  
 C-HEMBA1004312  
 C-HEMBA1004321//ZINC FINGER PROTEIN 184 (FRAGMENT).//2.3E-93//357aa//42%//Q99676  
 15 C-HEMBA1004323  
 C-HEMBA1004327  
 C-HEMBA1004330  
 C-HEMBA1004341  
 C-HEMBA1004366  
 C-HEMBA1004372  
 20 C-HEMBA1004389//"Homo sapiens zinc finger DNA binding protein 99 (ZNF281) mRNA, complete cds.  
 &quot;//0//1437bp//99%//AF125158  
 C-HEMBA1004394  
 C-HEMBA1004408//PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 10 (EC 5.2.1.8) (PPIASE) (ROTAMASE) (CY-  
 CLOPHILIN-10).//3.2E-32//148aa//52%//P52017  
 25 C-HEMBA1004429  
 C-HEMBA1004460  
 C-HEMBA1004461  
 C-HEMBA1004502  
 C-HEMBA1004554  
 30 C-HEMBA1004560  
 C-HEMBA1004610  
 C-HEMBA1004629  
 C-HEMBA1004632  
 C-HEMBA1004637  
 35 C-HEMBA1004670  
 C-HEMBA1004672  
 C-HEMBA1004697  
 C-HEMBA1004711  
 C-HEMBA1004725  
 40 C-HEMBA1004730  
 C-HEMBA1004734//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN  
 LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42).//9.9E-39//143aa//52%//P42743  
 C-HEMBA1004751  
 C-HEMBA1004752  
 45 C-HEMBA1004889//"Human C3f mRNA, complete cds."//6.70E-24//341aa//26%//U72515  
 C-HEMBA1004934  
 C-HEMBA1004944  
 C-HEMBA1004973  
 C-HEMBA1004977  
 50 C-HEMBA1005009//"Homo sapiens BAF53a (BAF53a) mRNA, complete cds."//0//1813bp//99%//  
 AF041474  
 C-HEMBA1005083  
 C-HEMBA1005113  
 C-HEMBA1005133  
 55 C-HEMBA1005185  
 C-HEMBA1005219//NUCLEAR PROTEIN SNF7.//5.3E-10//189aa//25%//P39929  
 C-HEMBA1005252//"Homo sapiens mRNA for KIAA0585 protein, partial cds."//1.2E-268//1215bp//  
 99%//AB011157

C-HEMBA1005296  
 C-HEMBA1005314  
 C-HEMBA1005331  
 C-HEMBA1005394  
 5 C-HEMBA1005403  
 C-HEMBA1005423//"Homo sapiens cyclin-dependent kinase inhibitor (CDKN2C) mRNA, complete cds.  
 &quot;//2E-213//537bp//99%//AF041248  
 C-HEMBA1005468  
 C-HEMBA1005469  
 10 C-HEMBA1005474  
 C-HEMBA1005517  
 C-HEMBA1005518  
 C-HEMBA1005528//CCR4-ASSOCIATED FACTOR 1 (CAF1).//3.1E-154//285aa//99%//Q60809  
 C-HEMBA1005558//NUCLEAR PROTEIN SNF7.//6.40E-16//170aa//31%//P39929  
 15 C-HEMBA1005576//"Homo sapiens mRNA for KIAA0463 protein, partial cds.&quot;//1.1E-181//835bp//  
 99%//AB007932  
 C-HEMBA1005582//"TROPOMYOSIN 1, NON-MUSCLE ISOFORM (TROPOMYOSIN II) (CYTOSKELETAL  
 TROPOMYOSIN).&quot;//0.00000009//213aa//27%//P09492  
 C-HEMBA1005583  
 20 C-HEMBA1005595//"DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC).&quot;//2.3E-54//562aa//29%//P34036  
 C-HEMBA1005609//Homo sapiens mRNA; cDNA DKFZp564K133 (from clone DKFZp564K133).//2.2e-315//  
 1448bp//99%//AL050012  
 C-HEMBA1005621//"Homo sapiens Mad2B protein (MAD2B) mRNA, complete cds.&quot;//2.9E-224//  
 1031bp//99%//AF139365  
 25 C-HEMBA1005666  
 C-HEMBA1005680  
 C-HEMBA1005685  
 C-HEMBA1005737//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT).//  
 4.4E-17//167aa//34%//P25296  
 30 C-HEMBA1005746  
 C-HEMBA1005755  
 C-HEMBA1005813  
 C-HEMBA1005822  
 C-HEMBA1005834  
 35 C-HEMBA1005884  
 C-HEMBA1005891  
 C-HEMBA1005909  
 C-HEMBA1005911  
 C-HEMBA1005931  
 40 C-HEMBA1005963  
 C-HEMBA1005991  
 C-HEMBA1006005  
 C-HEMBA1006031//"Homo sapiens mRNA for putative phospholipase, complete cds.&quot;//0//1413bp//  
 99%//AB019435  
 45 C-HEMBA1006067  
 C-HEMBA1006081  
 C-HEMBA1006091  
 C-HEMBA1006100  
 C-HEMBA1006108//"Homo sapiens mRNA for KIAA0943 protein, partial cds.&quot;//4.8E-245//764bp//  
 50 99%//AB023160  
 C-HEMBA1006121  
 C-HEMBA1006130//SEL-10 PROTEIN.//0.000000043//219aa//25%//Q93794  
 C-HEMBA1006155  
 C-HEMBA1006158//"Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene, complete cds.&quot;  
 //0//1551bp//99%//AF048693  
 55 C-HEMBA1006182  
 C-HEMBA1006198//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//1.9E-19//215aa//39%//P05142  
 C-HEMBA1006235//Homo sapiens clone 24422 mRNA sequence.//0//1615bp//99%//AF070557

C-HEMBA1006253//DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT111 PRECURSOR//0.00000002//  
62aa//53%//P42698  
C-HEMBA1006259  
C-HEMBA1006272//RETROVIRUS-RELATED PROTEASE (EC 3.4.23.-)//1.3E-123//200aa//73%//P10265  
5 C-HEMBA1006278//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANS-  
FERASE)//1E-210//490aa//77%//P25500  
C-HEMBA1006283//NUCLEAR POLYADENYLATED RNA-BINDING PROTEIN NAB2//0.000000012//176aa//  
30%//P32505  
C-HEMBA1006284  
10 C-HEMBA1006291//2-ARYLPROPIONYL-COA EPIMERASE (EC 5.---)//4.2E-12//215aa//23%//P70473  
C-HEMBA1006293  
C-HEMBA1006309//HYPOTHETICAL 54.2 KD PROTEIN IN ERP5-ORC6 INTERGENIC REGION//1.4E-48//  
248aa//43%//P38821  
15 C-HEMBA1006349  
C-HEMBA1006364  
C-HEMBA1006381  
C-HEMBA1006398//"Human L1 element L1.6 putative p150 gene, complete cds."//2E-277//1729bp//  
85%//U93563  
C-HEMBA1006445//"Homo sapiens putative tumor suppressor NOEY2 mRNA, complete cds."//1.4E-  
20 270//1224bp//100%//U96750  
C-HEMBA1006483  
C-HEMBA1006492  
C-HEMBA1006497  
C-HEMBA1006502  
25 C-HEMBA1006507//"Homo sapiens mRNA for KIAA0666 protein, partial cds."//0//2334bp//99%//  
AB014566  
C-HEMBA1006535  
C-HEMBA1006559//"Mus musculus PRAJA1 (Praja1) mRNA, complete cds."//2.8E-206//1107bp//83  
%//U06944  
30 C-HEMBA1006566  
C-HEMBA1006579  
C-HEMBA1006583  
C-HEMBA1006612  
C-HEMBA1006624//DNA/PANTOTHENATE METABOLISM FLAVOPROTEIN HOMOLOG//0.00000069//109aa//  
35 38%//Q58323  
C-HEMBA1006643  
C-HEMBA1006674  
C-HEMBA1006682  
C-HEMBA1006708//HYPOTHETICAL 46.4 KD TRP-ASP REPEATS CONTAINING PROTEIN IN PMC1-TFG2  
40 INTERGENIC REGION//3.3E-22//241aa//31%//P53196  
C-HEMBA1006717  
C-HEMBA1006744  
C-HEMBA1006754  
C-HEMBA1006767  
45 C-HEMBA1006789  
C-HEMBA1006832  
C-HEMBA1006885//"Homo sapiens gene for Proline synthetase associated, complete cds."//0//  
1467bp//96%//AB018566  
C-HEMBA1006900  
50 C-HEMBA1006926  
C-HEMBA1006941//Homo sapiens mRNA for putative thioredoxin-like protein//1.8E-226//1039bp//99%//  
AJ010841  
C-HEMBA1006973//"Homo sapiens rab3-GAP regulatory domain mRNA, complete cds."//5.6E-143//  
740bp//94%//AF004828  
55 C-HEMBA1006993  
C-HEMBA1007002  
C-HEMBA1007062  
C-HEMBA1007080

C-HEMBA1007087//HYPOTHETICAL PROTEIN MJ0162.//2E-45//304aa//32%//Q57626  
 C-HEMBA1007112//Homo sapiens mRNA; cDNA DKFZp586C1817 (from clone DKFZp586C1817).//0//1619bp//  
 99%//AL117450  
 C-HEMBA1007194//"Homo sapiens origin recognition complex subunit 6 (ORC6) mRNA, complete cds.  
 &quot;//0//1588bp//99%//AF139658  
 C-HEMBA1007206  
 C-HEMBA1007256  
 C-HEMBA1007267  
 C-HEMBA1007281  
 C-HEMBA1007300//"Homo sapiens 3',5'-cyclic nucleotide phosphodiesterase 10A1 (PDE10A) mRNA,  
 splice variant 1, complete cds.&quot;//0//1519bp//99%//AF127479  
 C-HEMBA1007301  
 C-HEMBA1007319  
 C-HEMBA1007320  
 C-HEMBA1007327  
 C-HEMBA1007347  
 C-HEMBB1000005  
 C-HEMBB1000030  
 C-HEMBB1000048  
 C-HEMBB1000099  
 C-HEMBB1000141  
 C-HEMBB1000198  
 C-HEMBB1000217//"Homo sapiens SUMO-1-activating enzyme E1 N subunit (SUA1) mRNA, complete cds.  
 &quot;//0//1038bp//99%//AF090385  
 C-HEMBB1000218  
 C-HEMBB1000274  
 C-HEMBB1000312  
 C-HEMBB1000402  
 C-HEMBB1000420  
 C-HEMBB1000480  
 C-HEMBB1000530  
 C-HEMBB1000550  
 C-HEMBB10000556//"Homo sapiens mRNA for KIAA0750 protein, complete cds.&quot;//6.3E-74//1213bp//  
 64%//AB018293  
 C-HEMBB1000586  
 C-HEMBB1000592  
 C-HEMBB1000593//"Homo sapiens transferrin receptor 2 alpha (TFR2) mRNA, complete cds.&quot;//1.3E-  
 107//503bp//99%//AF067864  
 C-HEMBB1000649  
 C-HEMBB1000693//"Homo sapiens neuroan1 mRNA, complete cds.&quot;//0//2952bp//94%//AF040723  
 C-HEMBB1000822  
 C-HEMBB1000826  
 C-HEMBB1000890  
 C-HEMBB1000915//SUBTILISIN-LIKE PROTEASE PACE4 PRECURSOR (EC 3.4.21.-).//1.10E-08//129aa//  
 31%//P29122  
 C-HEMBB1001008  
 C-HEMBB1001020//"Homo sapiens mRNA for KIAA0889 protein, complete cds.&quot;//0//1812bp//98%//  
 AB020696  
 C-HEMBB1001051  
 C-HEMBB1001112//"Homo sapiens sec61 homolog mRNA, complete cds.&quot;//6E-145//961bp//83%//  
 AF077032  
 C-HEMBB1001221  
 C-HEMBB1001234//65 KD YES-ASSOCIATED PROTEIN (YAP65).//5.4E-93//196aa//54%//P46938  
 C-HEMBB1001282//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).//7E-43//394aa//34%//  
 P16157  
 C-HEMBB1001302  
 C-HEMBB1001335  
 C-HEMBB1001337

C-HEMBB1001356  
 C-HEMBB1001364  
 C-HEMBB1001366  
 C-HEMBB1001367  
 5 C-HEMBB1001527  
 C-HEMBB1001537  
 C-HEMBB1002359  
 C-HEMBB1002415  
 C-HEMBB1002457  
 10 C-HEMBB1002492  
 C-HEMBB1002495  
 C-HEMBB1002502  
 C-HEMBB1002550//HYPOTHETICAL UOG-1 PROTEIN./.5E-28//266aa//33%//P27544  
 15 C-HEMBB1002600//"Homo sapiens tetraspan NET-5 mRNA, complete cds."//0//1417bp//99%//  
 AF089749  
 C-HEMBB1002607//"Homo sapiens vitamin D3 receptor interacting protein (DRIP80) mRNA, complete cds.  
 &quot;//2E-136//660bp//98%//AF105421  
 C-HEMBB1002684  
 C-HEMBB1002692  
 20 C-HEMBB1002697  
 C-HEMBB1002705//"Homo sapiens CGI-27 protein mRNA, complete cds."//7.80E-285//841bp//96%//  
 AF132961  
 C-MAMMA1000019  
 C-MAMMA1000020//H.sapiens mRNA for flavin-containing monooxygenase 5 (FM05).//8.2E-198//868bp//99%//  
 25 Z47553  
 C-MAMMA1000025  
 C-MAMMA1000055//TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)].//1.5E-90//323aa//48%//P47226  
 C-MAMMA1000069  
 C-MAMMA1000084  
 30 C-MAMMA1000139  
 C-MAMMA1000163  
 C-MAMMA1000171  
 C-MAMMA1000173//"Homo sapiens src homology 3 domain-containing protein HIP-55 mRNA, complete  
 cds.&quot;//2.6E-164//1044bp//87%//AF197060  
 35 C-MAMMA1000277  
 C-MAMMA1000278  
 C-MAMMA1000284//P.walti mRNA for mp associated protein 55./.2.2E-109//864bp//76%//X99836  
 C-MAMMA1000309  
 C-MAMMA1000312  
 40 C-MAMMA1000313  
 C-MAMMA1000361  
 C-MAMMA1000388//"Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds."//  
 0//1466bp//99%//AB015132  
 C-MAMMA1000395  
 45 C-MAMMA1000410  
 C-MAMMA1000416//HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III./.2.00E-30//119aa//  
 53%//Q09232  
 C-MAMMA1000421  
 C-MAMMA1000422  
 50 C-MAMMA1000468  
 C-MAMMA1000472  
 C-MAMMA1000490  
 C-MAMMA1000524  
 C-MAMMA1000567  
 55 C-MAMMA1000612//"Rattus norvegicus G beta-like protein GBL mRNA, complete cds."//1E-95//  
 1115bp//72%//AF051155  
 C-MAMMA1000623  
 C-MAMMA1000625//GYP7 PROTEIN./.2.1E-41//198aa//40%//P48365

C-MAMMA1000664  
 C-MAMMA1000670  
 C-MAMMA1000672//VITELLOGENIC CARBOXYPEPTIDASE PRECURSOR (EC 3.4.16.-).//4.4E-33//250aa//  
 33%//P42660  
 5 C-MAMMA1000713//L-RIBULOKINASE (EC 2.7.1.16).//7.70E-17//246aa//29%//P94524  
 C-MAMMA1000731//CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 1 (CHD-1).//1E-77//395aa//45%//  
 014646  
 C-MAMMA1000734//Homo sapiens mRNA for SEC63 protein.//0//1587bp//99%//AJ011779  
 C-MAMMA1000738//HYPOTHETICAL 116.5 KD PROTEIN C20G8.09C IN CHROMOSOME I.//9E-299//1033aa//  
 10 55%//P87115  
 C-MAMMA1000746  
 C-MAMMA1000775  
 C-MAMMA1000824//ACTIN.//6.2E-20//284aa//28%//P53500  
 C-MAMMA1000831  
 15 C-MAMMA1000841//PUTATIVE AMIDASE (EC 3.5.1.4).//7.8E-40//101aa//54%//027540  
 C-MAMMA1000842  
 C-MAMMA1000843  
 C-MAMMA1000856  
 C-MAMMA1000865  
 20 C-MAMMA1000875  
 C-MAMMA1000906  
 C-MAMMA1000908  
 C-MAMMA1000914  
 C-MAMMA1000956//Homo sapiens CLDN8 gene for claudin-8.//0//1767bp//99%//AJ250711  
 25 C-MAMMA1000968  
 C-MAMMA1000979  
 C-MAMMA1001008//"Homo sapiens aspartic-like protease mRNA, complete cds."//2.50E-276//  
 1263bp//99%//AF117892  
 C-MAMMA1001021  
 30 C-MAMMA1001041//"SPECTRIN BETA CHAIN, BRAIN (SPECTRIN, NON-ERYTHROID BETA CHAIN)  
 (FODRIN BETA CHAIN) (SPTBN1).";//1.6E-16//113aa//41%//Q01082  
 C-MAMMA1001059//Homo sapiens mRNA for DEAD Box Protein 5.//0//1440bp//99%//AJ237946  
 C-MAMMA1001075//"Homo sapiens CGI-72 protein mRNA, complete cds."//1.3E-181//397bp//98%//  
 AF151830  
 35 C-MAMMA1001078  
 C-MAMMA1001091  
 C-MAMMA1001105//OVO PROTEIN (SHAVEN BABY PROTEIN).//4E-49//125aa//68%//P51521  
 C-MAMMA1001110  
 C-MAMMA1001126  
 40 C-MAMMA1001139//SRE-2 PROTEIN.//5.80E-35//239aa//38%//Q09273  
 C-MAMMA1001143  
 C-MAMMA1001154  
 C-MAMMA1001181//ABC1 PROTEIN HOMOLOG PRECURSOR.//1.30E-07//81aa//45%//Q92338  
 C-MAMMA1001215  
 45 C-MAMMA1001244  
 C-MAMMA1001259//"Mus musculus F-box protein FBX18 mRNA, partial cds."//2.3E-271//1414bp//  
 89%//AF184275  
 C-MAMMA1001260//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME III.//2.1E-52//630aa//  
 30%//P34537  
 50 C-MAMMA1001343  
 C-MAMMA1001411//Homo sapiens mRNA; cDNA DKFZp56400823 (from clone DKFZp56400823).//0//2131bp//  
 99%//AL080121  
 C-MAMMA1001419  
 C-MAMMA1001476//URIDINE KINASE (EC 2.7.1.48) (URIDINE MONOPHOSPHOKINASE) (FRAGMENT).//  
 55 6.5E-129//260aa//92%//P52623  
 C-MAMMA1001510  
 C-MAMMA1001522  
 C-MAMMA1001576//"Human gamma-tubulin mRNA, complete cds."//7.5E-276//1561bp//90%//

M61764  
 C-MAMMA1001604  
 C-MAMMA1001620  
 C-MAMMA1001635  
 5 C-MAMMA1001649  
 C-MAMMA1001686  
 C-MAMMA1001692  
 C-MAMMA1001743//Y BOX BINDING PROTEIN-1 (Y-BOX TRANSCRIPTION FACTOR).//8.5E-32//171aa//36%//  
 P21573  
 10 C-MAMMA1001754//&quot;Homo sapiens CGI-11 protein mRNA, complete cds.&quot;//0//1837bp//98%//  
 AF132945  
 C-MAMMA1001757  
 C-MAMMA1001764  
 C-MAMMA1001768//CELL DIVISION CYCLE PROTEIN 48 HOMOLOG MJ1156.//3.8E-45//351aa//38%//Q58556  
 15 C-MAMMA1001771//M.musculus mRNA for semaphorin B.//2.60E-200//1272bp//79%//X85991  
 C-MAMMA1001790  
 C-MAMMA1001837//ZINC FINGER PROTEIN 29 (ZFP-29).//2.6E-77//507aa//38%//Q07230  
 C-MAMMA1001858  
 C-MAMMA1001868//TRICHOHYALIN.//2.7E-19//359aa//25%//P22793  
 20 C-MAMMA1001970  
 C-MAMMA1002042  
 C-MAMMA1002068  
 C-MAMMA1002153  
 C-MAMMA1002156  
 25 C-MAMMA1002170//40S RIBOSOMAL PROTEIN S2 (S4) (LLREP3 PROTEIN).//6E-66//157aa//70%//P15880  
 C-MAMMA1002174  
 C-MAMMA1002209  
 C-MAMMA1002219//&quot;Homo sapiens mRNA for KIAA1067 protein, partial cds.&quot;//1.1E-181//861bp//  
 98%//AB028990  
 30 C-MAMMA1002236//TRANSLATION INITIATION FACTOR EIF-2B GAMMA SUBUNIT (EIF-2B GDP-GTP EX-  
 CHANGE FACTOR).//8.8E-217//310aa//86%//P70541  
 C-MAMMA1002243  
 C-MAMMA1002268//&quot;Mus musculus sphingosine kinase (SPHK1a) mRNA, partial cds.&quot;//1E-190//  
 1624bp//76%//AF068748  
 35 C-MAMMA1002269  
 C-MAMMA1002292  
 C-MAMMA1002294  
 C-MAMMA1002297//Homo sapiens mRNA for Rab6 GTPase activating protein.//1.1E-214//881bp//97%//  
 AJ011679  
 40 C-MAMMA1002312  
 C-MAMMA1002329//M.musculus mRNA for semaphorin B.//3.80E-45//332bp//84%//X85991  
 C-MAMMA1002333  
 C-MAMMA1002351//FERRIPYOCHELIN BINDING PROTEIN.//0.000078//127aa//26%//P40882  
 C-MAMMA1002353  
 45 C-MAMMA1002355  
 C-MAMMA1002356  
 C-MAMMA1002362  
 C-MAMMA1002380  
 C-MAMMA1002384  
 50 C-MAMMA1002427  
 C-MAMMA1002470//PROBABLE NH(3)-DEPENDENT NAD(+) SYNTHETASE (EC 6.3.5.1).//1E-11//128aa//36%//  
 P47623  
 C-MAMMA1002485//&quot;Homo sapiens stanniocalcin-related protein mRNA, complete cds.&quot;//0//1822bp//  
 99%//AF098462  
 55 C-MAMMA1002494  
 C-MAMMA1002524//HYPOTHETICAL 117.8 KD PROTEIN IN STE2-FRS2 INTERGENIC REGION.//1.2E-34//  
 337aa//31%//P43571  
 C-MAMMA1002530//&quot;Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 gamma) mRNA, complete

cds."//0//1910bp//99%//AF065214  
 C-MAMMA1002554  
 C-MAMMA1002585//";Homo sapiens mRNA for KIAA0860 protein, complete cds."//0//1405bp//99%//  
 AB020667  
 5 C-MAMMA1002598  
 C-MAMMA1002619//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE K02C4.3 (EC 3.1.2.15)  
 (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING EN-  
 ZYME).//9.5E-16//159aa//37%//Q09931  
 C-MAMMA1002655//";Homo sapiens mRNA for ganglioside sialidase, complete cds."//0//1515bp//  
 10 99%//AB008185  
 C-MAMMA1002671//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL-AC-  
 TIVATING ENZYME).//1.1E-45//618aa//26%//P27550  
 C-MAMMA1002673  
 C-MAMMA1002684//";Homo sapiens mRNA for KIAA0214 protein, complete cds."//0//3174bp//99%//  
 15 D86987  
 C-MAMMA1002711  
 C-MAMMA1002769//";Homo sapiens cell cycle progression restoration 8 protein (CPR8) mRNA, complete  
 cds."//2.2E-25//330bp//77%//AF011794  
 C-MAMMA1002775  
 20 C-MAMMA1002782  
 C-MAMMA1002796  
 C-MAMMA1002807  
 C-MAMMA1002838  
 C-MAMMA1002842//";Mus musculus c-Cb1 associated protein CAP mRNA, complete cds."//2.6E-58//  
 25 373bp//81%//U58883  
 C-MAMMA1002869//PINCH PROTEIN (PARTICULARLY INTERESTING NEW CYS-HIS PROTEIN).//1.4E-160//  
 305aa//85%//P48059  
 C-MAMMA1002881//GLIOMA PATHOGENESIS-RELATED PROTEIN (RTVP-1 PROTEIN).//5.7E-30//214aa//  
 35 35%//P48060  
 C-MAMMA1002886  
 C-MAMMA1002890  
 C-MAMMA1002938//";Homo sapiens mRNA for KIAA0698 protein, complete cds."//8.4E-252//1139bp//  
 100%//AB014598  
 C-MAMMA1002964  
 35 C-MAMMA1003011//HESTONE MACRO-H2A.1.//2.7E-123//370aa//66%//Q02874  
 C-MAMMA1003013//DNA POLYMERASE BETA (EC 2.7.7.7).//7.4E-46//332aa//36%//P06746  
 C-MAMMA1003015  
 C-MAMMA1003019  
 C-MAMMA1003035//RIBOSOMAL LARGE SUBUNIT PSEUDOURIDINE SYNTHASE C (EC 4.2.1.70) (PSEU-  
 40 DOURIDYLATE SYNTHASE) (URACIL HYDROLYASE).//1.9E-13//108aa//33%//P23851  
 C-MAMMA1003039  
 C-MAMMA1003044  
 C-MAMMA1003049  
 C-MAMMA1003056  
 45 C-MAMMA1003057//MD6 PROTEIN.//3.1E-225//419aa//97%//Q60584  
 C-MAMMA1003066  
 C-MAMMA1003099  
 C-MAMMA1003104  
 C-MAMMA1003113//";Mus musculus COP9 complex subunit 7a (COPS7a) mRNA, complete cds."//  
 50 1.1E-234//1178bp//86%//AF071316  
 C-MAMMA1003127//MYOSIN I ALPHA (MMI-ALPHA).//2.2E-105//217aa//89%//P46735  
 C-MAMMA1003135  
 C-MAMMA1003146//";Homo sapiens mRNA for GaIT3 protein.//4.3E-218//996bp//99%//Y15062  
 C-MAMMA1003150//";Homo sapiens mRNA for KIAA1096 protein, partial cds."//0//1342bp//99%//  
 55 AB029019  
 C-MAMMA1003166//";Homo sapiens MLL septin-like fusion protein (MSF) mRNA, complete cds."//  
 3.10E-158//592bp//97%//AF123052  
 C-NT2RM1000032

C-NT2RM1000035//&quot;Human mRNA for KIAA0199 gene, partial cds.&quot;//0//2948bp//99%//D83782  
 C-NT2RM1000039//HYPOTHETICAL 41.4 KD PROTEIN IN SRLQ-HYPF INTERGENIC REGION (EC 1.18.1.-)  
 (ORF4) (ORF2).//2.90E-14//299aa//25%//P37596  
 C-NT2RM1000055//&quot;Homo sapiens mRNA for KIAA0829 protein, partial cds.&quot;//0//3111bp//99%//  
 AB020636  
 C-NT2RM1000059  
 C-NT2RM1000062  
 C-NT2RM1000118//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) (CAL-  
 CINEURIN REGULATORY SUBUNIT).//1.2E-10//150aa//28%//P87072  
 C-NT2RM1000119  
 C-NT2RM1000127  
 C-NT2RM1000131//&quot;Homo sapiens mRNA for KIAA0792 protein, complete cds.&quot;//0//2980bp//99%//  
 AB018335  
 C-NT2RM1000132//&quot;Homo sapiens NADH:ubiquinone oxidoreductas NDUFS6 subunit mRNA, nuclear gene  
 encoding mitochondrial protein, complete cds.&quot;//7.8E-110//516bp//99%//AF044959  
 C-NT2RM1000153//CYTOSOLIC PURINE 5'-NUCLEOTIDASE (EC 3.1.3.5).//3.3E-3 8//469aa//27%//P49902  
 C-NT2RM1000186//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) (CAL-  
 CINEURIN REGULATORY SUBUNIT).//1.2E-10//150aa//28%//P87072  
 C-NT2RM1000187//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE  
 SPAC10F6.02C.//1.1E-10//94aa//47%//042643  
 C-NT2RM1000199//Homo sapiens mRNA for type I transmembrane receptor (psk-1 gene).//0//2476bp//99%//  
 AJ245820  
 C-NT2RM1000244//&quot;Homo sapiens TRAF4 associated factor 1 mRNA, partial cds.&quot;//2E-126//592bp//  
 99%//U81002  
 C-NT2RM1000252//H.sapiens E-MAP-115 mRNA.//9.7E-35//569bp//64%//X73882  
 C-NT2RM1000256//&quot;Homo sapiens mRNA for Glutamine:fructose-6-phosphate amidotransferase, complete  
 cds.&quot;//0//3012bp//99%//AB016789  
 C-NT2RM1000260//&quot;Human mRNA for KIAA0130 gene, complete cds.&quot;//0//3139bp//98%//D50920  
 C-NT2RM1000271  
 C-NT2RM1000300  
 C-NT2RM1000314//&quot;Human mRNA for KIAA0159 gene, complete cds.&quot;//0//4349bp//99%//D63880  
 C-NT2RM1000354//&quot;Xenopus laevis chromosome condensation protein XCAP-G mRNA, complete cds.  
 &quot;//7.4E-245//2101bp//68%//AF111423  
 C-NT2RM1000355//&quot;Homo sapiens transmembrane protein BRI (BRI) mRNA, complete cds.&quot;//0//  
 1599bp//99%//AF152462  
 C-NT2RM1000365  
 C-NT2RM1000377//&quot;Homo sapiens dual specificity phosphatase MKP5 (MKP5) mRNA, complete cds.&quot;;  
 //3.2E-196//1016bp//94%//AF179212  
 C-NT2RM1000388//HYPOTHETICAL 27.7 KD PROTEIN IN CPT1-SPC98 INTERGENIC REGION.//  
 0.00000019//67aa//31%//P53915  
 C-NT2RM1000399  
 C-NT2RM1000430//&quot;Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.&quot;//  
 1.4E-185//1486bp//81%//AF084928  
 C-NT2RM1000555//&quot;Homo sapiens mRNA for KIAA0885 protein, complete cds.&quot;//0//2885bp//99%//  
 AB020692  
 C-NT2RM1000563//TRANSMISSION-BLOCKING TARGET ANTIGEN S230 PRECURSOR.//0.0000068//199aa//  
 30%//Q08372  
 C-NT2RM1000648//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//8.5E-75//301aa//39%//P43636  
 C-NT2RM1000661//&quot;Homo sapiens translation initiation factor 4e mRNA, complete cds.&quot;//4.3E-210//  
 960bp//99%//AF038957  
 C-NT2RM1000666//DNA-BINDING PROTEIN A.//2.2E-09//165aa//34%//P16989  
 C-NT2RM1000672  
 C-NT2RM1000691//Homo sapiens mRNA for PLU-1 protein.//0//3104bp//99%//AJ132440  
 C-NT2RM1000699  
 C-NT2RM1000741//&quot;Homo sapiens mRNA for KIAA0567 protein, partial cds.&quot;//1.1E-295//1338bp//  
 99%//AB011139  
 C-NT2RM1000742//&quot;Homo sapiens AC133 antigen mRNA, complete cds.&quot;//0//3524bp//99%//  
 AF027208

C-NT2RM1000746//"Homo sapiens polyamine modulated factor-1 (PMF1) mRNA, complete cds.&quot;//  
6.70E-227//1043bp//99%//AF141310  
C-NT2RM1000770//DXS6673E PROTEIN//1.4E-39//194aa//48%//Q14202  
C-NT2RM1000772//VEGETATTOLE INCOMPATIBILITY PROTEIN HET-E-1//7.3E-15//280aa//27%//Q00808  
5 C-NT2RM1000780  
C-NT2RM1000800//Mus musculus partial mRNA for B-IND1 protein (B-indl gene)//1.1E-98//571bp//89%//Z97207  
C-NT2RM1000802  
C-NT2RM1000811//"Homo sapiens AC133 antigen mRNA, complete cds.&quot;//0//3524bp//99%//  
AF027208  
10 C-NT2RM1000826//"Homo sapiens mRNA for KIAA0885 protein, complete cds.&quot;//0//2885bp//99%//  
AB020692  
C-NT2RM1000829  
C-NT2RM1000850//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN)//9.7E-42//333aa//36%//  
P16157  
15 C-NT2RM1000852//"Homo sapiens putative ATP-dependent RNA helicase ROK1 mRNA, complete cds.  
&quot;//0//2206bp//99%//AF077033  
C-NT2RM1000857//"Homo sapiens mRNA for KIAA0962 protein, partial cds.&quot;//0//3716bp//99%//  
AB023179  
C-NT2RM1000874//"Homo sapiens death effector domain-containing testicular molecule mRNA, complete  
20 cds.&quot;//1.4E-244//1113bp//99%//AF043733  
C-NT2RM1000882//"Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds.&quot;//4.30E-122//  
1394bp//69%//AF126799  
C-NT2RM1000885//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME III//1.8E-56//630aa//  
30 30%//P34537  
25 C-NT2RM1000894//DNA-DIRECTED RNA POLYMERASE 1135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA  
POLYMERASE I SUBUNIT 2) (RPA135)//0//1020aa//89%//P70700  
C-NT2RM1000898//"ACTIN, CYTOPLASMIC (ACTIN, MICRONUCLEAR).&quot;//8.9E-26//229aa//29%//  
P02583  
C-NT2RM1000905//"Homo sapiens HSPC021 mRNA, complete cds.&quot;//0//1480bp//99%//AF077207  
30 C-NT2RM1000924//HYPOTHETICAL 39.7 KD PROTEIN C34E10.2 IN CHROMOSOME III//1E-15//266aa//26%//  
P46577  
C-NT2RM1000927  
C-NT2RM1000962  
C-NT2RM1000978  
35 C-NT2RM1001003//"Homo sapiens alpha-catenin-like protein (CTNNAL1) mRNA, complete cds.&quot;//0//  
2230bp//99%//AF03233  
C-NT2RM1001043  
C-NT2RM1001066  
40 C-NT2RM1001072//"1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE GAM-  
MA 1 (EC 3.1.4.11) (PLC-GAMMA-1) (PHOSPHOLIPASE C-GAMMA-1) (PLC-II) (PLC-148).&quot;//8.3E-47//  
259aa//35%//P08487  
C-NT2RM1001085//"Rattus norvegicus brain specific cortactin-binding protein CBP90 mRNA, partial cds.  
&quot;//3.7E-32//460bp//64%//AF053768  
45 C-NT2RM1001102//"Human HEM45 mRNA, complete cds.&quot;//2.3E-27//482bp//63%//U88964  
C-NT2RM1001105  
C-NT2RM1001139//Homo sapiens mRNA; cDNA DKFZp564F0522 (from clone DKFZp564F0522).//0//1756bp//  
99%//AL049943  
C-NT2RM2000420  
50 C-NT2RM2000566//"Homo sapiens integrin alpha-7 mRNA, complete cds.&quot;//0//2519bp//96%//  
AF032108  
C-NT2RM2000609  
C-NT2RM2000612//"Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA,  
complete cds.&quot;//2.6E-106//1069bp//74%//U35776  
C-NT2RM2000735//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//2.9E-103//249aa//73%//P28160  
55 C-NT2RM2001588  
C-NT2RM2001605//Homo sapiens mRNA for PLU-1 protein.//0//3114bp//99%//AJ132440  
C-NT2RM2001613//"Homo sapiens sec61 homolog mRNA, complete cds.&quot;//0//2601bp//99%//  
AF084458

C-NT2RM2001632//KES 1 PROTEIN./.1.40E-31//342aa//34%//P35844  
 C-NT2RM2001648//&quot;Homo sapiens sec61 homolog mRNA, complete cds.&quot;//0//2421bp//99%//AF084458  
 C-NT2RM2001652//&quot;Homo sapiens guanine nucleotide exchange factor mRNA, complete cds.&quot;//0//2608bp//99%//AF111162  
 5 C-NT2RM2001659//ZINC/CADMIUM RESISTANCE PROTEIN./.3.4E-39//161aa//34%//P20107  
 C-NT2RM2001664//&quot;Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds.&quot;//0//2471bp//99%//AF044195  
 C-NT2RM2001668//&quot;Homo sapiens putative WHSC1 protein (WHSC1) mRNA, alternative splice product  
 10 ending in intron 11, complete cds.&quot;//6.2E-16//464bp//62%//AF083391  
 C-NT2RM2001671//&quot;Oryctolagus cuniculus sarcolemmal associated protein (SLAP1) mRNA, complete cds.  
 &quot;//0//1843bp//94%//U21155  
 C-NT2RM2001675  
 C-NT2RM2001681  
 15 C-NT2RM2001688//HYPOTHETICAL 33.8 KD PROTEIN C5H10.01 IN CHROMOSOME I./.4.60E-20//253aa//  
 30%//Q09674  
 C-NT2RM2001695//Homo sapiens clone H63 unknown mRNA./.0//2016bp//99%//AF103804  
 C-NT2RM2001696  
 C-NT2RM2001698//&quot;Homo sapiens XGalT-1 mRNA for galactosyltransferase I, complete cds.&quot;//6.2E-  
 20 253//1170bp//99%//AB028600  
 C-NT2RM2001700//&quot;ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC (EC 1.3.99.-) (VL-  
 CAD) (FRAGMENT).&quot;//5.7E-130//536aa//49%//P50544  
 C-NT2RM2001716  
 C-NT2RM2001723  
 25 C-NT2RM2001730//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE K02C4.3 (EC 3.1.2.15)  
 (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING EN-  
 ZYME).//7.2E-16//381aa//27%//Q09931  
 C-NT2RM2001743//&quot;Homo sapiens cell cycle progression 2 protein (CPR2) mRNA, complete cds.&quot;//  
 0//1498bp//99%//AF011792  
 30 C-NT2RM2001753//HYPOTHETICAL PROTEIN KIAA0210./.8.8E-11//119aa//36%//Q92609  
 C-NT2RM2001760//&quot;Homo sapiens sec61 homolog mRNA, complete cds.&quot;//0//2379bp//99%//  
 AF084458  
 C-NT2RM2001768  
 C-NT2RM2001771//ZINC FINGER PROTEIN 135./.6.4E-154//394aa//64%//P52742  
 35 C-NT2RM2001782//&quot;Homo sapiens GDP-mannose pyrophosphorylase A (GMPPA) mRNA, complete cds.  
 &quot;//0//1470bp//99%//AF135422  
 C-NT2RM2001784  
 C-NT2RM2001785//Homo sapiens mRNA; cDNA DKFZp586C201 (from clone DKFZp586C201).//0//2146bp//  
 99%//AL050118  
 40 C-NT2RM2001813  
 C-NT2RM2001823//CHD1 PROTEIN./.1.8E-106//631aa//39%//P32657  
 C-NT2RM2001839//&quot;Homo sapiens calumein (Calu) mRNA, complete cds.&quot;//0//2415bp//97%//  
 AF013759  
 C-NT2RM2001840  
 45 C-NT2RM2001855  
 C-NT2RM2001867//&quot;Homo sapiens mRNA for KIAA0943 protein, partial cds.&quot;//0//967bp//99%//  
 AB023160  
 C-NT2RM2001879  
 C-NT2RM2001983//&quot;Homo sapiens RGS-GAIP interacting protein GIPC mRNA, complete cds.&quot;//0//  
 50 1658bp//98%//AF089816  
 C-NT2RM2002145//&quot;Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.&quot;//  
 8.5E-191//1524bp//81%//AF084928  
 C-NT2RM4000027  
 C-NT2RM4000030//LAS1 PROTEIN./.5.6E-12//184aa//32%//P36146  
 55 C-NT2RM4000046//GOLIATH PROTEIN (G1 PROTEIN).//0.000008//112aa//31%//Q06003  
 C-NT2RM4000155//&quot;THREONYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.3) (THREONINE--  
 TRNA LIGASE) (THRRS).&quot;//1.2E-157//321aa//61%//P26639  
 C-NT2RM4000156//H.sapiens HPBRII-7 gene./.3.6E-21//785bp//60%//X67336

C-NT2RM4000167//&quot;Homo sapiens kinesin superfamily motor KIF4 mRNA, complete cds.&quot;//0//  
 1946bp//99%//AF071592  
 C-NT2RM4000199  
 C-NT2RM4000200  
 5 C-NT2RM4000202//ZINC FINGER PROTEIN MOK-2 (HOK-2).//4.9E-32//170aa//41%//Q16600  
 C-NT2RM4000233//&quot;Mus musculus semaphorin VIa mRNA, complete cds.&quot;//3.4E-231//1395bp//86%//  
 AF030430  
 C-NT2RM4000244  
 C-NT2RM4000251  
 10 C-NT2RM4000265  
 C-NT2RM4000324  
 C-NT2RM4000327  
 C-NT2RM4000356//RAS-RELATED PROTEIN RAB-17.//5.9E-80//213aa//75%//P35292  
 C-NT2RM4000425  
 15 C-NT2RM4000433//&quot;Mus musculus retinoic acid-responsive protein (Stra6) mRNA, complete cds.&quot;//  
 4.1E-271//2085bp//77%//AF062476  
 C-NT2RM4000514  
 C-NT2RM4000531//ZINC FINGER PROTEIN 29 (ZFP-29).//2.4E-89//389aa//43%//007230  
 C-NT2RM4000532  
 20 C-NT2RM4000534  
 C-NT2RM4000603  
 C-NT2RM4000611//VEGETABLE INCOMPATIBILITY PROTEIN HET-E-1.//2.9E-09//108aa//31%//Q00808  
 C-NT2RM4000616//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- AC-  
 TIVATING ENZYME).//2.7E-146//420aa//60%//P27550  
 25 C-NT2RM4000674//HYPOTHETICAL SYMPORTER SLL1374.//1.2E-28//180aa//30%//P74168  
 C-NT2RM4000689  
 C-NT2RM4000698  
 C-NT2RM4000700  
 30 C-NT2RM4000712//&quot;Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds.&quot;//1E-  
 136//1104bp//77%//AF022789  
 C-NT2RM4000717  
 C-NT2RM4000733//TRANSCRIPTION TERMINATION FACTOR RHO.//0.00000041//207aa//29%//P52154  
 C-NT2RM4000734//&quot;Homo sapiens mRNA for KIAA0760 protein, partial cds.&quot;//0//2273bp//99%//  
 AB018303  
 35 C-NT2RM4000741//&quot;Homo sapiens hSGT1 mRNA for hSgt1p, complete cds.&quot;//0//2184bp//99%//  
 D88208  
 C-NT2RM4000751//ZINC FINGER PROTEIN 184 (FRAGMENT).//3.9E-125//301aa//53%//Q99676  
 C-NT2RM4000764  
 C-NT2RM4000778  
 40 C-NT2RM4000787  
 C-NT2RM4000790  
 C-NT2RM4000795//&quot;Homo sapiens mRNA for KIAA0951 protein, complete cds.&quot;//0//1847bp//96%//  
 AB023168  
 C-NT2RM4000796  
 45 C-NT2RM4000798//&quot;Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 mRNA,  
 complete cds.&quot;//0//2603bp//99%//AF084521  
 C-NT2RM4000813  
 C-NT2RM4000820//VACUOLAR ATP SYNTHASE SUBUNIT AC45 PRECURSOR (EC 3.6.1.34) (V-ATPASE  
 AC45 SUBUNIT).//1.10E-24//138aa//44%//P40682  
 50 C-NT2RM4000833  
 C-NT2RM4000848  
 C-NT2RM4000852  
 C-NT2RM4000855  
 C-NT2RM4000887  
 55 C-NT2RM4000895  
 C-NT2RM4000950  
 C-NT2RM4000979  
 C-NT2RM4001002//Homo sapiens mRNA; cDNA DKFZp586G0518 (from clone DKFZp586G0518).//0//2259bp//

100%//AL050092  
 C-NT2RM4001032  
 C-NT2RM4001047//M025 PROTEIN//8E-140//333aa//80%//Q06138  
 C-NT2RM4001054//&quot;Homo sapiens sec61 homolog mRNA, complete cds.&quot;//3.1E-190//1315bp//81%//  
 5 AF077032  
 C-NT2RM4001084//HYPOTHETICAL 105.6 KD PROTEIN C16C9.06C IN CHROMOSOME I//0.000000032//  
 165aa//33%//Q09820  
 C-NT2RM4001116//HYPOTHETICAL 216.3 KD PROTEIN R06F6.8 IN CHROMOSOME II//5.9E-86//292aa//  
 48%//Q09417  
 10 C-NT2RM4001140//HOMEobox PROTEIN MSH-D//1E-11//103aa//38%//Q01704  
 C-NT2RM4001151  
 C-NT2RM4001155//ADRENAL MEDULLA 50 KD PROTEIN//4.1E-197//445aa//78%//Q27969  
 C-NT2RM4001160  
 C-NT2RM4001187  
 15 C-NT2RM4001191//&quot;Homo sapiens clone 24963 mRNA sequence, complete cds.&quot;//0//1950bp//99%//  
 AF131737  
 C-NT2RM4001200//ZINC FINGER PROTEIN 135//9.5E-135//375aa//60%//P52742  
 C-NT2RM4001203//&quot;Homo sapiens mRNA for KIAA0839 protein, partial cds.&quot;//0//3047bp//99%//  
 AB020646  
 20 C-NT2RM4001204//&quot;Homo sapiens mRNA for KIAA1089 protein, partial cds.&quot;//0//2349bp//99%//  
 AB029012  
 C-NT2RM4001217//&quot;Homo sapiens nuclear matrix protein NRP/B (NRPB) mRNA, complete cds.&quot;//  
 7.3E-148//1409bp//72%//AF059611  
 C-NT2RM4001256//&quot;Xenopus laevis putative Zic3 binding protein mRNA, complete cds.&quot;//4.30E-55//  
 25 289bp//77%//AF129131  
 C-NT2RM4001258  
 C-NT2RM4001309  
 C-NT2RM4001313//PHOSPHATIDYLINOSITOL 3-KINASE VPS34-LIKE (EC 2.7.1.137) (PI3-KINASE) (PTDINS-  
 3-KINASE) (PI3K)//3.50E-35//124aa//65%//P54676  
 30 C-NT2RM4001316//&quot;ACYL-COA DEHYDROGENASE, MEDIUM-CHAIN SPECIFIC PRECURSOR (EC  
 1.3.99.3) (MCAD).&quot;//2.3E-31//334aa//30%//P08503  
 C-NT2RM4001320//&quot;Homo sapiens mRNA for Neuroblastoma, complete cds.&quot;//1.8E-39//728bp//64%//  
 D89016  
 C-NT2RM4001340//UTR4 PROTEIN (UNKNOWN TRANSCRIPT 4 PROTEIN).//1E-28//171aa//37%//P32626  
 35 C-NT2RM4001344//HYPOTHETICAL GTP-BINDING PROTEIN IN POP2-HO1 INTERGENIC REGION//8.1E-  
 30//265aa//33%//P53742  
 C-NT2RM4001347//&quot;Homo sapiens NY-REN-25 antigen mRNA, partial cds.&quot;//0//2300bp//99%//  
 AF155103  
 C-NT2RM4001371//&quot;Homo sapiens IDN3 mRNA, partial cds.&quot;//0//2524bp//99%//AB019494  
 40 C-NT2RM4001382//&quot;Homo sapiens RanBP7/importin 7 mRNA, complete cds.&quot;//2.2E-237//1079bp//  
 99%//AF098799  
 C-NT2RM4001384  
 C-NT2RM4001410  
 45 C-NT2RM4001411//&quot;Mus musculus Pro-rich, PH, SH2 domain-containing signaling mediator (PSM) mRNA,  
 complete cds.&quot;//0//1962bp//87%//AF020526  
 C-NT2RM4001412//&quot;Homo sapiens nGAP mRNA, complete cds.&quot;//0//1918bp//99%//AF047711  
 C-NT2RM4001414  
 C-NT2RM4001437  
 50 C-NT2RM4001444//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE-TRNA LIGASE) (ILERS).//  
 1.4E-118//444aa//46%//P73505  
 C-NT2RM4001454  
 C-NT2RM4001455  
 C-NT2RM4001483//ZINC FINGER PROTEIN 136//5.1E-106//357aa//55%//P52737  
 55 C-NT2RM4001489//&quot;Homo sapiens mRNA for KIAA0685 protein, complete cds.&quot;//0//1810bp//99%//  
 AB014585  
 C-NT2RM4001522  
 C-NT2RM4001557//&quot;Homo sapiens mRNA for KIAA1040 protein, partial cds.&quot;//0//1547bp//97%//  
 AB028963

C-NT2RM4001565  
 C-NT2RM4001566//&quot;Homo sapiens mRNA for KIAA1114 protein, complete cds.&quot;//0//1900bp//99%//  
 AB029037  
 C-NT2RM4001582//&quot;Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds.&quot;//  
 5 1.5E-284//1082bp//90%//AF071317  
 C-NT2RM4001592//&quot;Homo sapiens mRNA for KIAA1122 protein, partial cds.&quot;//0//2170bp//99%//  
 AB032948  
 C-NT2RM4001594  
 C-NT2RM4001597//M.musculus red-1 gene.//2.1E-171//1414bp//78%//X92750  
 10 C-NT2RM4001611//SIS2 PROTEIN (HALOTOLERANCE PROTEIN HAL3).//2.6E-32//203aa//39%//Q12600  
 C-NT2RM4001629//&quot;MAGUK P55 SUBFAMILY MEMBER 3 (MPP3 PROTEIN) (DISCS, LARGE HOMOLOG  
 3).&quot;//1.5E-93//278aa//38%//Q13368  
 C-NT2RM4001650  
 C-NT2RM4001662  
 15 C-NT2RM4001666//HYPOTHETICAL 48.6 KD PROTEIN IN ALPA-GABP INTERGENIC REGION.//2.7E-84//  
 410aa//42%//P37339  
 C-NT2RM4001682  
 C-NT2RM4001710  
 C-NT2RM4001714//SEPTIN 2 HOMOLOG (FRAGMENT).//8.9E-141//354aa//72%//Q14141  
 20 C-NT2RM4001715  
 C-NT2RM4001731//&quot;Homo sapiens mRNA for KIAA1004 protein, partial cds.&quot;//0//1922bp//100%//  
 AB023221  
 C-NT2RM4001746  
 C-NT2RM4001754  
 25 C-NT2RM4001758//PUTATIVE SERINE/THREONINE-PROTEIN KINASE EMK (EC 2.7.1.-).//4.1E-186//639aa//  
 58%//Q05512  
 C-NT2RM4001783//ZINC FINGER PROTEIN HRX (ALL-1).//7.9E-66//311aa//35%//Q03164  
 C-NT2RM4001810//&quot;Homo sapiens mRNA for KIAA0863 protein, complete cds.&quot;//0//2377bp//99%//  
 AB020670  
 30 C-NT2RM4001813//LECTIN BRA-2.//0.00000048//114aa//30%//P17346  
 C-NT2RM4001823//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//2.9E-55//325aa//37%//P28160  
 C-NT2RM4001828//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//5.9E-161//481aa//56%//  
 P51523  
 C-NT2RM4001836  
 35 C-NT2RM4001841//&quot;Homo sapiens mRNA for KIAA0920 protein, complete cds.&quot;//0//1861bp//98%//  
 AB023137  
 C-NT2RM4001842  
 C-NT2RM4001856  
 C-NT2RM4001858//T-BOX CONTAINING PROTEIN TBX6L (FRAGMENT).//6.5E-22//126aa//46%//P79779  
 40 C-NT2RM4001865//Homo sapiens mRNA for atopy related autoantigen CALC.//4.3E-244//1248bp//94%//Y17711  
 C-NT2RM4001876//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1).//6.5E-23//184aa//  
 36%//Q15404  
 C-NT2RM4001880//PUTATIVE DNA HELICASE II HOMOLOG (EC 3.6.1.-).//5.9E-09//268aa//26%//P47486  
 C-NT2RM4001922//&quot;Homo-sapiens mRNA for KIAA0957 protein, complete cds.&quot;//0//2165bp//99%//  
 45 AB023174  
 C-NT2RM4001930//&quot;Homo sapiens dolichyl-P-Glc:Man9GlcNAc2-PP-dolichyl glucosyltransferase (ALG6)  
 mRNA, complete cds.&quot;//0//1930bp//99%//AF102851  
 C-NT2RM4001940//&quot;Homo sapiens timeless homolog mRNA, complete cds.&quot;//0//2087bp//99%//  
 AF098162  
 50 C-NT2RM4001953  
 C-NT2RM4001965  
 C-NT2RM4001969//R.norvegicus mRNA for IP63 protein.//2.6E-261//1563bp//84%//X99330  
 C-NT2RM4001979//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.8E-112//457aa//47%//  
 P51523  
 55 C-NT2RM4001984  
 C-NT2RM4001987//&quot;NEURAL CELL ADHESION MOLECULE 1, LARGE ISOFORM PRECURSOR (N-CAM  
 180) [CONTAINS: N-CAM 140].&quot;//3.2E-17//281aa//30%//P16170  
 C-NT2RM4002013//HYPOTHETICAL 89.4 KD TRP-ASP REPEATS CONTAINING PROTEIN IN PMT6-PCT1

INTERGENIC REGION.//6.9E-94//589aa//35%//P42935  
 C-NT2RM4002018  
 C-NT2RM4002034//&quot;Homo sapiens hiwi mRNA, partial cds.&quot;//1.9E-53//1585bp//60%//AF104260  
 C-NT2RM4002044  
 5 C-NT2RM4002054  
 C-NT2RM4002063//&quot;Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, complete cds.&quot;//0//1865bp//99%//U82267  
 C-NT2RM4002066//&quot;Homo sapiens thyroid hormone receptor-associated protein complex component TRAP230 mRNA, complete cds.&quot;//1.50E-211//1123bp//71%//AF117755  
 10 C-NT2RM4002075//RING CANAL PROTEIN (KELCH PROTEIN).//2.8E-105//556aa//41%//Q04652  
 C-NT2RM4002128  
 C-NT2RM4002140  
 C-NT2RM4002145//SLIT PROTEIN PRECURSOR.//1.40E-09//127aa//33%//P24014  
 C-NT2RM4002161//&quot;Homo sapiens laforin (EPM2A) mRNA, complete cds.&quot;//0//2671bp//99%//  
 15 AF084535  
 C-NT2RM4002174//MRP PROTEIN.//9.1E-68//264aa//51%//P21590  
 C-NT2RM4002189//&quot;GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLU-  
 COSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).&quot;//6.2E-33//688aa//27%//P08640  
 C-NT2RM4002205//&quot;ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G).&quot;//3E-  
 20 37//122aa//72%//Q07803  
 C-NT2RM4002213//&quot;Homo sapiens protein phosphatase methylesterase-1 (PME-1) mRNA, complete cds.  
 &quot;//0//2452bp//100%//AF157028  
 C-NT2RM4002226//GTPASE ACTIVATING PROTEIN ROTUND.//3.7E-19//147aa//41%//P40809  
 C-NT2RM4002251//&quot;ALPHA-1,3-MANNOSYL-GLYCOPROTEIN BETA-1,2-N-ACETYLGLUCOSAMINYL-  
 25 TRANSFERASE (EC 2.4.1.101) (N-GLYCOSYL-OLIGOSACCHARIDE-GLYCOPROTEIN N-ACETYLGLU-  
 COSAMINYLTRANSFERASE I) (GNT-I) (GLCNAC-TI).&quot;//2.2E-36//320aa//38%//P27808  
 C-NT2RM4002256  
 C-NT2RM4002266  
 C-NT2RM4002281  
 30 C-NT2RM4002287  
 C-NT2RM4002294  
 C-NT2RM4002301  
 C-NT2RM4002323//ANTIGEN GOR (FRAGMENT).//0.00000001//154aa//33 %//P48778.  
 C-NT2RM4002339  
 35 C-NT2RM4002344  
 C-NT2RM4002373//&quot;Homo sapiens mRNA for KIAA0649 protein, complete cds.&quot;//0//2666bp//99%//  
 AB014549  
 C-NT2RM4002374  
 C-NT2RM4002383  
 40 C-NT2RM4002409//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE-COA LIGASE) (ACYL- AC-  
 TIVATING ENZYME).//1.3E-29//275aa//30%//P27095  
 C-NT2RM4002438//&quot;Xenopus laevis putative Zic3 binding protein mRNA, complete cds.&quot;//1.1E-49//  
 611bp//70%//AF129131  
 C-NT2RM4002446  
 45 C-NT2RM4002452  
 C-NT2RM4002457  
 C-NT2RM4002460//&quot;ENV POLYPOLYPEPTIDE (COAT POLYPOLYPEPTIDE) [CONTAINS: COAT PROTEINS GP70,  
 GP20].&quot;//0.0000016//226aa//24%//P51515  
 C-NT2RM4002493  
 50 C-NT2RM4002527//VEGETABLE INCOMPATIBILITY PROTEIN HET-E-1.//8.9E-15//366aa//27%//Q00808  
 C-NT2RM4002532//PROTEIN HOM1.//2E-16//276aa//28%//P55137  
 C-NT2RM4002558//&quot;Homo sapiens fatty acid transport protein (FATP) mRNA, complete cds.&quot;//0//  
 1797bp//99%//AF055899  
 C-NT2RM4002567  
 55 C-NT2RM4002593  
 C-NT2RM4002594//MSP1 PROTEIN HOMOLOG.//2.7E-68//236aa//58%//P54815  
 C-NT2RM4002623//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE-TRNA LIGASE) (ASPRS).//  
 2.3E-101//488aa//45%//032038

C-NT2RP1000324  
 C-NT2RP1000363//&quot;Homo sapiens mRNA for KIAA0638 protein, partial cds.&quot;//0//1345bp//99%//  
 AB014538  
 5 C-NT2RP1000418  
 C-NT2RP1000513//&quot;Human NifU-like protein (hNifU) mRNA, partial cds.&quot;//6.50E-171//516bp//99%//  
 U47101  
 C-NT2RP1000721  
 C-NT2RP1000730  
 C-NT2RP1000767  
 10 C-NT2RP1000836  
 C-NT2RP1000902//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOME III//5.2E-20//306aa//  
 33%//Q09531  
 C-NT2RP1000943  
 C-NT2RP1001033//&quot;Homo sapiens delta-tubulin mRNA, complete cds.&quot;//2.10E-285//1290bp//100%//  
 15 AF201333  
 C-NT2RP1001073//&quot;Homo sapiens U6 snRNA-associated Sm-like protein LSm5 mRNA, complete cds.  
 &quot;//8.1E-107//504bp//99%//AF182291  
 C-NT2RP1001199  
 C-NT2RP1001248  
 20 C-NT2RP1001253//&quot;Homo sapiens oscillin (hLn) mRNA, complete cds.&quot;//0//2020bp//99%//AF029914  
 C-NT2RP1001286  
 C-NT2RP1001294//MICROTUBULE-ASSOCIATED PROTEIN YTM1//1.80E-38//258aa//32%//Q12024  
 C-NT2RP1001302//MICROTUBULE-ASSOCIATED PROTEIN YTM1//1.80E-38//258aa//32%//Q12024  
 C-NT2RP1001310//&quot;Homo sapiens mitochondrial carrier homolog 1 isoform a mRNA, partial cds; nuclear  
 25 gene for mitochondrial product.&quot;//0//1732bp//99%//AF176006  
 C-NT2RP1001361//&quot;Homo sapiens NADH-ubiquinone oxidoreductase subunit B14.5B homolog mRNA,  
 complete cds.&quot;//6.5E-116//541bp//100%//AF070652  
 C-NT2RP1001385//HYPOTHETICAL 48.8 KD PROTEIN IN SSU81-SCS2 INTERGENIC REGION//2.7E-22//  
 284aa//25%//P40074  
 30 C-NT2RP1001432  
 C-NT2RP2000040//&quot;Homo sapiens mRNA for KIAA0747 protein, partial cds.&quot;//0//2648bp//99%//  
 AB013290  
 C-NT2RP2000076//Homo sapiens partial mRNA for polyhomeotic 2 protein (PH2 gene)//7.9E-20//265bp//73%//  
 AJ242730  
 35 C-NT2RP2000098  
 C-NT2RP2000108  
 C-NT2RP2000257//PUTATIVE MITOCHONDRIAL CARRIER YIL006W//9.7E-41//278aa//36%//P40556  
 C-NT2RP2000258//ACTIVATOR 1 140 KD SUBUNIT (REPLICATION FACTOR C LARGE SUBUNIT) (A1 140 KD  
 40 SUBUNIT) (RF-C 140 KD SUBUNIT) (ACTIVATOR 1 LARGE SUBUNIT) (DNA-BINDING PROTEIN PO-GA).//  
 7.1E-12//213aa//23%//P35251  
 C-NT2RP2000289  
 C-NT2RP2000327  
 C-NT2RP2000337  
 C-NT2RP2000420//ZINC FINGER PROTEIN 165//8.5E-33//155aa//52%//P49910  
 45 C-NT2RP2000459  
 C-NT2RP2000498  
 C-NT2RP2000758  
 C-NT2RP2001137  
 C-NT2RP2001149  
 50 C-NT2RP2001168//VERPROLIN//1.5E-09//143aa//33%//P37370  
 C-NT2RP2001173//&quot;Homo sapiens mRNA for KIAA0480 protein, complete cds.&quot;//0//1780bp//99%//  
 AB007949  
 C-NT2RP2001174//GASTRULA ZINC FINGER PROTEIN XLCGF46.1 (FRAGMENT).//6E-10//88aa//38%//  
 P18722  
 55 C-NT2RP2001196  
 C-NT2RP2001226  
 C-NT2RP2001268//&quot;Homo sapiens mRNA for KIAA0810 protein, partial cds.&quot;//0//3301bp//98%//  
 AB018353

C-NT2RP2001290//BETA-SOLUBLE NSF ATTACHMENT PROTEIN (SNAP-BETA) (SNAP-ALPHA HOMOLOG)  
 (BRAIN PROTEIN 147) (FRAGMENT).//4.4E-91//179aa//99%//P28663  
 C-NT2RP2001295//ZINC/CADMIUM RESISTANCE PROTEIN.//8.3E-39//161aa//34%//P20107  
 C-NT2RP2001312  
 5 C-NT2RP2001327//&quot;TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12  
 PROTEIN).&quot;//5.5E-116//311aa//71%//Q13829  
 C-NT2RP2001328  
 C-NT2RP2001366  
 C-NT2RP2001378//MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).//2E-11//403aa//25%//Q02817  
 10 C-NT2RP2001392//MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR (EC 3.4.21.-).//8.4E-192//  
 581aa//54%//P93647  
 C-NT2RP2001394//Homo sapiens mRNA for SCML2 protein.//0//2068bp//99%//Y18004  
 C-NT2RP2001420//&quot;Mus musculus nuclear protein NIP45 mRNA, complete cds.&quot;//9E-112//742bp//  
 82%//U76759  
 15 C-NT2RP2001450  
 C-NT2RP2001467  
 C-NT2RP2001506  
 C-NT2RP2001511//&quot;Homo sapiens putative RNA-binding protein Q99 mRNA, complete cds.&quot;//3.2E-  
 297//2206bp//75 %//AF093097  
 20 C-NT2RP2001520//Homo sapiens mRNA for mitochondrial carrier protein ARALAR1.//0//2502bp//99%//Y14494  
 C-NT2RP2001536//&quot;Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete  
 cds.&quot;//0//2326bp//99%//AF035586  
 C-NT2RP2001560//VAV2 PROTEIN.//0.00000015//219aa//27%//Q60992  
 C-NT2RP2001576//HYPOTHETICAL 62.2 KD PROTEIN C4G8.12C IN CHROMOSOME 1.//8.2E-29//294aa/  
 25 31%//Q09837  
 C-NT2RP2001581  
 C-NT2RP2001597//&quot;RYANODINE RECEPTOR, CARDIAC MUSCLE.&quot;//0.000000036//127aa//36%//  
 P30957  
 C-NT2RP2001628  
 30 C-NT2RP2001663//ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-  
 GLYCERATE HYDRO-LYASE) (FRAGMENT).//1.1E-47//126aa//53%//P42897  
 C-NT2RP2001748//FARNESYL PYROPHOSPHATE SYNTHETASE (FPP SYNTHETASE) (FPS) (FARNESYL DI-  
 PHOSPHATE SYNTHETASE) (DIMETHYLALLYLTRANSFERASE (EC 2.5.1.1) / GERANYLTRANSTRANS-  
 FERASE (EC 2.5.1.10)) (KIAA0032).//5.40E-47//96aa//97%//P14324  
 35 C-NT2RP2001813  
 C-NT2RP2001883//&quot;Homo sapiens CGI-01 protein mRNA, complete cds.&quot;//0//2306bp//99%//  
 AF132936  
 C-NT2RP2001900//ACTIN-LIKE PROTEIN ARP5.//2.3E-38//395aa//30%//P53946  
 C-NT2RP2001947  
 40 C-NT2RP2001985//&quot;Homo sapiens high-risk human papilloma viruses E6 oncoproteins targeted protein  
 E6TP1 alpha mRNA, complete cds.&quot;//2.00E-38//435bp//67%//AF090989  
 C-NT2RP2001991//SODIUM- AND CHLORIDE-DEPENDENT TRANSPORTER NTT73.//6.5E-129//279aa//85%//  
 Q08469  
 C-NT2RP2002025//NG-CAM RELATED CELL ADHESION MOLECULE PRECURSOR (NR-CAM) (BRAVO).//  
 45 1.7E-47//247aa//52%//P35331  
 C-NT2RP2002058//&quot;Homo sapiens WD repeat protein WDR3 (WDR3) mRNA, complete cds.&quot;//0//  
 2510bp//99%//AF083217  
 C-NT2RP2002076//Homo sapiens clone 24804 mRNA sequence.7/1.5E-294//1334bp//99%//AF052183  
 C-NT2RP2002078//PECANEX PROTEIN.//1.8E-09//195aa//32%//P18490  
 50 C-NT2RP2002079//&quot;HISTONE H1, GONADAL.&quot;//4.4E-11//214aa//34%//P02256  
 C-NT2RP2002099//Homo sapiens mRNA for E1B-55kDa-associated protein.//0//3389bp//99%//AJ007509  
 C-NT2RP2002185//&quot;Homo sapiens ubiquilin mRNA, complete cds.&quot;//0//1789bp//99%//AF176069  
 C-NT2RP2002193//&quot;Homo sapiens PIAS3 mRNA for protein inhibitor of activated STAT3, complete cds.  
 &quot;//0//2809bp//99%//AB021868  
 55 C-NT2RP2002231  
 C-NT2RP2002235  
 C-NT2RP2002252//&quot;Mus musculus (clone pVzmSin3A9) mSin3A9 mRNA, complete cds.&quot;//0//3118bp//  
 91%//L38621

C-NT2RP2002292  
 C-NT2RP2002408  
 C-NT2RP2002442//HESA PROTEIN./.2.8E-14//163aa//30%//P46037  
 C-NT2RP2002464//DNA CROSS-LINK REPAIR PROTEIN PS02/SNM1./.6.50E-07//171aa//27%//P30620  
 5 C-NT2RP2002498  
 C-NT2RP2002503//ZINC FINGER PROTEIN 45 (BRC1744).//4.6E-144//537aa//49%//Q02386  
 C-NT2RP2002520//&quot;Homo sapiens transcription factor RFX-B (RFXB) mRNA, complete cds.&quot;//3.70E-34//668bp//61%//AF105427  
 C-NT2RP2002549  
 10 C-NT2RP2002609//2-HYDROXYMUCONIC SEMIALDEHYDE HYDROLASE (EC 3.1.1.-) (HMSH).//2.80E-08//109aa//37%//P19076  
 C-NT2RP2002706  
 C-NT2RP2002710//SH3-BINDING PROTEIN 3BP-1./.4.9E-85//489aa//43%//P55194  
 C-NT2RP2002800  
 15 C-NT2RP2002880//GLUCOSE REPRESSION MEDIATOR PROTEIN./.0.000039//206aa//23%//P14922  
 C-NT2RP2002891  
 C-NT2RP2002929//HYPOTHETICAL 46.2 KD TRP-ASP REPEATS CONTAINING PROTEIN D2013.2 IN CHROMOSOME II./.4.1E-87//395aa//40%//Q18964  
 C-NT2RP2002939//ZINC FINGER PROTEIN 136./.5.4E-70//282aa//42%//P52737  
 20 C-NT2RP2002993//DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135).//0//716aa//91%//P70700  
 C-NT2RP2003034  
 C-NT2RP2003099  
 C-NT2RP2003137//UBIQUITIN./.0.000026//70aa//30%//P13117  
 25 C-NT2RP2003157//&quot;Homo sapiens CGI-74 protein mRNA, complete cds.&quot;//0//2037bp//99%//AF151832  
 C-NT2RP2003158//&quot;Homo sapiens mRNA for proteasome subunit p58, complete cds.&quot;//0//2091bp//99%//D67025  
 C-NT2RP2003165  
 30 C-NT2RP2003243//Homo sapiens partial mRNA for putative p621 protein which interacts with transcription factor Sp1./.0//1544bp//99%//AJ242978  
 C-NT2RP2003277//&quot;Homo sapiens mRNA for KIAA0625 protein, partial cds.&quot;//0//3788bp//99%//AB014525  
 C-NT2RP2003286//PROBABLE RNA 3'-TERMINAL PHOSPHATE CYCLASE (EC 6.5.1.4) (RNA-3'-PHOSPHATE CYCLASE) (RNA CYCLASE).//4.1E-88//374aa//47%//Q23400  
 35 C-NT2RP2003297  
 C-NT2RP2003307//KINESIN LIGHT CHAIN (KLC).//2.2E-199//550aa//70%//Q07866  
 C-NT2RP2003308//CROOKED NECK PROTEIN./.5.4E-244//622aa//67%//P17886  
 C-NT2RP2003347//BREAST CANCER TYPE 1 SUSCEPTIBILITY PROTEIN HOMOLOG./.0.000022//261aa//24%//P48754  
 40 C-NT2RP2003391//Homo sapiens mRNA for nuclear transport receptor./.0//1509bp//99%//AJ133769  
 C-NT2RP2003393  
 C-NT2RP2003445  
 C-NT2RP2003466//&quot;Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds.&quot;/7//2194bp//99%//AF126799  
 45 C-NT2RP2003480//&quot;Homo sapiens zinc finger DNA binding protein 99 (ZNF281) mRNA, complete cds.&quot;//0//3012bp//99%//AF125158  
 C-NT2RP2003506//NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR).//5.4E-14//106aa//46%//P04175  
 50 C-NT2RP2003511  
 C-NT2RP2003513//&quot;Human mRNA for KIAA0270 gene, partial cds.&quot;//0//2137bp//97%//D87460  
 C-NT2RP2003567//&quot;Homo sapiens mRNA for KIAA0462 protein, partial cds.&quot;//0//2343bp//99%//AB007931  
 55 C-NT2RP2003604//&quot;Homo sapiens alpha-catenin-like protein (CTNNAL1) mRNA, complete cds.&quot;//0//2442bp//99%//AF030233  
 C-NT2RP2003691  
 C-NT2RP2003713//&quot;Homo sapiens ubiquitin-specific protease 3 (USP3) mRNA, complete cds.&quot;//0//2018bp//99%//AF073344

C-NT2RP2003760//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP).//0//869aa//  
 80%//P53620  
 C-NT2RP2003764  
 C-NT2RP2003769  
 5 C-NT2RP2003777  
 C-NT2RP2003840//HYPOTHETICAL 48.1 KD PROTEIN B0403.2 IN CHROMOSOME X.//3.7E-21//137aa//43%//  
 Q11076  
 C-NT2RP2003857//MYOTROPHIN (V-1 PROTEIN) (GRANULE CELL DIFFERENTIATION PROTEIN).//  
 10 0.0000016//117aa//29%//Q91955  
 C-NT2RP2003981//"Homo sapiens mRNA for KIAA0804 protein, partial cds."//0//3046bp//99%//  
 AB018347  
 C-NT2RP2003984//Homo sapiens mRNA; cDNA DKFZp564A026 (from clone DKFZp564A026).//0//2514bp//  
 99%//AL050367  
 C-NT2RP2004041//SYNAPSINS IA AND IB.//0.00000074//159aa//32%//P17599  
 15 C-NT2RP2004066//"Human DNA sequence from clone 134019 on chromosome 1p36.11-36.33, complete  
 sequence."//0//2410bp//99%//AL034555  
 C-NT2RP2004081  
 C-NT2RP2004124  
 C-NT2RP2004152  
 20 C-NT2RP2004165  
 C-NT2RP2004187//ZINC FINGER PROTEIN 38 (ZFP-38) (CTFIN51) (TRANSCRIPTION FACTOR RU49).//5.6E-  
 31//424aa//28%//007231  
 C-NT2RP2004239//"Homo sapiens Iok mRNA for protein kinase, complete cds."//0//3044bp//99%//  
 AB015718  
 25 C-NT2RP2004245  
 C-NT2RP2004364  
 C-NT2RP2004365  
 C-NT2RP2004366//"Homo sapiens mRNA for KIAA0986 protein, partial cds."//0//2790bp//97%//  
 AB023203  
 30 C-NT2RP2004373  
 C-NT2RP2004476//"Homo sapiens cyclin L ania-6a mRNA, complete cds."//0//2075bp//99%//  
 AF180920  
 C-NT2RP2004551  
 C-NT2RP2004568//PUTATIVE ATP-DEPENDENT RNA HELICASE C30D11.03.//3E-117//625aa//40%//Q09903  
 35 C-NT2RP2004600  
 C-NT2RP2004664//"Homo sapiens mRNA for KIAA0460 protein, partial cds."//0//2368bp//99%//  
 AB007929  
 C-NT2RP2004743  
 C-NT2RP2004768//SERINE/THREONINE-PROTEIN KINASE NRK1 (EC 2.7.1.-) (N-RICH KINASE 1).//1.3E-26//  
 40 190aa//41-%//P38692  
 C-NT2RP2004816//"Homo sapiens H beta 58 homolog mRNA, complete cds."//0//2144bp//96%//  
 AF054179  
 C-NT2RP2004861  
 C-NT2RP2004897  
 45 C-NT2RP2004933//"Homo sapiens mRNA for ZIP-kinase, complete cds."//0//2103bp//99%//AB007144  
 C-NT2RP2004978//ACTIN-LIKE PROTEIN ARP8.//3.3E-47//353aa//30%//Q12386  
 C-NT2RP2005038//DNA NUCLEOTIDYLEXOTRANSFERASE (EC 2.7.7.31) (TERMINAL ADDITION ENZYME)  
 (TERMINAL DEOXYNUCLEOTIDYLTRANSFERASE) (TERMINAL TRANSFERASE).//4E-91//218aa//44%//  
 Q92089  
 50 C-NT2RP2005162//"Homo sapiens aspartyl aminopeptidase mRNA, complete cds."//0//1615bp//99%//  
 AF005050  
 C-NT2RP2005204//"Homo sapiens SUMO-1-activating enzyme E1 N subunit (SUA1) mRNA, complete cds.  
 &quot;//0//1262bp//99%//AF090385  
 C-NT2RP2005227  
 55 C-NT2RP2005287  
 C-NT2RP2005288//"Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds."//0//  
 2992bp//99%//AF060219  
 C-NT2RP2005490//"Mus musculus D3Mm3e (D3Mm3e) mRNA, complete cds."//1.8E-175//1102bp//

83%//AF053628  
 C-NT2RP2005539//&quot;Homo sapiens mRNA for KIAA0850 protein, complete cds.&quot;//0//1560bp//99%//  
 AB020657  
 5 C-NT2RP2005605//QUEUINE TRNA-RIBOSYLTRANSFERASE (EC 2.4.2.29) (TRNA-GUANINE TRANSGLYC-  
 OSYLASE) (GUANINE INSERTION ENZYME).//8.2E-23//164aa//28%//032053  
 C-NT2RP2005722//&quot;Homo sapiens ZK1 mRNA for Kruppel-type zinc finger protein, complete cds.&quot;//  
 0//2545bp//99%//AB011414  
 C-NT2RP2005732  
 10 C-NT2RP2005784//&quot;Homo sapiens ubiquitin-conjugating enzyme variant Kua (UBE2V) mRNA, complete  
 cds.&quot;//0//2191bp//92%//AF155120  
 C-NT2RP2005812//HYPOTHETICAL 39.3 KD PROTEIN IN GCN4-WBP1 INTERGENIC REGION.//2.3E-39//  
 318aa//31%//P40004  
 C-NT2RP2005859//&quot;Homo sapiens mRNA for KIAA0863 protein, complete cds.&quot;//0//1649bp//99%//  
 AB020670  
 15 C-NT2RP2006023  
 C-NT2RP2006334//Homo sapiens mRNA; cDNA DKFZp434J154 (from clone DKFZp434J154).//0//2318bp//99%//  
 AL080155  
 C-NT2RP2006441  
 C-NT2RP3000002  
 20 C-NT2RP3000050//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.2E-150//490aa//  
 53%//Q05481  
 C-NT2RP3000055  
 C-NT2RP3000068  
 C-NT2RP3000080  
 25 C-NT2RP3000085//ACETYL-/PROPYONYL-COENZYME A CARBOXYLASE ALPHA CHAIN [CONTAINS: BIOTIN  
 CARBOXYLASE (EC 6.3.4.14); BIOTIN CARBOXYL CARRIER PROTEIN (BCCP)].//1.9E-123//436aa//50%//  
 P46401  
 C-NT2RP3000092  
 C-NT2RP3000109//P54 PROTEIN PRECURSOR.//0.0000065//358aa//22%//P13692  
 30 C-NT2RP3000134  
 C-NT2RP3000149  
 C-NT2RP3000197  
 C-NT2RP3000207//&quot;GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLU-  
 COSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).&quot;//2.9E-11//721aa//23%//P08640  
 35 C-NT2RP3000233//&quot;Human DNA sequence from clone 22D12 on chromosome Xq21.1-21.33. Contains a  
 novel protein similar to Drosophila Kelch (Ring Canal protein, KEL) and a heterogenous set of other types of  
 proteins. Contains ESTs and GSSs, complete sequence.&quot;//0//1462bp//99%//AL035424  
 C-NT2RP3000235  
 C-NT2RP3000247  
 40 C-NT2RP3000267  
 C-NT2RP3000299//&quot;Rattus norvegicus mRNA for Crk-associated substrate, p130, complete cds.&quot;//0//  
 2730bp//82%//D29766  
 C-NT2RP3000324  
 C-NT2RP3000341//&quot;Homo sapiens mitochondrial inner membrane preprotein translocase Tim17a mRNA,  
 45 nuclear gene encoding mitochondrial protein, complete cds.&quot;//1.5E-246//1124bp//99%//AF106622  
 C-NT2RP3000393//&quot;Rattus norvegicus DNA-binding protein PREB (Preb) mRNA, complete cds.&quot;//  
 5.8E-266//1373bp//86%//AF061817  
 C-NT2RP3000441//&quot;Homo sapiens squamous cell carcinoma antigen recognized by T cell (SART-2) mRNA,  
 complete cds.&quot;//3.40E-42//645bp//67%//AF098066  
 50 C-NT2RP3000449  
 C-NT2RP3000451  
 C-NT2RP3000456  
 C-NT2RP3000542  
 C-NT2RP3000561  
 55 C-NT2RP3000562//&quot;Homo sapiens putative RNA-binding protein Q99 mRNA, complete cds.&quot;//0//  
 2165bp//99%//AF093097  
 C-NT2RP3000578//HES1 PROTEIN.//1-3E-22//229aa//27%//P35843  
 C-NT2RP3000590//UVS-2 PROTEIN.//1.3E-22//458aa//24%//P33288

C-NT2RP3000592  
 C-NT2RP3000622  
 C-NT2RP3000624  
 C-NT2RP3000685  
 5 C-NT2RP3000736//HYPOTHETICAL PROTEIN KIAA0140//1.2E-166//305aa//99%//014153  
 C-NT2RP3000742//&quot;1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA  
 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III) (FRAGMENT).&quot;//4.1E-165//  
 371aa//49%//P10895  
 C-NT2RP3000753  
 10 C-NT2RP3000826  
 C-NT2RP3000865  
 C-NT2RP3000875//MEVALONATE KINASE (EC 2.7.1.36) (MK).//7.7E-87//175aa//98%//Q03426  
 C-NT2RP3001007  
 C-NT2RP3001055  
 15 C-NT2RP300111//&quot;Homo sapiens TRF-proximal protein mRNA, complete cds.&quot;//1.50E-149//731bp//  
 97%//AF097725  
 C-NT2RP3001120//ZINC FINGER PROTEIN 136//7.8E-170//512aa//58%//P52737  
 C-NT2RP3001126  
 C-NT2RP3001150//TRANSCRIPTION TERMINATION FACTOR RHO//0.00000031//207aa//29%//P52154  
 20 C-NT2RP3001232  
 C-NT2RP3001268//&quot;Homo sapiens zinc finger protein ZNF228 (ZNF228) mRNA, complete cds.&quot;//0//  
 3606bp//99%//AF198358  
 C-NT2RP3001272//Mus musculus mRNA for macrophage actin-associated-tyrosine-phosphorylated protein//  
 1.3E-99//669bp//83%//Y18101  
 25 C-NT2RP3001274//&quot;Homo sapiens mRNA for KIAA1037 protein, partial cds.&quot;//0//2254bp//99%//  
 AB028960  
 C-NT2RP3001281  
 C-NT2RP3001297  
 C-NT2RP3001318  
 30 C-NT2RP3001338//ZINC FINGER PROTEIN 81 (FRAGMENT).//2.4E-16//175aa//28%//P51508  
 C-NT2RP3001355//TRICARBOXYLATE TRANSPORT PROTEIN PRECURSOR (CITRATE TRANSPORT PRO-  
 TEIN) (CTP) (TRICARBOXYLATE CARRIER PROTEIN).//3.6E-25//129aa//34%//P32089  
 C-NT2RP3001374  
 35 C-NT2RP3001428//NUCLEOPROTEIN TPR.//1.4E-128//152aa//99%//P12270  
 C-NT2RP3001432  
 C-NT2RP3001447  
 C-NT2RP3001449//&quot;Human DNA sequence from clone 283E3 on chromosome 1p36.21-36.33. Contains the  
 alternatively spliced gene for Matrix Metalloproteinase in the Female Reproductive tract MIFR1, -2, MMP21/22A,  
 40 -B and -C, a novel gene, the alternatively spliced CDC2L2 gene for Cell Division Cycle 2-Like 2 (PITSRE, p58/GTA,  
 Galactosyltransferase Associated Protein Kinase) beta 1, beta 2-1, beta 2-2 and alpha 2-4, a 40S Ribosomal  
 Protein S7 pseudogene, part of the KIAA0447 gene, a novel alternatively spliced gene similar to many (archae)  
 bacterial, worm and yeast hypothetical genes, and the GNB1 gene for Guanine Nucleotide Binding Protein (G  
 protein), Beta polypeptide 1 (Transducin Beta chain 1). Contains putative CpG islands, ESTs, STSs and GSSs,  
 complete sequence.&quot;//0//1827bp//99%//AL031282  
 45 C-NT2RP3001453//ANTIGEN PEPTIDE TRANSPORTER 2 (APT2) (HISTOCOMPATIBILITY ANTIGEN MODIFI-  
 ER 2).//3.2E-90//157aa//59%//P36371  
 C-NT2RP3001459  
 C-NT2RP3001527//&quot;Human Spl40 protein (Spl40) mRNA, complete cds.&quot;//4.3E-290//793bp//93%//  
 U63420  
 50 C-NT2RP3001538//HYPOTHETICAL 39.0 KD PROTEIN T2.8D9.3 IN CHROMOSOME II//9.10E-10//158aa//  
 31%//Q10022  
 C-NT2RP3001580//&quot;Mus musculus strain C57BL/J germ cell-less protein (Gcl) mRNA, complete cds.&quot;  
 //0//1730bp//85%//AF163665  
 55 C-NT2RP3001587//&quot;Human anthracycline-associated resistance ARX mRNA, complete cds.&quot;//0//  
 2617bp//99%//U35832  
 C-NT2RP3001589  
 C-NT2RP3001607  
 C-NT2RP3001608

C-NT2RP3001671//"Homo sapiens mRNA for KIAA0850 protein, complete cds.";//0//2310bp//99%//  
AB020657

C-NT2RP3001672//"Homo sapiens Sex comb on midleg homolog 1 isoform 2 (SCMH1) mRNA, complete  
cds.";//0//2836bp//99%//AF149046

5 C-NT2RP3001678  
C-NT2RP3001688//"Homo sapiens glucocorticoid modulatory element binding protein-1 (GMEB1) mRNA,  
complete cds.";//0//1695bp//99%//AF099013

C-NT2RP3001690//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1//0.00000024//481aa//21%//  
P25386

10 C-NT2RP3001698  
C-NT2RP3001708//TWISTED GASTRULATION PROTEIN PRECURSOR//3.4E-33//161aa//32%//P54356

C-NT2RP3001716  
C-NT2RP3001752  
C-NT2RP3001792//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN M (HNRNP M)//1.8E-117//462aa//  
15 55%//P52272

C-NT2RP3001844  
C-NT2RP3001854//Homo sapiens mRNA; cDNA DKFZp564G013 (from clone DKFZp564G013).//0//1528bp//  
99%//AL050011

C-NT2RP3001855//HOMEobox PROTEIN PKNOX1 (HOMEobox PROTEIN PREP-1)//8.1E-125//302aa//  
20 60%//P55347

C-NT2RP3001898//"Homo sapiens mRNA for UDP-N-acetylglucosamine: alpha-1,3-D-mannoside beta-  
1,4-N-acetylglucosaminyltransferase IV, complete cds.";//0//1587bp//100%//AB000624

C-NT2RP3001931  
C-NT2RP3001969//TRICHOHYALIN//2.7E-11//442aa//23%//P37709

25 C-NT2RP3002002  
C-NT2RP3002004//H.sapiens mRNA for FAST kinase//1.50E-19211475bp//94%//X86779

C-NT2RP3002007//SAP1 PROTEIN//1.1E-68//474aa//32%//P39955

C-NT2RP3002014//HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III//5.30E-25//139aa//  
48%//Q09232

30 C-NT2RP3002045//"Homo sapiens mRNA for KIAA0899 protein, partial cds.";//0//33 85bp//99%//  
AB020706

C-NT2RP3002056//"Homo sapiens Rb binding protein homolog mRNA, partial cds.";//0//2374bp//99%//  
AF083249

C-NT2RP3002062//"Homo sapiens mRNA for KIAA0873 protein, partial cds.";//0//3764bp//99%//  
35 AB020680

C-NT2RP3002081//"Xenopus laevis chromosome condensation protein XCAP-G mRNA, complete cds.  
&quot;;//4.1E-233//1896bp//69%//AF111423

C-NT2RP3002097  
C-NT2RP3002108//DEC1 PROTEIN (MDM20 PROTEIN)//7.90E-09//181aa//22%//Q12387

40 C-NT2RP3002142  
C-NT2RP3002146  
C-NT2RP3002151//G1 TO S PHASE TRANSITION PROTEIN 1 HOMOLOG (GTP-BINDING PROTEIN  
GST1-HS)//2.8E-253//474aa//93%//P15170

C-NT2RP3002165//TRANSCRIPTIONAL REGULATOR PROTEIN HCNGP7//1.9E-151//223aa//91%//Q02614

45 C-NT2RP3002166  
C-NT2RP3002181  
C-NT2RP3002244  
C-NT2RP3002248  
C-NT2RP3002273//SCD6 PROTEIN//1.30E-09//295aa//28%//P45978

50 C-NT2RP3002276  
C-NT2RP3002304  
C-NT2RP3002501//THREONINE DEHYDRATASE CATABOLIC (EC 4.2.1.16) (THREONINE DEAMINASE)//  
3.70E-43//318aa//37%//P05792

C-NT2RP3002529//Homo sapiens mRNA for leucocyte vacuolar protein sorting//0//2276bp//99%//AJ133421

55 C-NT2RP3002566  
C-NT2RP3002587  
C-NT2RP3002590  
C-NT2RP3002631

C-NT2RP3002650//&quot;Mus musculus growth suppressor 1L (Gros1) mRNA, complete cds.&quot;//0//2109bp//87%//AF165163  
 C-NT2RP3002663//&quot;Homo sapiens putative glycolipid transfer protein mRNA, complete cds.&quot;//8.10E-263//1243bp//97%//AF103731  
 5 C-NT2RP3002671//ELONGATION FACTOR 2 (EF-2).//2.50E-73//179aa//36%//P13060  
 C-NT2RP3002763  
 C-NT2RP3002861  
 C-NT2RP3002911  
 C-NT2RP3002948//RING CANAL PROTEIN (KELCH PROTEIN).//2E-111//551aa//42%//Q04652  
 10 C-NT2RP3002953//&quot;Homo sapiens protocadherin beta 5 (PCDH-beta5) mRNA, complete cds.&quot;//0//2388bp//99%//AF152498  
 C-NT2RP3002988//&quot;Homo sapiens I<sub>k</sub>B kinase-b (IKK-beta) mRNA, complete cds.&quot;//1.8E-292//1325bp//99%//AF080158  
 C-NT2RP3003008  
 15 C-NT2RP3003101//&quot;Mouse mRNA for tetracycline transporter-like protein, complete cds.&quot;//3.6E-83//807bp//72%//D88315  
 C-NT2RP3003204  
 C-NT2RP3003278  
 C-NT2RP3003282//&quot;Homo sapiens dynamin (DNM) mRNA, complete cds.&quot;//0//2596bp//98%//L36983  
 20 C-NT2RP3003290//&quot;Mus musculus mRNA for Ndr1 related protein Ndr3, complete cds.&quot;//1.5e-310//1468bp//82%//AB033922  
 C-NT2RP3003302  
 C-NT2RP3003313//&quot;Homo sapiens thyroid hormone receptor-associated protein complex component TRAP80 mRNA, complete cds.&quot;//0//2476bp//99%//AF117657  
 25 C-NT2RP3003327//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)) (R052).//1.3E-35//178aa//44%//Q62191  
 C-NT2RP3003344  
 C-NT2RP3003353//HYPOTHETICAL 26.2 KD PROTEIN IN GDI1-COX15 INTERGENIC REGION.//2.80E-07//161aa//28%//P40084  
 30 C-NT2RP3003377  
 C-NT2RP3003385//&quot;Mus musculus SKD3 mRNA, complete cds.&quot;//0//2133bp//85%//U09874  
 C-NT2RP3003433  
 C-NT2RP3003490//&quot;Homo sapiens mRNA for KIAA0725 protein, partial cds.&quot;//0//2437bp//99%//AB018268  
 35 C-NT2RP3003491//&quot;Drosophila melanogaster Pelle associated protein Pellino (Pli) mRNA, complete cds.&quot;//5.6E-36//842bp//62%//AF091624  
 C-NT2RP3004206//CROOKED NECK PROTEIN.//1.4E-220//567aa//67%//P17886  
 C-NT2RP3004207//Homo sapiens mRNA for type I transmembrane receptor (psk-1 gene).//0//2445bp//100%//AJ245820  
 40 C-NT2RP3004209//&quot;Homo sapiens ubiquitin processing protease (Ubp-M) mRNA, complete cds.&quot;//0//2320bp//99%//AF126736  
 C-NT2RP3004242//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FACTIOGENITAL DYSPLASIA PROTEIN HOMOLOG).//4.7E-13//118aa//33%//P52734  
 C-NT2RP3004246  
 45 C-NT2RP3004258//&quot;Homo sapiens ZIS1 mRNA, complete cds.&quot;//0//1861bp//99%//AF065391  
 C-NT2RP3004262//&quot;Homo sapiens heat shock protein hsp40-3 mRNA, complete cds.&quot;//2.4E-248//1126bp//100%//AF088982  
 C-NT2RP3004341  
 C-NT2RP3004378  
 50 C-NT2RP3004424//Homo sapiens mRNA for stromal antigen 3 (STAG3 gene).//1E-66//364bp//93%//AJ007798  
 C-NT2RP3004428  
 C-NT2RP3004451  
 C-NT2RP3004454//&quot;Homo sapiens mRNA for KIAA0448 protein, complete cds.&quot;//0//2875bp//99%//AB007917  
 55 C-NT2RP3004472//GERM CELL-LESS PROTEIN.//1.6E-61//170aa//40%//Q01820  
 C-NT2RP3004498//&quot;Mus musculus ROSA 26 transcription AS ROSA26AS mRNA, complete cds.&quot;//2E-249//1777bp//80%//U83176  
 C-NT2RP3004504//M.musculus mRNA for CPEB protein.//1.9E-295//893bp//92%//Y08260

C-NT2RP3004507//MOB1 PROTEIN (MPS1 BINDER 1).//3.7E-37//190aa//39%//P40484  
 C-NT2RP3004534//&quot;Mouse oncogene (ect2) mRNA, complete cds.&quot;//0//2075bp//87%//L11316  
 C-NT2RP4000528//NPL4 PROTEIN//9.8E-86//515aa//37%//P33755  
 C-NT2RP4000907//&quot;Mouse NLRR-1 mRNA for leucine-rich-repeat protein, complete cds.&quot;//0//  
 5 2127bp//86%//D45913  
 C-NT2RP4001029//&quot;Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds.&quot;//0//1711bp//  
 90%//U20086  
 C-NT2RP4001336//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN//0.000016//  
 10 186aa//29%//024076  
 C-NT2RP4001389//KES1 PROTEIN//1.70E-31//342aa//34%//P35844  
 C-NT2RP4001442  
 C-NT2RP4001529//&quot;Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds.&quot;/1.70E-255//  
 15 1148bp//90%//U20086  
 C-NT2RP4001656//VACUOLAR BIOGENESIS PROTEIN END1 (PEP5 PROTEIN)//1.10E-45//310aa//27%//  
 P12868  
 C-OVARC1000106//&quot;TROPOMYOSIN 1, FUSION PROTEIN 33.&quot;//0.000032//165aa//27%//P49455  
 C-OVARC1000198  
 C-OVARC1000682//&quot;PROCESSING ALPHA-1,2-MANNOSIDASE (EC 3.2.1.-) (ALPHA-1,2-MANNOSI-  
 20 DASE 1B).&quot;//1.1E-209//293aa//95%//P39098  
 C-OVARC1000703  
 C-OVARC1000722//&quot;Homo sapiens chromosome 1q21-1q23 beta-1,4-galactosyltransferase mRNA, com-  
 plete cds.&quot;//0//759bp//98%//AF038661  
 C-OVARC1000730  
 C-OVARC1000746//MATERNAL EFFECT PROTEIN STAUFEN//0.000000017//78aa//48%//P25159  
 25 C-OVARC1000781  
 C-OVARC1000787  
 C-OVARC10008347//Homo sapiens mRNA for atopy related autoantigen CALCJ/2.8E-258//1183bp//99%//Y17711  
 C-OVARC1000846//NUCLEOLIN (PROTEIN C23).//0.0000097//109aa//30%//P08199  
 C-OVARC1000850//&quot;Homo sapiens PB39 mRNA, complete cds.&quot;//0//2095bp//99%//AF045584  
 30 C-OVARC1000862//M.musculus mRNA for FT1//5.9E-226//1498bp//81%//Z67963  
 C-OVARC1000876//MOB1 PROTEIN (MPS1 BINDER 1).//2.2E-50//206aa//52%//P40484  
 C-OVA-RC1000883  
 C-OVARC1000886  
 C-OVARC1000912  
 35 C-OVARC1000915//&quot;Homo sapiens histone deacetylase 5 mRNA, complete cds.&quot;//1.60E-121//591bp//  
 97%//AF132608  
 C-OVARC1000924  
 C-OVARC1000964  
 C-OVARC1000984  
 40 C-OVARC1001004  
 C-OVARC1001010  
 C-OVARC1001011  
 C-OVARC1001032  
 C-OVARC1001044  
 45 C-OVARC1001055//PRE-B CELL ENHANCING FACTOR PRECURSOR//1.9E-35//76aa//98%//P43490  
 C-OVARC1001068//&quot;Homo sapiens Era GTPase A protein (HERA-A) mRNA, partial cds.&quot;//0//1819bp//  
 99%//AF082657  
 C-OVARC1001074  
 C-OVARC1001092//&quot;Homo sapiens mRNA for JM5 protein, complete CDS (clone IMAGE 53337,  
 50 LLNLc110F185707 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin)).&quot;//2E-214//769bp//97%//  
 AJ005897  
 C-OVARC1001107//&quot;Homo sapiens protein methyltransferase (JBP1) mRNA, complete cds.&quot;//6.1E-  
 276//594bp//98%//AF167572  
 C-OVARC1001154//&quot;Homo sapiens clone 24720 epithelin 1 and 2 mRNA, complete cds.&quot;//2.3E-296//  
 55 1561bp//93%//AF055008  
 C-OVARC1001161  
 C-OVARC1001167  
 C-OVARC1001170

C-OVARC1001171//"Homo sapiens translation initiation factor 3 47 kDa subunit mRNA, complete cds.&quot;;  
 //5.7E-151//436bp//92%//U94855  
 C-OVARC1001173  
 C-OVARC1001176  
 5 C-OVARC1001180//UBIQUITIN-LIKE PROTEIN DSK2//1.1E-11//221aa//25%//P48510  
 C-OVARC1001188  
 C-OVARC1001232//"CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT  
 (CPSF 100 KD SUBUNIT).&quot;//5.10E-22//83aa//37%//Q10568  
 C-OVARC1001270  
 10 C-OVARC1001271//NUCLEOLAR TRANSCRIPTION FACTOR 1 (UPSTREAM BINDING FACTOR 1) (UBF-1).//  
 0.0000014//224aa//26%//P25976  
 C-OVARC1001306//N-MYC PROTO-ONCOGENE PROTEIN//0.00000073//247aa//27%//P18444  
 C-OVARC1001344  
 C-OVARC1001369  
 15 C-OVARC1001372//"Homo sapiens mRNA for KIAA0897 protein, partial cds.&quot;//0//840bp//97%//  
 AB020704  
 C-OVARC1001391  
 C-OVARC1001399  
 C-OVARC1001417//"Homo sapiens thyroid hormone receptor-associated protein complex component  
 20 TRAP170 mRNA, complete cds.&quot;//0//1715bp//99%//AF135802  
 C-OVARC1001419//"Homo sapiens GOK (STIM1) mRNA, complete cds.&quot;//4.9E-48//586bp//69%//  
 U52426  
 C-OVARC1001436//ENL PROTEIN//0.00000009//81aa//39%//Q03111  
 C-OVARC1001453  
 25 C-OVARC1001476//"Mus musculus YGR163w mRNA homologue, complete cds.&quot;//1.80E-187//  
 510bp//89%//AB017616  
 C-OVARC1001480  
 C-OVARC1001489  
 C-OVARC1001506//POLYCYSTIN PRECURSOR (AUTOSOMAL DOMINANT POLYCYSTIC KIDNEY DISEASE  
 30 PROTEIN 1).//0//777aa//91%//P98161  
 C-OVARC1001525  
 C-OVARC1001555//NGG1-INTERACTING FACTOR 3//4.4E-19//130aa//40%//P53081  
 C-OVARC1001577//Homo sapiens SRp46 splicing factor transcribed retropseudogene//0//1167bp//100%//  
 AF031165  
 35 C-OVARC1001600  
 C-OVARC1001610//"Homo sapiens choline/ethanolaminephosphotransferase (CEPT1) mRNA, complete  
 cds.&quot;//0//1870bp//99%//AF068302  
 C-OVARC1001702  
 C-OVARC1001703//"Mus musculus ARL-6 interacting protein-2 (Aip-2) mRNA, complete cds.&quot;//3.5E-  
 40 16//399bp//61%//AF133670  
 C-OVARC1001711//CORNIFIN B (SMALL PROLINE-RICH PROTEIN 1B) (SPR1B) (SPR1 B).//2.80E-10//106aa//  
 38%//Q62267  
 C-OVARC1001713//ENDOZEPINE-RELATED PROTEIN PRECURSOR (MEMBRANE-ASSOCIATED DI-  
 AZEPAM BINDING INHIBITOR) (MA-DBI).//4.4E-40//195aa//41%//P07106  
 45 C-OVARC1001726//APICAL-LIKE PROTEIN (APXL PROTEIN).//4.3E-16//116aa//43%//Q13796  
 C-OVARC1001731//"TROPOMYOSIN ALPHA CHAIN, FIBROBLAST ISOFORM F2.&quot;//4E-122//  
 282aa//85%//P08942  
 C-OVARC1001745  
 C-OVARC1001762//"N-TERMINAL ACETYLTRANSFERASE 1 (EC 2.3.1.88) (AMINO-TERMINAL, ALPHA-  
 50 AMINO, ACETYLTRANSFERASE 1).&quot;//6.4E-85//514aa//34%//P12945  
 C-OVARC1001766//"Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete  
 cds.&quot;//0//963bp//99%//U97670  
 C-OVARC1001767//"Homo sapiens mRNA for KIAA0675 protein, complete cds.&quot;//0//2083bp//99%//  
 AB014575  
 55 C-OVARC1001768  
 C-OVARC1001791  
 C-OVARC1001795  
 C-OVARC1001802

C-OVARC1001809//"Mus musculus sphingosine kinase (SPHK1a) mRNA, partial cds.";//2.7E-190//  
 1624bp//76%//AF068748  
 C-OVARC1001828  
 C-OVARC1001846  
 5 C-OVARC1001861  
 C-OVARC1001879  
 C-OVARC1001880  
 C-OVARC1001883  
 C-OVARC1001916  
 10 C-OVARC1001928  
 C-OVARC1001942//"N-TERMINAL ACETYLTRANSFERASE 1 (EC 2.3.1.88) (AMINO-TERMINAL, ALPHA-  
 AMINO, ACETYLTRANSFERASE 1).";//3.1E-81//497aa/35%//P12945  
 C-OVARC1001943//"Mus musculus DEBT-91 mRNA, complete cds.";//0//2035bp//87%//AF143859  
 C-OVARC1001950  
 15 C-OVARC1001987//"Rattus norvegicus DNA-binding protein PREB (Preb) mRNA, complete cds.";//  
 2.3E-220//652bp//84%//AF061817  
 C-OVARC1002050//"Homo sapiens mRNA for actin binding protein ABP620, complete cds.";//0//  
 1019bp//99%//AB029290  
 C-OVARC1002082  
 20 C-OVARC1002107  
 C-OVARC1002127//SODIUM-INDEPENDENT ORGANIC ANION TRANSPORTER 2 (BRAIN DIGOXIN CARRI-  
 ER PROTEIN) (BRAIN-SPECIFIC ORGANIC ANION TRANSPORTER) (OATP-B1).//5.4E-52//306aa/35%//  
 035913  
 C-OVARC1002138//SAP1 PROTEIN.//7.6E-60//128aa//59%//P39955  
 25 C-OVARC1002156  
 C-OVARC1002158  
 C-PLACE100004//"Homo sapiens IDN3-B mRNA, complete cds.";//0//2365bp//99%//AB019602  
 C-PLACE1000040//TRANSFORMING PROTEIN P21/K-RAS 2B.//1.4E-17//185aa//32%//P08643  
 C-PLACE1000048  
 30 C-PLACE1000050  
 C-PLACE1000061//Human ribosomal protein L37a mRNA sequence.//7.9E-54//190bp//94%//L22154  
 C-PLACE1000081//"Human SEC7 homolog Tic (TIC) mRNA, complete cds.";//0//2077bp//99%//  
 U63127  
 C-PLACE1000094  
 35 C-PLACE1000133//TRANSCRIPTION FACTOR BTF3 (RNA POLYMERASE B TRANSCRIPTION FACTOR 3).//  
 1.8E-62//158aa//81%//P20290  
 C-PLACE1000214  
 C-PLACE1000236  
 C-PLACE1000246  
 40 C-PLACE1000292  
 C-PLACE1000308  
 C-PLACE1000332  
 C-PLACE1000453  
 C-PLACE1000583//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//1.60E-47//207aa//46%//  
 45 P51522  
 C-PLACE1000599  
 C-PLACE1000610//MSN5 PROTEIN.//0.0000026//136aa//26%//P52918  
 C-PLACE1000653//"Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.";//  
 0//1992bp//99%//AF180371  
 50 C-PLACE1000656//"Homo sapiens mRNA for JM4 protein, complete CDS (clone IMAGE 546750 and  
 LLNLc110F1857Q7 (RZPD Berlin)).";//2.1E-277//1260bp//99%//AJ005896  
 C-PLACE1000706//"Homo sapiens transcriptional intermediary factor 1 gamma mRNA, complete cds.";  
 //0//1366bp//99%//AF119043  
 C-PLACE1000712  
 55 C-PLACE1000749  
 C-PLACE1000769//"Homo sapiens CGI-18 protein mRNA, complete cds.";//0//1985bp//98%//  
 AF132952  
 C-PLACE1000786//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FA-

CIOGENITAL DYSPLASIA PROTEIN HOMOLOG).//7.10E-09//59aa//47%//P52734  
 C-PLACE1000849  
 C-PLACE1000856//&quot;Homo sapiens mRNA for KIAA0974 protein, partial cds.&quot;//0//1310bp//100%//  
 AB023191  
 5 C-PLACE1000931  
 C-PLACE1000987//&quot;Homo sapiens mRNA for KIAA0724 protein, complete cds.&quot;//0//1749bp//99%//  
 AB018267  
 C-PLACE1001010  
 C-PLACE1001015  
 10 C-PLACE1001024  
 C-PLACE1001062//&quot;Homo sapiens PAC clone DJ1049N15 from 7q31.2-7q32, complete sequence.&quot;//  
 2.7E-32//470bp//71%//AC006020  
 C-PLACE1001104  
 C-PLACE1001168  
 15 C-PLACE1001171//MYOTUBULARIN//7.1E-84//198aa//73%//Q13496  
 C-PLACE1001185//&quot;Homo sapiens mRNA for KIAA0943 protein, partial cds.&quot;//0//1668bp//99%//  
 AB023160  
 C-PLACE1001238//&quot;Mouse mRNA for RNA polymerase I associated factor (PAF53), complete cds.&quot;//  
 2E-202//1333bp//80%//D14336  
 20 C-PLACE1001280  
 C-PLACE1001294//M.musculus GEG-154 mRNA//4.3E-221//1057bp//78%//X7I642  
 C-PLACE1001304//&quot;Homo sapiens zinc finger protein dp mRNA, complete cds.&quot;//0//2421bp//99%//  
 AF153201  
 C-PLACE1001311  
 25 C-PLACE1001323  
 C-PLACE1001351  
 C-PLACE1001414  
 C-PLACE1001440  
 C-PLACE1001456  
 30 C-PLACE1001517//&quot;Homo sapiens gene for glycosylphosphatidylinositol anchor attachment 1 (GPAA1),  
 complete cds.&quot;//4.60E-112//392bp//87%//AB002137  
 C-PLACE1001602//CCR4-ASSOCIATED FACTOR 1 (CAF1).//5.7E-130//244aa//99%//Q60809  
 C-PLACE1001632//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.4E-118//429aa//48%//  
 P51523  
 35 C-PLACE1001634  
 C-PLACE1001640  
 C-PLACE1001672//PROBABLE AMINOTRANSFERASE T01B11.2 (EC 2.6.1.-).//4.3E-66//174aa//45%//P91408  
 C-PLACE1001705  
 C-PLACE1001716  
 40 C-PLACE1001720  
 C-PLACE1001745  
 C-PLACE1001748//&quot;Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.&quot;//0//2602bp//99%//  
 AF061243  
 C-PLACE1001771//Homo sapiens mRNA for transient receptor potential protein  
 45 TRP6.//0//2900bp//99%//AJ006276  
 C-PLACE1001799  
 C-PLACE1001845//&quot;Mus musculus cyclin ania-6a mRNA, complete cds.&quot;//3.30E-31//925bp//62%//  
 AF159159  
 C-PLACE1001897  
 50 C-PLACE1002090//SIGNAL RECOGNITION PARTICLE 72 KD PROTEIN (SRP72).//6.5E-58//112aa//100%//  
 076094  
 C-PLACE1002157  
 C-PLACE1002171//TRANSCRIPTION REGULATORY PROTEIN SWI3 (SWI/SNF COMPLEX COMPONENT  
 SWI3) (TRANSCRIPTION FACTOR TYE2).//0.00005//179aa//23%//P32591  
 55 C-PLACE1002227  
 C-PLACE1002259  
 C-PLACE1002319  
 C-PLACE1002395//&quot;Mus musculus mRNA for UBE-1c1, UBE-1c2, UBE-1c3, complete cds.&quot;//7.9E-

100//966bp//75%//AB030505  
 C-PLACE1002477  
 C-PLACE1002493//"Homo sapiens signal transducing adaptor molecule 2A (STAM2) mRNA, complete cds.  
 &quot;//1.7E-113//545bp//98%//AF042273  
 5 C-PLACE1002500  
 C-PLACE1002514  
 C-PLACE1002532//HOMEobox PROTEIN DLX-5.//1.2E-152//289aa//96%//P70396  
 C-PLACE1002537  
 C-PLACE1002571//ACTIN-LIKE PROTEIN 13E.//5E-99//386aa//48%//P45890  
 10 C-PLACE10025 83//"GLUTAMATE RECEPTOR, IONOTROPIC KAINATE 2 PRECURSOR (GLUTAMATE  
 RECEPTOR 6) (GLUR-6) (GLUTAMATE RECEPTOR BETA-2) (GLUR BETA-2) (FRAGMENT)."//5.6E-34//  
 76aa//98%//P39087  
 C-PLACE1002598//OLIGORIBONUCLEASE (EC 3.1.-.-).//5.5E-17//76aa//56%//P45340  
 C-PLACE1002625  
 15 C-PLACE1002655//ADSEVERIN (SCINDERIN)(SC).//2.5E-278//543aa//92%//Q28046  
 C-PLACE1002768  
 C-PLACE1002782//"Rattus norvegicus zinc transporter (ZnT-2) mRNA, complete cds."//3.8E-43//  
 385bp//77%//U50927  
 C-PLACE1002816//HISTONE DEACETYLASE HDA1.//2.20E-48//217aa//46%//P53973  
 20 C-PLACE1002853  
 C-PLACE1002908//"Homo sapiens XGalT-1 mRNA for galactosyltransferase I, complete cds."//0//  
 1654bp//99%//AB028600  
 C-PLACE1002962  
 C-PLACE1002968  
 25 C-PLACE1002991//PUTATIVE AMIDASE (EC 3.5.1.4).//1.4E-78//496aa//37%//Q49091  
 C-PLACE1003025  
 C-PLACE1003027//"Homo sapiens mRNA for KIAA0516 protein, partial cds."//2.1e-314//1417bp//  
 100%//AB011088  
 C-PLACE1003044//"Homo sapiens mRNA for KIAA0829 protein, partial cds."//0//1382bp//96%//  
 30 AB020636  
 C-PLACE1003176  
 C-PLACE1003238//PROBABLE G PROTEIN-COUPLED RECEPTOR KIAA0001.//4.9E-76//309aa//47%//  
 Q15391  
 C-PLACE1003256  
 35 C-PLACE1003258//EARLY EMBRYOGENESIS ZYG-11 PROTEIN.//7.9E-22//70aa7/47%//P21541  
 C-PLACE1003343  
 C-PLACE1003361  
 C-PLACE1003366//"Homo sapiens otoferlin (OTOF) mRNA, complete cds."//1.4E-78//542bp//67%//  
 AF107403  
 40 C-PLACE1003373  
 C-PLACE1003375  
 C-PLACE1003394//"Sprague-Dawley (clone LRB13) RAB14 mRNA, complete. cds."//2.30E-150//  
 774bp//94%//M83680  
 C-PLACE1003420//PUTATIVE MITOCHONDRIAL CARRIER YIL006W.//1.3E-40//278aa//36%//P40556  
 45 C-PLACE1003454  
 C-PLACE1003478  
 C-PLACE1003516  
 C-PLACE1003519//H.sapiens hnRNP-E2 mRNA.//5.1E-218//905bp//99%//X78136  
 C-PLACE1003521//HYPOTHETICAL HELICASE C28H8.3 IN CHROMOSOME III.//0.0000011//101aa//32%//  
 50 Q09475  
 C-PLACE1003528  
 C-PLACE1003537//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHE-  
 ROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPO-  
 NENT).//7.7E-68//404aa//33%//P32802  
 55 C-PLACE1003566  
 C-PLACE1003584  
 C-PLACE1003593  
 C-PLACE1003605//HAP5 TRANSCRIPTIONAL

ACTIVATOR./.0.00000023//82aa//35%//Q02516  
 C-PLACE1003618  
 C-PLACE1003638  
 C-PLACE1003738//ZINC FINGER PROTEIN 135./.9.6E-118//350aa//46%//P52742  
 5 C-PLACE1003760//&quot;Homo sapiens tetraspanin TM4-A mRNA, complete cds.&quot;//5.2E-289//1313bp//  
 97%//AF133423  
 C-PLACE1003768  
 C-PLACE1003795  
 C-PLACE1003886  
 10 C-PLACE1003888//&quot;Homo sapiens mRNA for KIAA1092 protein, partial cds.&quot;//0//2057bp//99%//  
 AB029015  
 C-PLACE1003903//CTP SYNTHASE (EC 6.3.4.2) (UTP-AMMONIA LIGASE) (CTP SYNTHETASE).//1.4E-243//  
 584aa//74%//P17812  
 C-PLACE1003915//&quot;PROBABLE ARGINYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.19) (AR-  
 15 GININE- -TRNA LIGASE) (ARGRS).&quot;//2.4E-108//581aa//40%//Q05506  
 C-PLACE1004118  
 C-PLACE1004256//&quot;Mus musculus short coiled coil protein SCOCO (Scoc) mRNA, complete cds.&quot;//  
 2E-93//960bp//76%//AF115778  
 C-PLACE1004274  
 20 C-PLACE1004284  
 C-PLACE1005331  
 C-PLACE1005739//Homo sapiens mRNA; cDNA DKFZp564A032 (from clone DKFZp564A032).//0//2190bp//  
 99%//AL050267  
 C-PLACE1005828  
 25 C-PLACE1005876//&quot;CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT  
 (CPSF 100 KD SUBUNIT).&quot;//0//730aa//99%//Q10568  
 C-PLACE1005890//BEM46 PROTEIN (FRAGMENT).//9.9E-42//224aa//43%//P54069  
 C-PLACE1006157//E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1)  
 (ELAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E).//2E-28//236aa//  
 30 30%//P98110  
 C-PLACE1007053  
 C-PLACE1007068  
 C-PLACE1008368//RING CANAL PROTEIN (KELCH PROTEIN).//5.3E-26//309aa//30%//Q04652  
 C-PLACE1009921  
 35 C-PLACE1010401  
 C-PLACE1010856  
 C-PLACE1010857  
 C-PLACE1010917  
 C-PLACE1010925  
 40 C-PLACE1010926//&quot;Homo sapiens mRNA for KIAA0554 protein, partial cds.&quot;//0//1160bp//100%//  
 AB011126  
 C-PLACE1010942//&quot;Homo sapiens intersectin long isoform (ITSN) mRNA, complete cds.&quot;//0//1440bp//  
 99%//AF114487  
 C-PLACE1010944  
 45 C-PLACE1010954  
 C-PLACE1010960//ACTIN-LIKE PROTEIN 13E.//5.3E-98//297aa//48%//P45890  
 C-PLACE1011026  
 C-PLACE1011046//&quot;1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 1  
 (EC 3.1.4.11) (PLC-BETA-1) (PHOSPHOLIPASE C-BETA-1) (PLC-I) (PLC-154).&quot;//0//646aa//97%//P10894  
 50 C-PLACE1011054  
 C-PLACE1011057  
 C-PLACE1011109//&quot;ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G).&quot;//1.50E-  
 22//63aa//88%//Q07803  
 C-PLACE1011114//PROBABLE ATP-DEPENDENT RNA HELICASE HAS1.//2.9E-71//190aa//44%//Q03532  
 55 C-PLACE1011133  
 C-PLACE1011143  
 C-PLACE1011165  
 C-PLACE1011185//INSERTION ELEMENT IS1 PROTEIN INSB.//1.3E-89//167aa//100%//P03830

C-PLACE1011219//PROBABLE OXIDOREDUCTASE (EC 1.-.-.-).//3.2E-12//212aa//29%//Q03326  
 C-PLACE1011221  
 C-PLACE1011263//Homo sapiens mRNA; cDNA DKFZp564O043 (from clone DKFZp564O043).//0//2487bp//  
 99%//AL050390  
 5 C-PLACE1011325  
 C-PLACE1011332//"Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.";//  
 7.2E-151//697bp//99%//AF102265  
 C-PLACE1011340//"Homo sapiens IDN3-B mRNA, complete cds.";//1.20E-74//380bp//97%//  
 AB019602  
 10 C-PLACE1011399//"Homo sapiens CGI-72 protein mRNA, complete cds.";//3.2E-90//427bp//99%//  
 AF151830  
 C-PLACE1011433//"Homo sapiens mRNA for KIAA0530 protein, partial cds.";//0//1946bp//99%//  
 AB011102  
 C-PLACE1011452  
 15 C-PLACE1011465  
 C-PLACE1011472//"Homo sapiens mRNA for KIAA0712 protein, complete cds.";//0//2022bp//99%//  
 AB018255  
 C-PLACE1011477//"Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.";//0//2040bp//99%//  
 AF065482  
 20 C-PLACE1011492//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT).//  
 4.90E-11//147aa//32%//P52178  
 C-PLACE1011520  
 C-PLACE1011563  
 C-PLACE1011567  
 25 C-PLACE1011576//"Human Kruppel related zinc finger protein (HTF10) mRNA, complete cds.";//0//  
 1791bp//82%//L11672  
 C-PLACE1011586  
 C-PLACE1011643  
 C-PLACE1011649  
 30 C-PLACE1011664//CROOKED NECK PROTEIN.//1.6E-187//505aa//64%//P17886  
 C-PLACE1011682  
 C-PLACE1011719  
 C-PLACE1011729  
 35 C-PLACE1011858//Homo sapiens mRNA; cDNA DKFZp586C021 (from clone DKFZp586C021).//0//1490bp//  
 99%//AL050287  
 C-PLACE1011874  
 C-PLACE1011875//"Homo sapiens mRNA for KIAA0580 protein, partial cds.";//4.1E-112//524bp//  
 100%//AB011152  
 C-PLACE1011923//"Homo sapiens serum-inducible kinase mRNA, complete cds.";//0//2782bp//99%//  
 40 AF059617  
 C-PLACE1011982  
 C-PLACE2000014//HYPOTHETICAL HELICASE C28H8.3 IN CHROMOSOME III.//2.6E-42//104aa//49%//  
 Q09475  
 C-PLACE2000015//EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN  
 45 EPS15) (AF-1P PROTEIN).//1.1E-116//364aa//45%//P42566  
 C-PLACE2000017  
 C-PLACE2000021//"Homo sapiens TRF1-interacting ankyrin-related ADP-ribose polymerase mRNA, com-  
 plete cds.";//2.7E-107//981bp//74%//AF082556  
 C-PLACE2000047  
 50 C-PLACE2000062//"Homo sapiens mRNA for type II membrane protein similar to HIV gp120-binding C-type  
 lectin, complete cds, clone:HP01347.";//6.3E-166//656bp//94%//AB015629  
 C-PLACE2000100  
 C-PLACE2000111  
 C-PLACE2000172  
 55 C-PLACE2000187  
 C-PLACE2000216//"Dog nonerythroid beta-spectrin mRNA, 3' end.";//3.2E-253//1799bp//83%//L02897  
 C-PLACE2000246//"Homo sapiens mRNA for KIAA0795 protein, partial cds.";//4.60E-172//796bp//  
 99%//AB018338

C-PLACE2000317  
C-PLACE2000341//"Homo sapiens sodium-dependent multivitamin transporter (SMVT) mRNA, complete cds.";//0//1554bp//99%//AF069307  
C-PLACE2000366  
5 C-PLACE2000373//F-SPONDIN PRECURSOR//8.6E-16//371aa//28%//P35446  
C-PLACE2000394  
C-PLACE2000398//LAR PROTEIN PRECURSOR (LEUKOCYTE ANTIGEN RELATED) (EC 3.1.3.48)//6.3E-37//  
90aa//98%//P10586  
C-PLACE2000411//"Homo sapiens mRNA for KIAA1037 protein, partial cds.";//0//2515bp//99%//  
10 AB028960  
C-PLACE2000425  
C-PLACE2000427//PROBABLE HELICASE MOT1//1.2E-26//200aa//27%//P32333  
C-PLACE2000433  
C-PLACE2000438//"POLYPEPTIDE N-ACETYLGLACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PRO-  
15 TEIN- UDP ACETYLGLACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N-ACETYLGLAC-  
TOSAMINYLTRANSFERASE)(GALNAC-T1).";//2.1E-86//348aa//41%//Q10472  
C-PLACE2000458//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN)//2.5E-25//  
165aa//40%//P33450  
C-PLACE2000477//"Homo sapiens putative secreted protein (ZSIG11) mRNA, complete cds.";//6.7E-  
20 127//671bp//94%//AF072733  
C-PLACE3000009  
C-PLACE3000020//"Homo sapiens type III adenylyl cyclase (AC-III) mRNA, complete cds.";//0//  
2253bp//99%//AF033861  
C-PLACE3000103  
25 C-PLACE3000142  
C-PLACE3000145//TENSIN//1E-108//277aa//75%//Q04205  
C-PLACE3000156  
C-PLACE3000157  
C-PLACE3000197  
30 C-PLACE3000208  
C-PLACE3000226//"Homo sapiens mRNA for KIAA0962 protein, partial cds.";//0//4805bp//99%//  
AB023179  
C-PLACE3000242//"Homo sapiens mRNA for KIAA1114 protein, complete cds.";//0//2786bp//96%//  
AB029037  
35 C-PLACE3000363  
C-PLACE3000405  
C-PLACE3000416//"Homo sapiens mRNA for actin binding protein ABP620, complete cds.";//1.80E-  
141//565bp//98%//AB029290  
C-PLACE3000477  
40 C-PLACE4000106//"Homo sapiens mRNA for KIAA0462 protein, partial cds.";//0//6702bp//99%//  
AB007931  
C-PLACE4000323  
C-PLACE4000326//NAM7 PROTEIN (NONSENSE-MEDIATED mRNA DECAY PROTEIN 1) (UP-FRAMESHIFT  
SUPPRESSOR 1)//8.10E-24//319aa//31%//P30771  
45 C-PLACE4000369//"Homo sapiens mRNA for KIAA1025 protein, partial cds.";//0//4830bp//99%//  
AB028948  
C-PLACE4000445//Homo sapiens mRNA; cDNA DKFZp434C212 (from clone DKFZp434C212)//0//2565bp//  
99%//AL080196  
50 C-PLACE4000558//"Homo sapiens mRNA for KIAA0729 protein, partial cds.";//0//1051bp//97%//  
AB018272  
C-PLACE4000581//FIBROPELLIN I PRECURSOR (EPIDERMAL GROWTH FACTOR-RELATED PROTEIN 1)  
(UEGF-1)//9.3E-70//226aa//52%//P10079  
C-PLACE4000593  
55 C-PLACE4000612//POL POLYPROTEIN [CONTAINS: PROTEASE (EC 3.4.23.-); REVERSE TRANSCRIPTASE  
(EC 2.7.7.49); ENDONUCLEASE].//7.1E-154//340aa//40%//P21414  
C-PLACE4000670  
C-THYRO1000026  
C-THYRO1000085//"PAIRED BOX PROTEIN PAX-8, ISOFORMS 8A/8B.";//2E-72//155aa//92%//

Q06710  
 C-THYRO1000107  
 C-THYRO1000111  
 C-THYRO1000132//"Homo sapiens echinoderm microtubule-associated protein homolog HuEMAP mRNA, complete cds.&quot;//1.1E-159//824bp//95%//U97018  
 C-THYRO1000156  
 C-THYRO1000173//"Homo sapiens AP-mu chain family member mu1B (HSMU1B) mRNA, complete cds.&quot;//0//1713bp//99%//AF020797  
 C-THYRO1000186  
 10 C-THYRO1000187  
 C-THYRO1000241  
 C-THYRO1000279  
 C-THYRO1000327//"Homo sapiens autocrine motility factor receptor (AMFR) mRNA, complete cds.&quot;//0//1567bp//99%//AF124145  
 15 C-THYRO1000452  
 C-THYRO1000471  
 C-THYRO1000484  
 C-THYRO1000502  
 C-THYRO1000505  
 20 C-THYRO1000585//"Homo sapiens protein associated with Myc mRNA, complete cds.&quot;//0//1901bp//99%//AF075587  
 C-THYRO1000596  
 C-THYRO1000662//"Homo sapiens XPV mRNA for DNA polymerase eta, complete cds.&quot;//0//2341 bp//99%//AB024313  
 25 C-THYRO1000666//Mus musculus mRNA for kinesin like protein 9 //0//2001bp//86%//AJ132889  
 C-THYRO1000715  
 C-THYRO1000734  
 C-THYRO1000748//RHO-GAP HEMATOPOIETIC PROTEIN C1 (P115) (KIAA0131).//3.30E-96//335aa//52%//P98171  
 30 C-THYRO1000756//"ALPHA-N-ACETYLGLUCOSAMINIDE ALPHA-2,6-SIALYLTRANSFERASE (EC 2.4.99.-) (ST6GALNACIII) (STY).&quot;//1.8E-55//243aa//42%//Q64686  
 C-THYRO1000777  
 C-THYRO1000783//"Xenopus laevis tail-specific thyroid hormone up-regulated (gene 5) mRNA, complete cds.&quot;//2.4E-157//1656bp//70%//U37373  
 35 C-THYRO1000787  
 C-THYRO1000793  
 C-THYRO1000796  
 C-THYRO1000843  
 C-THYRO1000852//"Human branched chain aminotransferase precursor (BCATm) mRNA, nuclear gene encoding mitochondrial protein, complete cds.&quot;//3.3E-147//790bp//93%//U68418  
 40 C-THYRO1000865  
 C-THYRO1000895  
 C-THYRO1000926//"Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds.&quot;//0//2387bp//99%//AF079529  
 45 C-THYRO1000951//DIHYDROXYACETONE KINASE 2 (EC 2.7.1.29) (GLYCERONE KINASE).//5E-83//566aa//37%//P43550  
 C-THYRO1000952  
 C-THYRO1000983//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B).//6.30E-17//143aa//39%//P35132  
 50 C-THYRO1001003//UBIQUITIN-CONJUGATING ENZYME E2-21.2 KD (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN).//5.90E-14//84aa//41%//P52491  
 C-THYRO1001031  
 C-THYRO1001062  
 C-THYRO1001100//ZINC FINGER X-LINKED PROTEIN ZXDA (FRAGMENT).//1.2E-67//245aa//62%//P98168  
 55 C-THYRO1001133  
 C-THYRO1001134//"Homo sapiens CGI-78 protein mRNA, complete cds.&quot;//0//1898bp//99%//AF151835  
 C-THYRO1001173

C-THYRO1001213  
 C-THYRO1001321  
 C-THYRO1001322  
 C-THYRO1001365  
 5 C-THYRO1001401  
 C-THYRO1001411  
 C-THYRO1001434  
 C-THYRO1001534  
 C-THYRO1001541  
 10 C-THYRO1001559  
 C-THYRO1001570  
 C-THYRO1001595  
 C-THYRO1001605  
 C-THYRO1001617//Homo sapiens cDNA for dihydroxyacetone phosphate acyltransferase (DAP-AT).//0//1784bp//  
 15 99%//AJ002190  
 C-THYRO1001656//"Homo sapiens Leman coiled-coil protein (LCCP) mRNA, complete cds."//4.1E-  
 273//1947bp//82%//AF175968  
 C-THYRO1001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59 kDa isoform.//0//1820bp//99%//  
 AJ225089  
 20 C-THYRO1001673  
 C-THYRO1001703//NIFR3-LIKE PROTEIN.//2.90E-32//282aa//32%//P45672  
 C-THYRO1001706  
 C-THYRO1001738//TUBULIN-TYROSINE LIGASE (EC 6.3.2.25) (TTL).//2.4E-20//217aa//30%//P38584  
 C-THYRO1001745  
 25 C-THYRO1001793  
 C-THYRO1001809//MYOCYTE NUCLEAR FACTOR (MNF).//1.4E-74//158aa//89%//P42128  
 C-THYRO1001895  
 C-THYRO1001907  
 C-VESEN1000122  
 30 C-Y79AA1000037//DNA-BINDING PROTEIN BMI-1.//2.4E-30//80aa//60%//P25916  
 C-Y79AA1000059//"Homo sapiens immunophilin homolog ARA9 mRNA, complete cds."//2.9E-70//  
 1040bp//65%//U78521  
 C-Y79AA1000065  
 C-Y79AA1000131  
 35 C-Y79AA1000181//"Homo sapiens CGI-01 protein mRNA, complete cds."//0//1858bp//99%//  
 AF132936  
 C-Y79AA1000202  
 C-Y79AA1000214//"Homo sapiens histone H2A.F/Z variant (H2AV) mRNA, complete cds."//7.1E-71//  
 345bp//100%//AF081192  
 40 C-Y79AA1000230  
 C-Y79AA1000258  
 C-Y79AA1000268//"Mus musculus Nip21 mRNA, complete cds."//2.10E-50//648bp//64%//AF035207  
 C-Y79AA1000313//CALPHOTIN.//0.000011//336aa//23%//Q02910  
 C-Y79AA1000328//SEL-10 PROTEIN.//0.00000067//219aa//25 %//Q93794  
 45 C-Y79AA1000355  
 C-Y79AA1000368//REDUCED VIABILITY UPON STARVATION PROTEIN 161.//4E-20//261 aa//27%//P25343  
 C-Y79AA1000420  
 C-Y79AA1000469//"Mus musculus ancient ubiquitous 46 kDa protein AUP1 precursor (Aup1) mRNA, com-  
 plete cds."//8.30E-252//1207bp//85%//U41736  
 50 C-Y79AA1000480  
 C-Y79AA1000540  
 C-Y79AA1000560//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE  
 CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA  
 C SUBUNIT).//0//652aa//98%//P17427  
 55 C-Y79AA1000574//Homo sapiens clone H17 unknown mRNA.//0//1932bp//99%//AF103801  
 C-Y79AA1000627//"Homo sapiens zinc finger protein (ZF5128) mRNA, complete cds."//2E-287//203  
 lbp//82%//AF060503  
 C-Y79AA1000705//M.musculus mRNA of enhancer-trap-locus 1.//5.80E-254//1477bp//84%//X69942

C-Y79AA1000734//"Homo sapiens peroxisomal biogenesis factor (PEX11b) mRNA, complete cds.";//0//1594bp//99%//AF093670  
 C-Y79AA1000748//"Homo sapiens CGI-05 protein mRNA, complete cds.";//1.9E-239//1367bp//91%//AF152097  
 5 C-Y79AA1000752//PUTATIVE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN X (HNRNP X) (CBP).//4.9E-91//200aa/64%//Q61990  
 C-Y79AA1000774  
 C-Y79AA1000782//CYTOSOLIC PURINE 5'-NUCLEOTEDASE (EC 3.1.3.5).//3E-37//469aa/27%//P49902  
 10 C-Y79AA1000784//"Homo sapiens RanBP7/importin 7 mRNA, complete cds.";//1.10E-236//1076bp//99%//AF098799  
 C-Y79AA1000794//"Homo sapiens actin-associated protein 2E4/kaptin (2E4) mRNA, 2E4-1 allele, complete cds.";//0//1610bp//99%//AF105369  
 15 C-Y79AA1000800//"Homo sapiens putative secreted protein (ZSIG11) mRNA, complete cds.";//1.6E-284//1288bp//99%//AF072733  
 C-Y79AA1000805  
 C-Y79AA1000824  
 C-Y79AA1000833//TUBULIN ALPHA-1 CHAIN.//5E-173//220aa/79%//P05209  
 C-Y79AA1000850  
 C-Y79AA1000962//"MYOSIN HEAVY CHAIN, NON-MUSCLE (ZIPPER PROTEIN) (MYOSIN II).";//4.2E-17//430aa/27%//Q99323  
 20 C-Y79AA1000968//"Rattus norvegicus initiation factor eIF-2B gamma subunit (eIF-2B gamma) mRNA, complete cds.";//3.9E-248//1468bp//87%//U38253  
 C-Y79AA1000976  
 C-Y79AA1001023  
 25 C-Y79AA1001041  
 C-Y79AA1001048//"ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (VLCAD).";//3.1E-138//583aa/47%//P45953  
 C-Y79AA1001077  
 C-Y79AA1001078  
 30 C-Y79AA1001145  
 C-Y79AA1001177  
 C-Y79AA1001185  
 C-Y79AA1001211//"Homo sapiens origin recognition complex subunit 6 (ORC6) mRNA, complete cds.";//0//1435bp//99%//AF139658  
 35 C-Y79AA1001228  
 C-Y79AA1001233//ESTRADIOL 17 BETA-DEHYDROGENASE 1 (EC 1.1.1.62) (17-BETA-HSD 1) (17-BETA-HYDROXYSTEROID DEHYDROGENASE 1).//7.7E-50//228aa/42%//P51657  
 C-Y79AA1001236//"Homo sapiens mRNA for JM23 protein, complete coding sequence (clone IMAGE 34581 and IMAGE 45355 and LLNLc110I133Q7 (RZPD Berlin)).";//0//1653bp//99%//AJ005892  
 40 C-Y79AA1001281  
 C-Y79AA1001312//ZINC FINGER PROTEIN MLZ-4 (ZINC FINGER PROTEIN 46).//0.000000023//193aa/30%//Q03309  
 C-Y79AA1001323//"Mus musculus mRNA for GSG1, complete cds.";//3.3E-172//1171bp//83%//D87325  
 45 C-Y79AA1001391//HOMEobox protein HOX-A13 (HOX-1J).//1.2E-58//178aa/66%//P31271  
 C-Y79AA1001394//CELL DIVISION PROTEIN FTSH HOMOLOG (EC 3.4.24.-).//1.2E-13//230aa/32%//O83746  
 C-Y79AA1001402//"Homo sapiens paraneoplastic cancer-testis-brain antigen (MA4) mRNA, partial cds.";//8.50E-65//784bp//62%//AF083115  
 C-Y79AA1001493//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B).//3.80E-18//151aa/38%//P35132  
 50 C-Y79AA1001533//"Mouse mRNA for RNA polymerase I associated factor (PAF53), complete cds.";//4.5E-193//1333bp//80%//D14336  
 C-Y79AA1001541  
 C-Y79AA1001548//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA (EC 2.7.1.67) (PI4-KINASE) (PTDINS-4-KINASE) (PI4K-ALPHA).//7.5E-76//85aa/90%//P42356  
 55 C-Y79AA1001555  
 C-Y79AA1001581//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME).//1.9E-40//482aa/27%//P27550

C-Y79AA1001585  
 C-Y79AA1001603//"POLYPEPTIDE N-ACETYLGALACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PROTEIN- UDP ACETYLGALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N-ACETYLGALACTOSAMINYLTRANSFERASE) (GALNAC-T1)."//1.7E-84//313aa//48%//Q07537  
 5 C-Y79AA1001613//ZINC FINGER PROTEIN 132//3.8E-91//209aa//41%//P52740  
 C-Y79AA1001665  
 C-Y79AA1001679//"Homo sapiens lambda-crystallin mRNA, complete cds."//3.4e-310//1430bp//98%//AF077049  
 10 C-Y79AA1001696//"Homo sapiens mRNA for KIAA1109 protein, partial cds."//0//1669bp//100%//AB029032  
 C-Y79AA1001705//"Homo sapiens p53 regulated PA26-T2 nuclear protein (PA26) mRNA, complete cds."//3.4E-47//626bp//68%//AF033120  
 C-Y79AA1001711//"Human 60-kdal ribonucleoprotein (Ro) mRNA, complete cds."//1.2E-258//1185bp//99%//J04137  
 15 C-Y79AA1001781  
 C-Y79AA1001805  
 C-Y79AA1001827//"Homo sapiens mammalian inositol hexakisphosphate kinase 2 (IP6K2) mRNA, complete cds."//0//1689bp//98%//AF177145  
 C-Y79AA1001846  
 20 C-Y79AA1001923  
 C-Y79AA1001963//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C//1E-10//94aa//47%//O42643  
 C-Y79AA1002027//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42)//9.9E-39//143aa//52%//P42743  
 25 C-Y79AA1002083//H.sapiens mRNA for MUF1 protein//5E-163//752bp//99%//X86018  
 C-Y79AA1002089  
 C-Y79AA1002115  
 C-Y79AA1002125  
 C-Y79AA1002204  
 30 C-Y79AA1002208//ANKYRIN//8.1E-34//188aa//38%//Q02357  
 C-Y79AA1002209//"Homo sapiens CGI-04 protein mRNA, complete cds."//0//1617bp//99%//AF132939  
 C-Y79AA1002229//DNA CROSS-LINK REPAIR PROTEIN PSO2/SNM1//7.10E-17//213aa//31%//P30620  
 35 C-Y79AA1002246//SYNAPTOTAGMIN V//1.6E-28//286aa//32%//000445  
 C-Y79AA1002298  
 C-Y79AA1002307//"Homo sapiens astrotactin2 (ASTN2) mRNA, complete cds."//0//1209bp//99%//AF116574  
 C-Y79AA1002311//R.norvegicus mRNA for cytosolic resiniferatoxin-binding protein//2.9E-186//1130bp//82%//X67877  
 40 C-Y79AA1002351  
 C-Y79AA1002407  
 C-Y79AA1002433//"Homo sapiens chromatin-specific transcription elongation factor FACT 140 kDa subunit mRNA, complete cds."//0//1545bp//96%//AF152961  
 C-Y79AA1002472//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7)//1.5E-136//472aa//49%//Q05481  
 45

## Homology Search Result Data 13.

[0333] Data obtained by the homology search for full-length nucleotide sequences and deduced amino acid sequences. Each data includes Clone name, Definition in hit data, P value, Length of sequence to be compared, Homology, and Accession number (No.) of hit data. These items are shown in this order and separated by a double-slash mark, //.

C-HEMBA1000042  
 C-HEMBA1000141//Homo sapiens SUMO-1-specific protease (SSP1) mRNA, complete cds//0//1135bp//100%//AF196304  
 55 C-HEMBA1000150//H.sapiens gene for U5 snRNP-specific 200kD protein//2.50E-153//525bp//91%//Z70200  
 C-HEMBA1000213  
 C-HEMBA1000243

C-HEMBA1000244  
C-HEMBA1000251  
C-HEMBA1000338  
C-HEMBA1000357  
5 C-HEMBA1000376  
C-HEMBA1000428  
C-HEMBA1000469  
C-HEMBA1000497  
C-HEMBA1000561//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//3.40E-37//674aa//  
10 25%//Q05481  
C-HEMBA1000569//GPI-ANCHORED PROTEIN P137.//6.50E-19//265aa//32%//Q60865  
C-HEMBA1000575  
C-HEMBA1000591//PTB-ASSOCIATED SPLICING FACTOR (PSF).//2.20E-17//198aa//40%//P23246  
15 C-HEMBA1000673  
C-HEMBA1000702  
C-HEMBA1000722  
C-HEMBA1000726  
C-HEMBA1000876  
C-HEMBA1000942  
20 C-HEMBA1000943  
C-HEMBA1000960  
C-HEMBA1000985  
C-HEMBA1001019//CELL DIVISION CONTROL PROTEIN 2 HOMOLOG (EC 2.7.1.-) (P34 PROTEIN KINASE)  
(CYCLIN-DEPENDENT KINASE 1) (CDK1).//3.10E-10//70aa//58%//P06493  
25 C-HEMBA1001020  
C-HEMBA1001024  
C-HEMBA1001026  
C-HEMBA1001051  
C-HEMBA1001060  
30 C-HEMBA1001071//PROCOLLAGEN ALPHA 1(III) CHAIN PRECURSORS.//1.50E-92//82aa//100%//P02461  
C-HEMBA1001077//Homo sapiens transcriptional intermediary factor 1 gamma mRNA, complete cds.//2.00E-80//  
432bp//94%//AF119043  
C-HEMBA1001099  
C-HEMBA1001121  
35 C-HEMBA1001123  
C-HEMBA1001208  
C-HEMBA1001213  
C-HEMBA1001226  
C-HEMBA1001247  
40 C-HEMBA1001299  
C-HEMBA1001319  
C-HEMBA1001323  
C-HEMBA1001327  
C-HEMBA1001361  
45 C-HEMBA1001375  
C-HEMBA1001377  
C-HEMBA1001383  
C-HEMBA1001391  
C-HEMBA1001411  
50 C-HEMBA1001432  
C-HEMBA1001433  
C-HEMBA1001435  
C-HEMBA1001442  
C-HEMBA1001463  
55 C-HEMBA1001515  
C-HEMBA1001522  
C-HEMBA1001557  
C-HEMBA1001566

C-HEMBA1001589  
C-HEMBA1001608  
C-HEMBA1001636  
C-HEMBA1001647  
5 C-HEMBA1001651  
C-HEMBA1001658  
C-HEMBA1001675//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS9//5.40E-09//101aa//35%//  
P54787  
C-HEMBA1001712  
10 C-HEMBA1001734//CADHERIN-11 PRECURSOR (OSTEOBLAST-CADHERIN) (OB-CADHERIN) (OSF-4)//  
1.10E-38//87aa//96%//P55288  
C-HEMBA1001745  
C-HEMBA1001750  
15 C-HEMBA1001784  
C-HEMBA1001791  
C-HEMBA1001803  
C-HEMBA1001820  
C-HEMBA1001835  
C-HEMBA1001888  
20 C-HEMBA1001912  
C-HEMBA1001915  
C-HEMBA1001918  
C-HEMBA1001940  
C-HEMBA1001942  
25 C-HEMBA1001964  
C-HEMBA1002022  
C-HEMBA1002039  
C-HEMBA1002100  
C-HEMBA1002113  
30 C-HEMBA1002119  
C-HEMBA1002139//LIM AND SH3 DOMAIN PROTEIN LASP-1 (MLN 50)//7.10E-05//51aa//49%//Q14847  
C-HEMBA1002160  
C-HEMBA1002162  
35 C-HEMBA1002166  
C-HEMBA1002185  
C-HEMBA1002204  
C-HEMBA1002328  
C-HEMBA1002337  
C-HEMBA1002348  
40 C-HEMBA1002381  
C-HEMBA1002486  
C-HEMBA1002498  
C-HEMBA1002538  
C-HEMBA1002552  
45 C-HEMBA1002555//Homo sapiens mSin3A associated polypeptide p30 mRNA, complete cds//5.30E-51//768bp//  
68%//AF055993  
C-HEMBA1002558  
C-HEMBA1002621  
C-HEMBA1002629  
50 C-HEMBA1002645  
C-HEMBA1002659  
C-HEMBA1002661  
C-HEMBA1002666  
C-HEMBA1002678  
55 C-HEMBA1002679  
C-HEMBA1002712  
C-HEMBA1002716  
C-HEMBA1002742

C-HEMBA1002746//DNA POLYMERASE BETA (EC 2.7.7.7).//5.00E-37//268aa//34%//P06746  
 C-HEMBA1002748  
 C-HEMBA1002780  
 C-HEMBA1002801  
 5 C-HEMBA1002826  
 C-HEMBA1002833  
 C-HEMBA1002921  
 C-HEMBA1002934  
 C-HEMBA1002944  
 10 C-HEMBA1002968  
 C-HEMBA1003034  
 C-HEMBA1003037  
 C-HEMBA1003071//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COMPLEX ACID LABILE CHAIN  
 PRECURSOR (ALS).//1.30E-09//121aa//40%//P35858  
 15 C-HEMBA1003078  
 C-HEMBA1003083  
 C-HEMBA1003086  
 C-HEMBA1003098//Homo sapiens NY-REN-6 antigen mRNA, partial cds.//6.20E-273//1253bp//99%//AF155096  
 C-HEMBA1003133  
 20 C-HEMBA1003142  
 C-HEMBA1003166  
 C-HEMBA1003197  
 C-HEMBA1003202  
 C-HEMBA1003220  
 25 C-HEMBA1003229  
 C-HEMBA1003276  
 C-HEMBA1003278  
 C-HEMBA1003328  
 C-HEMBA1003373  
 30 C-HEMBA1003597  
 C-HEMBA1003598  
 C-HEMBA1003656  
 C-HEMBA1003680//PUTATIVE AMINOPEPTIDASE ZK353.6 IN CHROMOSOME III (EC 3.4.11.-).//2.40E-92//  
 423aa//47%//P34629  
 35 C-HEMBA1003733  
 C-HEMBA1003742  
 C-HEMBA1003760//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN)  
 (MEMBER OF PAS PROTEIN 1) (MOP1) (HIF1 ALPHA).//3.70E-124//347aa//55%//Q16665  
 C-HEMBA1003803  
 40 C-HEMBA1003854  
 C-HEMBA1003926  
 C-HEMBA1003939  
 C-HEMBA1003987  
 C-HEMBA1004012  
 45 C-HEMBA1004015  
 C-HEMBA1004193  
 C-HEMBA1004225  
 C-HEMBA1004241  
 C-HEMBA1004267  
 50 C-HEMBA1004295//Homo sapiens NY-REN-25 antigen mRNA, partial cds.//9.40E-31//381bp//65%//AF155103  
 C-HEMBA1004354//CHL1 PROTEIN.//9.90E-26//130aa//42%//P22516  
 C-HEMBA1004356//H.sapiens MSSP-2 mRNA.//3.00E-243//573bp//98%//X77494  
 C-HEMBA1004396  
 C-HEMBA1004405  
 55 C-HEMBA1004433  
 C-HEMBA1004538  
 C-HEMBA1004542  
 C-HEMBA1004573

C-HEMBA1004577  
 C-HEMBA1004604//Homo sapiens COP9 complex subunit 7a mRNA, complete cds.//0//1612bp//99%//AF193844  
 C-HEMBA1004617  
 C-HEMBA1004631  
 5 C-HEMBA1004705  
 C-HEMBA1004733  
 C-HEMBA1004748  
 C-HEMBA1004778  
 C-HEMBA1004803  
 10 C-HEMBA1004807  
 C-HEMBA1004820  
 C-HEMBA1004865  
 C-HEMBA1004880  
 C-HEMBA1004900  
 15 C-HEMBA1004909  
 C-HEMBA1004960  
 C-HEMBA1004978  
 C-HEMBA1004980  
 C-HEMBA1004983  
 20 C-HEMBA1004995  
 C-HEMBA1005019//Homo sapiens mRNA for KIAA0648 protein, partial cds.//0//2212bp//99%//AB014548  
 C-HEMBA1005029//Homo sapiens CGI-13 protein mRNA, complete cds.//0//1487bp//99%//AF132947  
 C-HEMBA1005035  
 C-HEMBA1005039  
 25 C-HEMBA1005047//RAS-RELATED PROTEIN RAB-24 (RAB-16).//3.40E-101//106aa//98%//P35290  
 C-HEMBA1005050  
 C-HEMBA1005062  
 C-HEMBA1005066  
 C-HEMBA1005075  
 30 C-HEMBA1005079  
 C-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete cds.//0//2762bp//99%//  
 AF080561  
 C-HEMBA1005123  
 C-HEMBA1005149  
 35 C-HEMBA1005152  
 C-HEMBA1005201//Homo sapiens CGI-07 protein mRNA, complete cds.//0//1608bp//99%//AF132941  
 C-HEMBA1005202//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//1.90E-179//361aa//95%//  
 Q00004  
 C-HEMBA1005223  
 40 C-HEMBA1005232  
 C-HEMBA1005241  
 C-HEMBA1005275  
 C-HEMBA1005293  
 C-HEMBA1005311  
 45 C-HEMBA1005338//Homo sapiens mRNA for matrilin-4, partial.//3.90E-241//1095bp//99%//AJ007581  
 C-HEMBA1005359//ZINC FINGER PROTEIN 137.//3.90E-85//206aa//69%//P52743  
 C-HEMBA1005367//Homo sapiens melastatin 1 (MLSN1) mRNA, complete cds.//9.00E-77//620bp//74%//  
 AF071787  
 C-HEMBA1005374  
 50 C-HEMBA1005382  
 C-HEMBA1005411  
 C-HEMBA1005426  
 C-HEMBA1005443  
 C-HEMBA1005447  
 55 C-HEMBA1005497  
 C-HEMBA1005500  
 C-HEMBA1005506  
 C-HEMBA1005508

C-HEMBA1005526  
C-HEMBA1005530//Homo sapiens anaphase-promoting complex subunit 7 (APC7) mRNA, complete cds.//0//  
1578bp//98%//AF191340  
C-HEMBA1005548//Homo sapiens MAFB/Kreisler basic region/leucine zipper transcription factor (MAFB) mRNA,  
5 complete cds.//1.00E-220//1014bp//99%//AF134157  
C-HEMBA1005552  
C-HEMBA1005568  
C-HEMBA1005588  
C-HEMBA1005593  
10 C-HEMBA1005606  
C-HEMBA1005616  
C-HEMBA1005627  
C-HEMBA1005670  
C-HEMBA1005679  
15 C-HEMBA1005699  
C-HEMBA1005705  
C-HEMBA1005732//Human mRNA for KIAA1293 gene, complete cds.//5.50E-102//317bp//98%//D14697  
C-HEMBA1005815//CALPAIN, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM ACTIVATED NEU-  
TRAL PROTEINASE) (CANP) (MU/M-TYPE).//2.00E-36//342aa//33%//P00789  
20 C-HEMBA1005852  
C-HEMBA1005894  
C-HEMBA1005921  
C-HEMBA1006035  
C-HEMBA1006036  
25 C-HEMBA1006090  
C-HEMBA1006138  
C-HEMBA1006173  
C-HEMBA1006252  
C-HEMBA1006268//Homo sapiens HQ0024c mRNA, complete cds.//3.50E-157//845bp//92%//AF073836  
30 C-HEMBA1006347//MALES-ABSENT ON THE FIRST PROTEIN (EC 2.3.1.-).//1.60E-130//332aa//62%//002193  
C-HEMBA1006359//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//3.50E-105//381aa//54%//P28160  
C-HEMBA1006380  
C-HEMBA1006416  
35 C-HEMBA1006421  
C-HEMBA1006424  
C-HEMBA1006426  
C-HEMBA1006446  
C-HEMBA1006485//PUROMYCIN-SENSITIVE AMINOPEPTIDASE (EC 3.4.11.-) (PSA).//1.90E-81//153aa//  
97%//P55786  
40 C-HEMBA1006486  
C-HEMBA1006494  
C-HEMBA1006546  
C-HEMBA1006562  
C-HEMBA1006595  
45 C-HEMBA1006597  
C-HEMBA1006631  
C-HEMBA1006639  
C-HEMBA1006652//60S RIBOSOMAL PROTEIN L7.//2.40E-44//206aa//47%//P14148  
C-HEMBA1006659  
50 C-HEMBA1006665  
C-HEMBA1006676  
C-HEMBA1006695  
C-HEMBA1006709  
C-HEMBA1006758//Homo sapiens protocadherin beta 13 (PCDH-beta13) mRNA, complete cds.//0//1832bp//  
91%//AF152492  
55 C-HEMBA1006780  
C-HEMBA1006807//Homo sapiens mRNA for SPOP.//5.70E-125//1109bp//75%//AJ000644  
C-HEMBA1006824

C-HEMBA1006865  
 C-HEMBA1006921  
 C-HEMBA1006949  
 5 C-HEMBA1006976//H.sapiens mRNA for Gal-beta(1-3/1-4)GlcNAc alpha-2,3-sialyltransferase./1.90E-80//  
 447bp//89%//X74570  
 C-HEMBA1007051  
 C-HEMBA1007052  
 C-HEMBA1007066  
 C-HEMBA1007073  
 10 C-HEMBA1007078  
 C-HEMBA1007085  
 C-HEMBA1007113  
 C-HEMBA1007121//Homo sapiens bisphosphate 3'-nucleotidase mRNA, complete cds./1.70E-252//1118bp//  
 92%//AF125042  
 15 C-HEMBA1007129  
 C-HEMBA1007147  
 C-HEMBA1007151//Homo sapiens synphilin 1 mRNA, complete cds./0//1900bp//99%//AF076929  
 C-HEMBA1007178  
 20 C-HEMBA1007203//Homo sapiens mRNA for KIAA0214 protein, complete cds./0//1212bp//98%//D86987  
 C-HEMBA1007224//Homo sapiens SUMO-1-specific protease (SSP1) mRNA, complete cds./0//1590bp//99%//  
 AF196304  
 C-HEMBA1007243//Chinese hamster hprt mRNA, complete cds./2.00E-58//650bp//70%//J00060  
 C-HEMBA1007251  
 C-HEMBA1007288  
 25 C-HEMBA1007322  
 C-HEMBA1007341  
 C-HEMBB1000050  
 C-HEMBB1000054  
 C-HEMBB1000059  
 30 C-HEMBB1000089  
 C-HEMBB1000113  
 C-HEMBB1000144//GUANYLATE CYCLASE ACTIVATING PROTEIN 2 (GCAP 2) (RETINAL GUANYLYL CYCLASE ACTIVATOR PROTEIN P24).//1.40E-24//71aa//77%//P51177  
 C-HEMBB1000173  
 35 C-HEMBB1000175  
 C-HEMBB1000272  
 C-HEMBB1000317//FIBULIN-1, ISOFORM D PRECURSOR./7.10E-62//458aa//35%//P37888  
 C-HEMBB1000318  
 C-HEMBB1000336  
 40 C-HEMBB1000341  
 C-HEMBB1000343  
 C-HEMBB1000354  
 C-HEMBB1000374  
 C-HEMBB1000434  
 45 C-HEMBB1000441  
 C-HEMBB1000491  
 C-HEMBB1000493  
 C-HEMBB1000510  
 C-HEMBB1000652  
 50 C-HEMBB1000672  
 C-HEMBB1000684  
 C-HEMBB1000709  
 C-HEMBB1000726  
 C-HEMBB1000770  
 55 C-HEMBB1000827  
 C-HEMBB1000831  
 C-HEMBB1000883  
 C-HEMBB1000888

C-HEMBB1000893  
 C-HEMBB1000913  
 C-HEMBB1000996  
 C-HEMBB1001004  
 5 C-HEMBB1001047  
 C-HEMBB1001060  
 C-HEMBB1001114  
 C-HEMBB1001119  
 C-HEMBB1001133  
 10 C-HEMBB1001142  
 C-HEMBB1001177  
 C-HEMBB1001208  
 C-HEMBB1001209  
 C-HEMBB1001249  
 15 C-HEMBB1001253  
 C-HEMBB1001254  
 C-HEMBB1001271  
 C-HEMBB1001304  
 C-HEMBB1001317  
 20 C-HEMBB1001348  
 C-HEMBB1001394  
 C-HEMBB1001410  
 C-HEMBB1001424  
 C-HEMBB1001426  
 25 C-HEMBB1001429//Homo sapiens leucine aminopeptidase mRNA, complete cds.//0//1933bp//99%//AF061738  
 C-HEMBB1001436  
 C-HEMBB10014437//Rattus norvegicus pyruvate dehydrogenase phosphatase isoenzyme 1 mRNA, complete  
 cds.//3.00E-130//553bp//86%//AF062740  
 C-HEMBB1001449  
 30 C-HEMBB1001458  
 C-HEMBB1001521  
 C-HEMBB1001531  
 C-HEMBB1001535  
 C-HEMBB1001536  
 35 C-HEMBB1001564  
 C-HEMBB1001565  
 C-HEMBB1001585  
 C-HEMBB1001588  
 C-HEMBB1001603  
 40 C-HEMBB1001618  
 C-HEMBB1001635  
 C-HEMBB1001653  
 C-HEMBB1001668  
 C-HEMBB1001673//Homo sapiens mRNA for KIAA0646 protein, complete cds.//0//2035bp//99%//AB014546  
 45 C-HEMBB1001685  
 C-HEMBB1001695  
 C-HEMBB1001707  
 C-HEMBB1001735  
 C-HEMBB1001736//EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 9 (EIF3 P116) (EIF3  
 50 P110).//4.60E-15//391aa//25%//P55884  
 C-HEMBB1001747  
 C-HEMBB1001749//TRANSCRIPTIONAL ACTIVATOR GCN5//1.70E-16//84aa//47%//Q03330  
 C-HEMBB1001753  
 C-HEMBB1001756  
 55 C-HEMBB1001760  
 C-HEMBB1001785  
 C-HEMBB1001797  
 C-HEMBB1001802//Human desmin mRNA, complete cds.//0//1523bp//98%//U59167

C-HEMBB1001816  
 C-HEMBB1001831//Homo sapiens PAM COOH-terminal interactor protein 1 (PCIP1) mRNA complete cds.//0//  
 1514bp//99%//AF056209  
 C-HEMBB1001839//GASTRULA ZINC FINGER PROTEIN XLCGF42.1 (FRAGMENT).//6.90E-11//87aa//35%//  
 5 P18720  
 C-HEMBB1001850  
 C-HEMBB1001863  
 C-HEMBB1001868  
 C-HEMBB1001874  
 10 C-HEMBB1001880  
 C-HEMBB1001899  
 C-HEMBB1001906  
 C-HEMBB1001910  
 C-HEMBB1001911  
 15 C-HEMBB1001921  
 C-HEMBB1001922  
 C-HEMBB1001930  
 C-HEMBB1001944  
 C-HEMBB1001945  
 20 C-HEMBB1001947  
 C-HEMBB1001950//PROBABLE OXYGEN-INDEPENDENT COPROPORPHYRINOGEN III OXIDASE (EC 1.-.-.)  
 (COPROPORPHYRINOGENASE) (COPROGEN OXIDASE).//1.60E-41//370aa//31%//P54304  
 C-HEMBB1001952  
 C-HEMBB1001957  
 25 C-HEMBB1001962  
 C-HEMBB1001983  
 C-HEMBB1001990  
 C-HEMBB1001996  
 C-HEMBB1002002  
 30 C-HEMBB1002005  
 C-HEMBB1002042//CYTOCHROME P450 4C1 (EC 1.14.14.1) (CYPIVC1).//2.70E-49//139aa//55%//P29981  
 C-HEMBB1002043  
 C-HEMBB1002045  
 C-HEMBB1002049  
 35 C-HEMBB1002050  
 C-HEMBB1002068  
 C-HEMBB1002092  
 C-HEMBB1002139  
 C-HEMBB1002142  
 40 C-HEMBB1002190  
 C-HEMBB1002193  
 C-HEMBB1002217//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.10E-132//399aa//  
 44%//Q05481  
 C-HEMBB1002218  
 45 C-HEMBB1002232  
 C-HEMBB1002247  
 C-HEMBB1002249  
 C-HEMBB1002266//NEURONAL PROTEIN.//2.10E-46//121aa//76%//P41737  
 C-HEMBB1002327  
 50 C-HEMBB1002329  
 C-HEMBB1002342//Homo sapiens mRNA for putative thioredoxin-like protein.//1.10E-274//1249bp//99%//  
 AJ010841  
 C-HEMBB1002358  
 C-HEMBB1002371  
 55 C-HEMBB1002387  
 C-HEMBB1002409  
 C-HEMBB1002425  
 C-HEMBB1002442//LIN-10 PROTEIN.//9.70E-14//121aa//31%//P34692

C-HEMBB1002453  
 C-HEMBB1002458  
 C-HEMBB1002477//Human Grb2-associated binder-1 mRNA, complete cds././/7.70E-258//774bp//99%//U43885  
 C-HEMBB1002489  
 5 C-HEMBB1002510//GYP7 PROTEIN././/3.10E-50//192aa//42%//P48365  
 C-HEMBB1002520  
 C-HEMBB1002522  
 C-HEMBB1002545  
 C-HEMBB1002579  
 10 C-HEMBB1002582  
 C-HEMBB1002596  
 C-HEMBB1002603  
 C-HEMBB1002610  
 C-HEMBB1002613  
 15 C-HEMBB1002617  
 C-HEMBB1002623  
 C-HEMBB1002635  
 C-HEMBB1002677  
 C-HEMBB1002683  
 20 C-HEMBB1002699  
 C-HEMBB1002702  
 C-MAMMA1000009  
 C-MAMMA1000043  
 25 C-MAMMA1000045//ENV POLYPROTEIN [CONTAINS: SURFACE PROTEIN GP85; MEMBRANE PROTEIN GP37].//1.90E-07//249aa//27%//P03396  
 C-MAMMA1000057  
 C-MAMMA1000085//PUTATIVE CYSTEINYLY-TRNA SYNTHETASE C29E6.06C (EC 6.1.1.16) (CYSTEINE--  
 TRNA LIGASE) (CYSRS).//2.10E-90//427aa//39%//Q09860  
 C-MAMMA1000092  
 30 C-MAMMA1000103  
 C-MAMMA1000117  
 C-MAMMA1000129  
 C-MAMMA1000133  
 C-MAMMA1000155  
 35 C-MAMMA1000175  
 C-MAMMA1000198  
 C-MAMMA1000241  
 C-MAMMA1000251  
 C-MAMMA1000254  
 40 C-MAMMA1000287  
 C-MAMMA1000307  
 C-MAMMA1000331  
 C-MAMMA1000339  
 C-MAMMA1000340  
 45 C-MAMMA1000348  
 C-MAMMA1000356  
 C-MAMMA1000360  
 C-MAMMA1000402  
 C-MAMMA1000414  
 50 C-MAMMA1000431  
 C-MAMMA1000444  
 C-MAMMA1000458  
 C-MAMMA1000500  
 C-MAMMA1000522  
 55 C-MAMMA1000576  
 C-MAMMA1000583  
 C-MAMMA1000594  
 C-MAMMA1000605

C-MAMMA1000616  
 C-MAMMA1000643  
 C-MAMMA1000684//Homo sapiens 7-60 mRNA, complete cds.//0//2402bp//99%//AF109134  
 C-MAMMA1000696  
 5 C-MAMMA1000707  
 C-MAMMA1000714  
 C-MAMMA1000720  
 C-MAMMA1000744  
 C-MAMMA1000761  
 10 C-MAMMA1000776  
 C-MAMMA1000798  
 C-MAMMA1000839  
 C-MAMMA1000851  
 C-MAMMA1000863  
 15 C-MAMMA1000867  
 C-MAMMA1000876  
 C-MAMMA1000880  
 C-MAMMA1000883  
 C-MAMMA1000921  
 20 C-MAMMA1000931  
 C-MAMMA1000941  
 C-MAMMA1000957  
 C-MAMMA1000962  
 C-MAMMA1000975  
 25 C-MAMMA1000987  
 C-MAMMA1001003  
 C-MAMMA1001030//LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR (LH/CG-R) (LSH-R)  
 (LUTEINIZING HOROMINE RECEPTOR) (FRAGMENT).//1.20E-26//276aa//28%//Q90674  
 C-MAMMA1001038//MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC  
 30 2.7.1.117) (MLCK) [CONTAINS: TELOKIN].//2.60E-107//190aa//95%//Q15746  
 C-MAMMA1001082  
 C-MAMMA1001162  
 C-MAMMA1001186  
 C-MAMMA1001191  
 35 C-MAMMA1001206  
 C-MAMMA1001220  
 C-MAMMA1001243  
 C-MAMMA1001249  
 C-MAMMA1001256  
 40 C-MAMMA1001268  
 C-MAMMA1001271  
 C-MAMMA1001274  
 C-MAMMA1001292  
 C-MAMMA1001305//RHO-GTPASE-ACTIVATING PROTEIN 1 (GTPASE-ACTIVATING PROTEIN RHOGAP)  
 45 (RHO-RELATED SMALL GTPASE PROTEIN ACTIVATOR) (CDC42 GTPASE-ACTIVATING PROTEIN)  
 (P50-RHOGAP).//2.20E-98//283aa//63%//Q07960  
 C-MAMMA1001324  
 C-MAMMA1001341  
 C-MAMMA1001388//LEUCINE-RICH ALPHA-2-GLYCOPROTEIN (LRG).//1.40E-165//312aa//99%//P02750  
 50 C-MAMMA1001397  
 C-MAMMA1001408  
 C-MAMMA1001420  
 C-MAMMA1001442  
 C-MAMMA1001452  
 55 C-MAMMA1001465  
 C-MAMMA1001487  
 C-MAMMA1001501//CALPAIN 1, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM-ACTIVATED NEU-  
 TRAL PROTEINASE) (CANP) (MU-TYPE).//5.70E-55//86aa//97%//P07384

C-MAMMA1001547  
 C-MAMMA1001551  
 C-MAMMA1001575  
 C-MAMMA1001590  
 5 C-MAMMA1001600  
 C-MAMMA1001606  
 C-MAMMA1001627//Homo sapiens mRNA for transcription factor TBX6././/5.20E-189//871bp//99%//AJ007989  
 C-MAMMA1001663  
 C-MAMMA1001670  
 10 C-MAMMA1001671  
 C-MAMMA1001679//F-ACTIN CAPPING PROTEIN BETA SUBUNIT (CAPZ).//0.00000058//29aa//100%//P47756  
 C-MAMMA1001711  
 C-MAMMA1001735//TUBULIN BETA-5 CHAIN (BETA-TUBULIN CLASS-V).//5.90E-240//445aa//97%//P09653  
 15 C-MAMMA1001744  
 C-MAMMA1001745  
 C-MAMMA1001751//Homo sapiens tandem pore domain potassium channel TWIK-2 (KCNK6) mRNA, complete  
 cds.//0//2332bp//99%//AF117708  
 C-MAMMA1001783  
 C-MAMMA1001788  
 20 C-MAMMA1001806  
 C-MAMMA1001812  
 C-MAMMA1001815  
 C-MAMMA1001817  
 C-MAMMA1001818  
 25 C-MAMMA1001820//Rattus norvegicus mRNA for PAG608 gene././/1.30E-198//1157bp//80%//Y13148  
 C-MAMMA1001824  
 C-MAMMA1001851  
 C-MAMMA1001854  
 C-MAMMA1001864  
 30 C-MAMMA1001878  
 C-MAMMA1001890  
 C-MAMMA1001907  
 C-MAMMA1001908  
 C-MAMMA1001931  
 35 C-MAMMA1001969  
 C-MAMMA1002011  
 C-MAMMA1002032  
 C-MAMMA1002041  
 C-MAMMA1002047  
 40 C-MAMMA1002056  
 C-MAMMA1002058  
 C-MAMMA1002078  
 C-MAMMA1002082  
 C-MAMMA1002084  
 45 C-MAMMA1002093  
 C-MAMMA1002094  
 C-MAMMA1002118  
 C-MAMMA1002125  
 C-MAMMA1002132  
 50 C-MAMMA1002140  
 C-MAMMA1002143//Homo sapiens Cdc42 effector protein 4 mRNA, complete cds7/1.70E-252//1170bp//99%//  
 AF099664  
 C-MAMMA1002145  
 C-MAMMA1002198//THIOREDOXIN PEROXIDASE 1 (THIOREDOXIN-DEPENDENT PEROXIDE REDUCTASE  
 55 1) (THIOL-SPECIFIC ANTIOXIDANT PROTEIN) (TSA) (PRP) (NATURAL KILLER CELL ENHANCING FACTOR  
 B) (NKEF-B).//5.20E-61//60aa//90%//P32119  
 C-MAMMA1002230  
 C-MAMMA1002250

C-MAMMA1002282  
 C-MAMMA1002293  
 C-MAMMA1002298  
 C-MAMMA1002299  
 5 C-MAMMA1002308  
 C-MAMMA1002310  
 C-MAMMA1002311  
 C-MAMMA1002322  
 C-MAMMA1002339  
 10 C-MAMMA1002352  
 C-MAMMA1002359  
 C-MAMMA1002360  
 C-MAMMA1002392  
 C-MAMMA1002411  
 15 C-MAMMA1002413  
 C-MAMMA1002417  
 C-MAMMA1002428//LYSOSOME MEMBRANE PROTEIN II (LIMP II) (85 KD LYSOSOMAL MEMBRANE  
 SIALOGLYCOPROTEIN) (LGP85) (CD36 ANTIGEN-LIKE 2).//1.10E-24//96aa//68%//Q14108  
 C-MAMMA1002434  
 20 C-MAMMA1002446  
 C-MAMMA1002454  
 C-MAMMA1002461  
 C-MAMMA1002475  
 C-MAMMA1002556  
 25 C-MAMMA1002566  
 C-MAMMA1002612  
 C-MAMMA1002622//VILLIN.//7.20E-35//53aa//64%//P02640  
 C-MAMMA1002637//KINESIN LIGHT CHAIN (KLC).//1.30E-198//550aa//70%//Q07866  
 C-MAMMA1002650//Mus musculus ODA-8S protein mRNA, complete cds.//5.40E-57//480bp//68%//AF194030  
 30 C-MAMMA1002699//Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds.//4.3e-317//  
 1942bp//85%//AF018261  
 C-MAMMA1002727  
 C-MAMMA1002748  
 C-MAMMA1002758  
 35 C-MAMMA1002780  
 C-MAMMA1002820  
 C-MAMMA1002833  
 C-MAMMA1002843  
 C-MAMMA1002895  
 40 C-MAMMA1002937//ZINC FINGER PROTEIN 135.//8.30E-99//393aa//43%//P52742  
 C-MAMMA1003004  
 C-MAMMA1003047//Homo sapiens protein inhibitor of activated STAT protein PIASy mRNA, complete cds.//0//  
 1533bp//99%//AF077952  
 C-NT2RM1000001//D.melanogaster sap47-2 mRNA.//1.50E-10//417bp//62%//X80110  
 45 C-NT2RM1000018//Human mRNA for KIAA0066 gene, partial cds.//0//3376bp//99%//D31886  
 C-NT2RM1000037//Homo sapiens mRNA for KIAA0690 protein, partial cds.//0//3551bp//99%//AB014590  
 C-NT2RM1000086//Homo sapiens mRNA for KIAA0661 protein, complete cds.//0//3035bp//96%//AB014561  
 C-NT2RM1000421//RIBONUCLEASE INHIBITOR.//4.40E-21//372aa//30%//P10775 C-NT2RM1000499  
 C-NT2RM1001059//NUCLEAR POLYADENYLATED RNA-BINDING PROTEIN NAB4.//3.60E-11//180aa//28%//  
 50 Q99383  
 C-NT2RM1001092//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//3.60E-115//332aa//  
 52%//Q05481  
 C-NT2RM2001592//Homo sapiens mRNA for KIAA1067 protein, partial cds.//0//3471bp//99%//AB028990  
 C-NT2RM2001635//Homo sapiens mRNA for KIAA0618 protein, complete cds.//0//1632bp//99%//AB014518  
 55 C-NT2RM2001637  
 C-NT2RM2001641  
 C-NT2RM2001670//ZINC FINGER PROTEIN 29 (ZFP-29).//6.50E-104//407aa//43%//Q07230  
 C-NT2RM2001699

C-NT2RM2001706  
C-NT2RM2001718  
C-NT2RM2001727//Homo sapiens mRNA for KIAA0462 protein, partial cds./0//2892bp//99%//AB007931  
C-NT2RM2001805  
5 C-NT2RM4000086  
C-NT2RM4000215//MAK16 PROTEIN./1.30E-68//295aa//49%//P10962  
C-NT2RM4000414  
C-NT2RM4000590//RING CANAL PROTEIN (KELCH PROTEIN).//1.00E-59//595aa//28%//Q04652  
C-NT2RM4000634  
10 C-NT2RM4000657//Homo sapiens mRNA for KIAA1069 protein, partial cds./0//1412bp//100%//AB028992  
C-NT2RM4000783  
C-NT2RM4000857//LEUCINE-RICH ALPHA-2-GLYCOPROTEIN (LRG).//6.70E-22//250aa//29%//P02750  
C-NT2RM4000971  
C-NT2RM4000996//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//8.00E-211//738aa//  
15 50%//Q05481  
C-NT2RM4001092//ZINC FINGER PROTEIN GLO3./3.10E-24//265aa//33%//P38682  
C-NT2RM4001178//PROBABLE ATP-DEPENDENT RNA HELICASE HAS1./1.10E-48//218aa//43%//Q03532  
C-NT2RM4001569  
C-NT2RM4001819//Human p58/GTA (galactosyltransferase associated protein kinase) mRNA, complete cds./  
20 8.10E-300//1395bp//98%//M37712  
C-NT2RM4001905  
C-NT2RM4001938//Homo sapiens mRNA for KIAA0898 protein, partial cds./0//2234bp//99%//AB020705  
C-NT2RM4002062//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA LIGASE) (ASPRS).//  
1.90E-31//80aa//52%//P36419  
25 C-NT2RM4002073//Mus musculus fatty acid transport protein 3 mRNA, partial cds./9.30E-293//1751bp//83%//  
AF072758  
C-NT2RM4002093//Homo sapiens neural polypyrimidine tract binding protein (PTB) mRNA, complete cds./0//  
2550bp//99%//AF176085  
C-NT2RM4002109//Homo sapiens kinesin superfamily motor KIF4 mRNA, complete cds./0//2572bp//99%//  
30 AF071592  
C-NT2RM4002146//Homo sapiens MAGOH mRNA, complete cds./6.90E-70//454bp//85%//AF035940  
C-NT2RM4002194//Mus musculus semaphorin Vla mRNA, complete cds./5.20E-297//1753bp//87%//AF030430  
C-NT2RM4002390  
C-NT2RM4002398  
35 C-NT2RM4002420  
C-NT2RM4002534  
C-NT2RM4002565//Mus musculus Sec8 mRNA, complete cds./0//1915bp//87%//AF022962  
C-NT2RM4002571//H.sapiens mRNA for UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase (T2).//  
4.60E-78//921bp//69%//X85019  
40 C-NT2RP1000358//Homo sapiens mRNA; cDNA DKFZp564C186 (from clone DKFZp564C186).//0//1938bp//  
88%//AL050019  
C-NT2RP1000522//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THI-  
OLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING EN-  
ZYME 1).//8.20E-83//345aa//47%//Q61068  
45 C-NT2RP1000609//Homo sapiens mRNA; cDNA DKFZp586C201 (from clone DKFZp586C201).//0//2165bp//  
99%//AL050118  
C-NT2RP1000677//SODIUM-INDEPENDENT ORGANIC ANION TRANSPORTER (ORGANIC ANION TRANS-  
PORTING POLYPEPTIDE).//1.20E-78//483aa//31%//P46721  
C-NT2RP1000701//Homo sapiens phospholipase A2 activating protein (PLA2P) mRNA, complete cds./0//  
50 1687bp//99%//AF145020  
C-NT2RP1000834//Homo sapiens alpha-methylacyl-CoA racemase mRNA, complete cds./1.80E-176//829bp//  
98%//AF047020  
C-NT2RP1000860//Homo sapiens KL04P mRNA, complete cds./0//1555bp//99%//AF064094  
C-NT2RP1000916  
55 C-NT2RP1000944  
C-NT2RP1001079//Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, complete cds./0//2085bp//99%//  
U82267  
C-NT2RP1001080//PROBABLE ATP-DEPENDENT RNA HELICASE DBP9./2.30E-116//319aa//46%//Q06218

C-NT2RP1001113  
C-NT2RP1001173//Homo sapiens mRNA; cDNA DKFZp566D1146 (from clone DKFZp566D1146).//0//2333bp//  
99%//AL080222  
C-NT2RP1001177//Rattus norvegicus histone macroH2A1.2 mRNA, complete cds.//5.20E-108//1278bp//69%//  
5 U79139  
C-NT2RP1001185//Human isovaleryl-coA dehydrogenase (IVD) mRNA, complete cds.//1.90E-158//729bp//99%//  
M34192  
C-NT2RP1001247//Homo sapiens TGF-beta type secreted signaling protein LEFTYA mRNA, complete cds.//0//  
2006bp//100%//AF081513  
10 C-NT2RP1001311  
C-NT2RP1001313//Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds.//7.50E-121//1394bp//69%//  
AF126799  
C-NT2RP2000001//Homo sapiens mRNA for KIAA1111 protein, partial cds.//0//3188bp//99%//AB029034  
C-NT2RP2000027  
15 C-NT2RP2000183//DIHYDROPYRIMIDINASE RELATED PROTEIN-2 (DRP-2) (NEURAL SPECIFIC PROTEIN  
NSP60).//3.30E-16//114aa//44%//002675  
C-NT2RP2000198  
C-NT2RP2000523//APOLIPOPROTEIN B MRNA EDITING PROTEIN (HEPR) (APOBEC-1).//6.00E-16//124aa//  
34%//P41238  
20 C-NT2RP2000551  
C-NT2RP2000644  
C-NT2RP2000660//SAP1 PROTEIN.//5.20E-68//474aa//32%//P39955  
C-NT2RP2000678  
C-NT2RP2000715  
25 C-NT2RP2000842//Human lysophosphatidic acid receptor homolog mRNA, complete cds.//0//1562bp//99%//  
U80811  
C-NT2RP2000970  
C-NT2RP2001347  
C-NT2RP2001460//TRICHOHYALIN.//1.00E-14//521aa//24%//P37709  
30 C-NT2RP2001613//MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT TOM40 (MOM38 PROTEIN) (TRANSLO-  
CASE OF OUTER MEMBRANE 40 KD SUBUNTD.//6.10E-12//184aa//31%//P24391  
C-NT2RP2001634//Homo sapiens alpha-catenin-like protein mRNA, complete cds.//0//2445bp//99%//U97067  
C-NT2RP2001660//Homo sapiens putative 13 S Golgi transport complex 90kD subunit brain-specific isoform mR-  
NA, complete cds.//0//1287bp//99%//AF058718  
35 C-NT2RP2001677  
C-NT2RP2001678  
C-NT2RP2001720  
C-NT2RP2001740//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THI-  
OLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING EN-  
ZYME 1).//7.90E-52//220aa//44%//Q61068  
40 C-NT2RP2001756//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.70E-49//411aa//32%//  
P51523  
C-NT2RP2001839//SCY1 PROTEIN.//5.40E-32//621aa//24%//P53009  
C-NT2RP2001861  
45 C-NT2RP2001869//ZINC FINGER PROTEIN 191.//7.10E-26//126aa//52%//014754  
C-NT2RP2001876//ALLOGRAFT INFLAMMATORY FACTOR-1 (AIF-1) (IONIZED CALCIUM BINDING ADAPTER  
MOLECULE 1).//1.20E-45//141aa//65%//P55008  
C-NT2RP2001898//Human inositol polyphosphate 5-phosphatase (5ptase) mRNA, 3' end.//0//2518bp//98%//  
M74161  
50 C-NT2RP2001936  
C-NT2RP2001943  
C-NT2RP2001946  
C-NT2RP2002032  
C-NT2RP2002033  
55 C-NT2RP2002041  
C-NT2RP2002047  
C-NT2RP2002066//Rattus norvegicus transmembrane receptor Unc5H2 mRNA, complete cds.//1.60E-226//  
1301bp//88%//U87306

C-NT2RP2002124//Homo sapiens mRNA for KIAA1097 protein, partial cds./0//1772bp//95%//AB029020  
 C-NT2RP2002172  
 C-NT2RP2002219  
 5 C-NT2RP2002256//Homo sapiens retinoic acid hydroxylase mRNA, complete cds./0//1528bp//98%//AF005418  
 C-NT2RP2002316  
 C-NT2RP2002373  
 C-NT2RP2002439  
 C-NT2RP2002475  
 C-NT2RP2002546  
 10 C-NT2RP2002591//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.20E-155//562aa//50%//  
 P51523  
 C-NT2RP2002606//Rattus norvegicus Rabin3 mRNA, complete cds./9.20E-147//874bp//87%//U19181  
 C-NT2RP2002643  
 15 C-NT2RP2002727//Rattus norvegicus tulip 2 mRNA, complete cds./3.50E-74//727bp//72%//AF041107  
 C-NT2RP2002736  
 C-NT2RP2002740  
 C-NT2RP2002741//Homo sapiens mRNA for Neuroblastoma, complete cds./9.90E-54//964bp//64%//D89016  
 C-NT2RP2002752  
 C-NT2RP2002753  
 20 C-NT2RP2002857  
 C-NT2RP2003000//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PRO-  
 TEIN).//1.90E-11//132aa//38%//Q13829  
 C-NT2RP2003073  
 C-NT2RP2003164//Homo sapiens mRNA for protein kinase..//0//2313bp//99%//AJ132545  
 25 C-NT2RP2003206  
 C-NT2RP2003228//H.sapiens P1-Cdc21 mRNA./0//2870bp//98%//X74794  
 C-NT2RP2003230//Rattus norvegicus endo-alpha-D-mannosidase (Enman) mRNA, complete cds./2.60E-186//  
 1551bp//77%//AF023657  
 C-NT2RP2003237  
 30 C-NT2RP2003272//Homo sapiens ubiquilin mRNA, complete cds./0//1789bp//99%//AF176069  
 C-NT2RP2003280  
 C-NT2RP2003293  
 C-NT2RP2003394//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1//5.50E-13//302aa//26%//  
 P25386  
 35 C-NT2RP2003401//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THI-  
 OLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING EN-  
 ZYME 1).//9.60E-78//346aa//43%//061068  
 C-NT2RP2003456  
 40 C-NT2RP2003517//Human c-sis/platelet-derived growth factor 2 (SIS/PDGF2) mRNA, complete cds./0//1746bp//  
 95%//M12783  
 C-NT2RP2003522//Homo sapiens zinc finger DNA binding protein 99 (ZNF281) mRNA, complete cds./0//1764bp//  
 99%//AF125158  
 C-NT2RP2003559  
 45 C-NT2RP2003564//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)).//  
 2.10E-59//270aa//46%//P19474  
 C-NT2RP2003581  
 C-NT2RP2003643//Mus musculus mRNA for CMP-N-acetylneuraminc acid synthetase./9.40E-243//1624bp//  
 82%//AJ006215  
 50 C-NT2RP2003702//Homo sapiens 17 beta-hydroxysteroid dehydrogenase type VII (HSD17B7) mRNA, complete  
 cds./2.1e-313//978bp//99%//AF098786  
 C-NT2RP2003704//Homo sapiens mRNA for ATP-dependent metalloprotease YME1L./1.80E-72//350bp//100%//  
 AJ132637  
 C-NT2RP2003727  
 C-NT2RP2003751  
 55 C-NT2RP2003781//HYPOTHETICAL 36.7 KD PROTEIN AH6.2 IN CHROMOSOME II./5.50E-63//253aa//50%//  
 Q09201  
 C-NT2RP2003825  
 C-NT2RP2003871

C-NT2RP2003885  
C-NT2RP2003912//SERINE/THREONINE-PROTEIN KINASE NEK1 (EC 2.7.1.-) (NIMA-RELATED PROTEIN KI-  
NASE 1).//6.10E-183//387aa//87%//P51954  
C-NT2RP2003976//Homo sapiens mRNA for KIAA0447 protein, complete cds.//0//2866bp//98%//AB007916  
5 C-NT2RP2003988  
C-NT2RP2004013//TRANSCRIPTION FACTOR BTF3 (RNA POLYMERASE B TRANSCRIPTION FACTOR 3).//  
2.30E-53//141aa//78%//P20290  
C-NT2RP2004098//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLA-  
SE).//5.40E-30//319aa//31%//Q01513  
10 C-NT2RP2004142  
C-NT2RP2004170//Homo sapiens mRNA for transducin (beta) like 1 protein.//1.10E-138//1236bp//74%//Y12781  
C-NT2RP2004194//Rattus norvegicus Golgi SNARE GS15 mRNA, complete cds.//3.80E-52//397bp//82%//  
AF003998  
C-NT2RP2004207  
15 C-NT2RP2004226  
C-NT2RP2004232//Homo sapiens EPK2 mRNA for serine/threonine kinase, complete cds.//0//2272bp//99%//  
AB015982  
C-NT2RP2004242//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H).//  
9.90E-12//427aa//26%//P19246  
20 C-NT2RP2004270//PROTEIN PTM1 PRECURSOR.//1.40E-16//334aa//24%//P32857  
C-NT2RP2004321  
C-NT2RP2004339  
C-NT2RP2004347  
25 C-NT2RP2004396//Homo sapiens mRNA for activator of S phase Kinase, complete cds.//5.40E-243//1108bp//  
99%//AB028069  
C-NT2RP2004399  
C-NT2RP2004400  
C-NT2RP2004412  
C-NT2RP2004425//Mus musculus axotrophin mRNA, complete cds.//0//2321bp//86%//AF155739  
30 C-NT2RP2004490  
C-NT2RP2004523  
C-NT2RP2004538//Mus musculus kinesin-like protein KIF1B (Kif1b) mRNA, complete cds.//0//1387bp//86%//  
AF090190  
C-NT2RP2004580  
35 C-NT2RP2004587//Homo sapiens mRNA for KIAA0888 protein, partial cds.//0//2886bp//100%//AB020695  
C-NT2RP2004594  
C-NT2RP2004681  
C-NT2RP2004709  
C-NT2RP2004710//Homo sapiens mRNA for KIAA1014 protein, partial cds.//0//2587bp//100%//AB023231  
40 C-NT2RP2004732//Homo sapiens mRNA for KIAA0884 protein, partial cds.//0//1774bp//99%//AB020691  
C-NT2RP2004767  
C-NT2RP2004775  
C-NT2RP2004961//Rattus norvegicus KRAB/zinc finger suppressor protein 1 (KS1) mRNA, complete cds.//1.00E-  
228//1666bp//75%//U56732  
45 C-NT2RP2004962  
C-NT2RP2004982  
C-NT2RP2005003//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)).//  
1.80E-99//376aa//43%//P19474  
C-NT2RP2005018  
50 C-NT2RP2005020  
C-NT2RP2005022  
C-NT2RP2005031  
C-NT2RP2005116//Homo sapiens mRNA for KIAA0664 protein, partial cds.//0//4069bp//99%//AB014564  
C-NT2RP2005139//2-5A-DEPENDENT RIBONUCLEASE (EC 3.1.26.-) (2-5A-DEPENDENT RNAASE) (RNASE  
L) (RIBONUCLEASE 4) (FRAGMENT).//0.00000022//139aa//35%//Q05921  
55 C-NT2RP2005168//Homo sapiens mRNA for E1B-55kDa-associated protein.//0//2769bp//98%//AJ007509  
C-NT2RP2005254  
C-NT2RP2005325//Homo sapiens LIM-homeodomain protein HLHX2 (LHX2) mRNA, complete cds.//0//1643bp//

99%//AF124735  
 C-NT2RP2005336//TRICHOHYALIN//5.40E-10//545aa//22%//P37709  
 C-NT2RP2005344//PROBABLE CALCIUM-TRANSPORTING ATPASE 5 (EC 3.6.1.38).//2.10E-124//636aa//  
 38%//P32660  
 5 C-NT2RP2005360  
 C-NT2RP2005407//OXYSTEROL-BINDING PROTEIN//5.30E-63//410aa//40%//P22059  
 C-NT2RP2005454  
 C-NT2RP2005457//Homo sapiens NADH-ubiquinone oxidoreductase subunit B14.5B homolog mRNA, complete  
 cds.//1.20E-130//608bp//99%//AF070652  
 10 C-NT2RP2005476//Human p190-B (pl90-B) mRNA, complete cds.//3.40E-108//668bp//88%//U17032  
 C-NT2RP2005491//PARAMYOSIN (PMY) (ANTIGEN B).//0.00000015//279aa//26%//P35418  
 C-NT2RP2005496//ZINC FINGER PROTEIN 135.//2.90E-146//398aa//59%//P52742  
 C-NT2RP2005501  
 C-NT2RP2005531//PROTEIN 4.1 (BAND 4.1) (P4.1).//5.50E-70//393aa//39%//P11171  
 15 C-NT2RP2005600//Homo sapiens mRNA for KIAA1020 protein, partial cds.//0//2554bp//99%//AB028943  
 C-NT2RP2005645  
 C-NT2RP2005694//X-LINKED RETINITIS PIGMENTOSA GTPASE REGULATOR.//2.60E-10//175aa//27%//  
 Q92834  
 C-NT2RP2005701//ZINC-FINGER PROTEIN RFP (RET FINGER PROTEIN).//3.00E-63//323aa//39%//Q62158  
 20 C-NT2RP2005741  
 C-NT2RP2005806  
 C-NT2RP2005815  
 C-NT2RP2005841  
 C-NT2RP2005882  
 25 C-NT2RP2005942//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANSFERASE).//1.50E-67//388aa//44%//P25500  
 C-NT2RP2006103  
 C-NT2RP2006166  
 C-NT2RP2006258  
 30 C-NT2RP2006261  
 C-NT2RP2006321  
 C-NT2RP2006454  
 C-NT2RP2006598//Homo sapiens retinoid X receptor interacting protein mRNA, complete cds.//3.10E-295//  
 1193bp//99%//AF113538  
 35 C-NT2RP3000046//MITOCHONDRIAL GTPASE MSS1 PRECURSOR.//4.60E-78//421aa//37%//P32559  
 C-NT2RP3000047//NPL4 PROTEIN.//1.10E-85//526aa//36%//P33755  
 C-NT2RP3000418  
 C-NT2RP3000439//HYPOTHETICAL 46.4 KD PROTEIN IN FFH-GRPE INTERGENIC REGION.//2.90E-  
 1511319aa//26%//P37908  
 40 C-NT2RP3000487  
 C-NT2RP3000512//Human HOX2G mRNA from the Hox2 locus.//0//1934bp//99%//X16667  
 C-NT2RP3000526  
 C-NT2RP3000603//NEUROGENIC DIFFERENTIATION FACTOR 1.//3.70E-11//90aa//42%//Q13562  
 C-NT2RP3000605//Mus musculus mRNA for wizL, complete cds.//0//2232bp//82%//AB012265  
 45 C-NT2RP3000628  
 C-NT2RP3000739//ATROPHIN-1 (DENTATORUBRAL-PALLIDOLUYSIAN ATROPHY PROTEIN).//1.40E-24//  
 155aa//37%//Q10149  
 C-NT2RP3000845//PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78 (EC 2.7.1.).//8.30E-108//331aa//  
 50 50%//P27448  
 C-NT2RP3000968//40S RIBOSOMAL PROTEIN S15A.//1.90E-46//73aa//98%//P39027  
 C-NT2RP3001057//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//9.00E-201//584aa//  
 54%//Q05481  
 C-NT2RP3001113//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//2.90E-11//631aa//23%//  
 P25386  
 55 C-NT2RP3001245//Homo sapiens mRNA for KIAA0923 protein, complete cds.//0//2659bp//99%//AB023140  
 C-NT2RP3001253//NUF1 PROTEIN (SPINDLE POLY BODY SPACER PROTEIN SPC110).//1.70E-10//540aa//  
 23%//P32380  
 C-NT2RP3001356

C-NT2RP3001383  
 C-NT2RP3001399//SSU72 PROTEIN././/1.30E-16//84aa//52%//P53538  
 C-NT2RP3001554//MICROTUBULE-ASSOCIATED PROTEIN 1B [CONTAINS: LIGHT CHAIN LC1].//1.40E-76//  
 388aa//32%//P46821

5 C-NT2RP3001712//Homo sapiens HP1-BP74 protein mRNA, complete cds././/0//1788bp//99%//AF113534  
 C-NT2RP3001724//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds././/1.10E-  
 240//902bp//99%//AF054177  
 C-NT2RP3001727//Rattus norvegicus implantation-associated protein (IAG2) mRNA, partial cds././/6.90E-132//  
 774bp//88%//AF008554

10 C-NT2RP3001730//SEPTIN 2 HOMOLOG (FRAGMENT).//7.10E-132//294aa//84%//Q14141  
 C-NT2RP3001739  
 C-NT2RP3001777  
 C-NT2RP3001857//VEGETABLE INCOMPATIBILITY PROTEIN HET-E-1././/1.20E-14//242aa//24%//Q00808  
 C-NT2RP3001943//Homo sapiens mRNA for KIAA0675 protein, complete cds././/0//3747bp//99%//AB014575

15 C-NT2RP3001944  
 C-NT2RP3002033  
 C-NT2RP3002054  
 C-NT2RP3002063//Homo sapiens mRNA for KIAA1033 protein, partial cds././/0//2830bp//99%//AB028956  
 C-NT2RP3002099

20 C-NT2RP3002102  
 C-NT2RP3002147  
 C-NT2RP3002163  
 C-NT2RP3002173  
 C-NT2RP3002255

25 C-NT2RP3002303//PROBABLE UNDECAPRENYL PYROPHOSPHATE SYNTHETASE (EC 2.5.1.31) (UPP SYN-  
 THETASE) (DI-TRANS-POLY-CIS-DECAPRENYLCISTRANSFERASE).//8.60E-49//243aa//43%//Q58767  
 C-NT2RP3002343  
 C-NT2RP3002351//Human mRNA for NAD-dependent methylene tetrahydrofolate dehydrogenase cyclohydrolase  
 (EC 1.5.1.15).//4.20E-70//590bp//76%//X16396

30 C-NT2RP3002399//DNA REPLICATION LICENSING FACTOR MCM4 (CDC21 HOMOLOG)(P1-CDC21).//8.60E-  
 79//416aa//34%//P33991  
 C-NT2RP3002455//Homo sapiens mRNA for KIAA0678 protein, partial cds././/0//3811bp//99%//AB014578  
 C-NT2RP3002545//Homo sapiens mRNA; cDNA DKFZp586G0518 (from clone DKFZp586G0518).//0//2499bp//  
 99%//AL050092

35 C-NT2RP3002549//HYPOTHETICAL 26.6 KD PROTEIN T19C3.4 IN CHROMOSOME III.//5.80E-40//161aa//  
 52%//Q10010  
 C-NT2RP3002602//PROBABLE PROTEIN DISULFIDE ISOMERASE ER-60 PRECURSOR (EC 5.3.4.1) (ERP60)  
 (58 KD MICROSOMAL PROTEIN) (P58) (HIP-70) (Q-2).//2.90E-19//173aa//28%//P11598

40 C-NT2RP3002603  
 C-NT2RP3002628//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//2.50E-26//  
 90aa//42%//P38660  
 C-NT2RP3002659  
 C-NT2RP3002660  
 C-NT2RP3002682//Homo sapiens CGI-145 protein mRNA, complete cds././/0//1596bp//98%//AF151903

45 C-NT2RP3002687  
 C-NT2RP3002688//Mouse mRNA for kinesin-like protein (Kifib), complete cds././/1.10E-93//1205bp//69%//D17577  
 C-NT2RP3002701  
 C-NT2RP3002785//LETHAL(2)DENTICLELESS PROTEIN (DTL83 PROTEIN).//2.50E-55//187aa//39%//Q24371  
 C-NT2RP3002869//Mus musculus semaphorin VIa mRNA, complete cds././/2.50E-232//1282bp//85%//AF030430

50 C-NT2RP3002876  
 C-NT2RP3002877  
 C-NT2RP3002909//Homo sapiens mRNA for KIAA0771 protein, partial cds././/0//2085bp//94%//AB018314  
 C-NT2RP3002969//Homo sapiens mRNA for Acyl-CoA synthetase 3, complete cds././/0//2722bp//99%//D89053  
 C-NT2RP3002972//Halocynthia roretzi mRNA for HrPET-1, complete cds././/3.90E-52//899bp//64%//AB029333

55 C-NT2RP3003032//Homo sapiens okadaic acid-inducible and cAMP-regulated phosphoprotein 19 (ARPP-19) mR-  
 NA, complete cds././/0//2656bp//99%//AF084555  
 C-NT2RP3003061//ANKYRIN././/1.40E-20//200aa//37%//Q02357  
 C-NT2RP3003071//NEUROGENIC PROTEIN BIG BRAIN././/1.10E-05//258aa//24%//P23645

C-NT2RP3003078  
 C-NT2RP3003139  
 C-NT2RP3003145//Mus musculus metallocarboxypeptidase CPX-1 mRNA, complete cds./0//2251bp//81%//  
 AF07773 8  
 5 C-NT2RP3003150  
 C-NT2RP3003197//HYPOTHETICAL 33.8 KD PROTEIN C5H10.01 IN CHROMOSOME 1./5.70E-09//169aa//  
 31%//Q09674  
 C-NT2RP3003203//Rattus norvegicus golgi stacking protein homolog GRASP55 mRNA, complete cds./2.00E-  
 210//1851bp//76%//AF110267  
 10 C-NT2RP3003210  
 C-NT2RP3003212//Rattus norvegicus lamina associated polypeptide 1C (LAP1C) mRNA, complete cds./4.30E-  
 187//1750bp//75%//U20286  
 C-NT2RP3003230//Homo sapiens mRNA for hCRNN4, complete cds./0//2350bp//99%//AB030656  
 15 C-NT2RP3003242//Homo sapiens stanniocalcin-related protein mRNA, complete cds./0//2366bp//99%//  
 AF098462  
 C-NT2RP3003251//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A))(RO(SS-A)).//  
 4.20E-86//366aa//48%//P19474  
 C-NT2RP3003301//MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR (EC 3.4.21.-).//1.10E-170//  
 585aa//54%//064948  
 20 C-NT2RP3003311  
 C-NT2RP3003409//Human DHHC-domain-containing cysteine-rich protein mRNA, complete cds./9.20E-45//  
 782bp//65%//U90653  
 C-NT2RP3003427  
 C-NT2RP3003543  
 25 C-NT2RP3003552  
 C-NT2RP3003555//HYPOTHETICAL 32.6 KD PROTEIN IN MET30-PIG2 INTERGENIC REGION./4.50E-30//  
 191aa//40%//P40529  
 C-NT2RP3003564  
 C-NT2RP3003589//Homo sapiens ras-related GTP-binding protein mRNA, complete cds./0//3131bp//94%//  
 30 AF106681  
 C-NT2RP3003621  
 C-NT2RP3003625  
 C-NT2RP3003656  
 C-NT2RP3003659//HES1 PROTEIN./5.90E-22//229aa//27%//P35843  
 35 C-NT2RP3003686  
 C-NT2RP3003701//F-SPONDIN PRECURSOR./1.80E-17//324aa//26%//P35446  
 C-NT2RP3003716//SLIT PROTEIN PRECURSOR./6.60E-10//150aa//34%//P24014  
 C-NT2RP3003726//Homo sapiens spermatogenesis associated PD1 mRNA, complete cds./0//2568bp//99%//  
 U28164  
 40 C-NT2RP3003795  
 C-NT2RP3003805  
 C-NT2RP3003809//SAV PROTEIN./1.10E-131//576aa//41%//Q07590  
 C-NT2RP3003819  
 C-NT2RP3003825//PHOSPHATIDYLCHOLINE TRANSFER PROTEIN (PC-TP)./9.60E-19//174aa//31%//  
 45 P02720  
 C-NT2RP3003831//Homo sapiens ENOGL-1 (alias ENGL-a) mRNA for endonuclease G-like protein-1, complete  
 cds./2.2e-316//1436bp//99%//AB020523  
 C-NT2RP3003833  
 C-NT2RP3003842  
 50 C-NT2RP3003846//Homo sapiens mRNA for putative phospholipase, complete cds./4.80E-277//1255bp//99%//  
 AB019435  
 C-NT2RP3003870//Homo sapiens mRNA for KIAA0800 protein, complete cds./0//2557bp//99%//AB018343  
 C-NT2RP3003876  
 C-NT2RP3003914//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-)  
 55 (DUGT)./2.20E-20//76aa//64%//Q09332  
 C-NT2RP3003918//Homo sapiens VAMP-associated protein B (VAP-B) mRNA, complete cds./0//2191bp//99%//  
 AF086628  
 C-NT2RP3003989

C-NT2RP3004016//TRANSCRIPTION INTERMEDIARY FACTOR 1-BETA (NUCLEAR COREPRESSOR KAP-1) (KRAB-ASSOCIATED PROTEIN 1).//1.50E-17//226aa//26%//Q13263  
 C-NT2RP3004070  
 C-NT2RP3004145  
 5 C-NT2RP3004215  
 C-NT2RP3004253  
 C-NT2RP3004282//Homo sapiens torsinA (DYT1) mRNA, complete cds.//5.10E-24//597bp//61 %//AF007871  
 C-NT2RP3004348//R.norvegicus mRNA for cytosolic resiniferatoxin-binding protein.//1.10E-185//1130bp//82%//  
 X67877  
 10 C-NT2RP3004490//Homo sapiens PAC clone 166H1 from 12q, complete sequence.//0//1778bp//99%//AC003982  
 C-NT2RP3004503  
 C-NT2RP3004566//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.20E-95//434aa//43%//  
 P51523  
 15 C-NT2RP3004670//Homo sapiens GN6ST mRNA for N-acetylglucosamine-6-O-sulfotransferase (GlcNAc6ST),  
 complete cds.//0//2393bp//99%//AB014679  
 C-NT2RP4000023  
 C-NT2RP4000218  
 C-NT2RP4000424  
 C-NT2RP4001213//ZINC FINGER PROTEIN 184 (FRAGMENT).//5.70E-141//511aa//43%//Q99676  
 20 C-NT2RP4001447  
 C-NT2RP4001841  
 C-NT2RP4001849//SH3-BINDING PROTEIN 3BP-1.//1.40E-85//489aa//43%//P55194  
 C-NT2RP4002047//GTP-BINDING PROTEIN LEPA.//1.50E-168//601aa//52%//067618  
 C-NT2RP4002075  
 25 C-NT2RP4002083  
 C-OVARC1000001//Homo sapiens mRNA for actin binding protein ABP620, complete cds.//7.00E-217//683bp//  
 99%//AB029290  
 C-OVARC1000008  
 C-OVARC1000017  
 30 C-OVARC1000058  
 C-OVARC1000068  
 C-OVARC1000071//Homo sapiens NTF2-related export protein NXT1 (NXT1) mRNA, complete cds.//1.50E-47//  
 727bp//67%//AF156957  
 C-OVARC1000085//Human mRNA for proteasome subunit HC5.//1.00E-151//699bp//100%//D00761  
 35 C-OVARC1000109  
 C-OVARC1000114  
 C-OVARC1000145  
 C-OVARC1000240  
 C-OVARC1000302  
 40 C-OVARC1000408  
 C-OVARC1000414  
 C-OVARC1000440  
 C-OVARC1000442  
 C-OVARC1000496  
 45 C-OVARC1000556//RIBOSOMAL PROTEIN S6 KINASE II ALPHA 2 (EC 2.7.1.-) (S6KII-ALPHA 2) (P90-RSK 2)  
 (RIBOSOMAL S6 KINASE 3) (RSK3) (PP90RSK3).//3.30E-67//132aa//95%//015349  
 C-OVARC1000557  
 C-OVARC1000578  
 C-OVARC1000622  
 50 C-OVARC1000679//Homo sapiens myosin-IXa mRNA, complete cds.//0//808bp//99%//AF117888  
 C-OVARC1000681  
 C-OVARC1000700  
 C-OVARC1000724  
 C-OVARC1000751//PROBABLE PROTEIN PHOSPHATASE 2C T23F11.1 (EC 3.1.3.16) (PP2C).//5.60E-11//  
 55 74aa//37%//P49596  
 C-OVARC1000800//MITOCHONDRIAL STRESS-70 PROTEIN PRECURSOR (75 KD GLUCOSE REGULATED  
 PROTEIN) (GRP 75).//3.90E-46//78aa//98%//035501  
 C-OVARC1000885//OXIDOREDUCTASE UCPA (EC 1.---).//1.30E-32//170aa//34%//P37440

C-OVARC1000936//COAT PROTEIN GP37 (ENV PROTEIN GP37).//0.0000054//135aa//28%//P03398  
 C-OVARC1000937//S-PHASE ENTRY CYCLIN 6.//4.90E-10//61aaaa//49%//P32943  
 C-OVARC1000960  
 C-OVARC1000971  
 5 C-OVARC1000999//ANKYRIN HOMOLOG PRECURSOR.//4.10E-11//189aa//32%//Q06527  
 C-OVARC1001000  
 C-OVARC1001029  
 C-OVARC1001040  
 C-OVARC1001051//EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN  
 10 EPS15) (AF-1P PROTEIN).//1.10E-08//216aa//23%//P42566  
 C-OVARC1001113//Homo sapiens diaphanous 1 (HDIA1) mRNA, complete cds.//5.1e-310//1588bp//93%//  
 AF051782  
 C-OVARC1001118  
 C-OVARC1001129  
 15 C-OVARC1001169  
 C-OVARC1001240  
 C-OVARC1001261  
 C-OVARC1001339  
 C-OVARC1001342//40S RIBOSOMAL PROTEIN S8.//1.40E-110//207aa//99%//P09058  
 20 C-OVARC1001357  
 C-OVARC1001442  
 C-OVARC1001611  
 C-OVARC1001813  
 C-OVARC1002112//Homo sapiens histone macroH2A1.2 mRNA, complete cds.//0//1760bp//99%//AF054174  
 25 C-OVARC1002143  
 C-OVARC1002165//3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 2 (EC 1.3.99.5) (STEROID 5-ALPHA-  
 REDUCTASE 2) (SR TYPE 2).//7.60E-08//114aa//37%//P31213  
 C-OVARC1002182//BETA-TRCP (BETA-TRANSDUCIN REPEAT-CONTAINING PROTEIN) (BTRCP).//1.70E-  
 09//207aa//30%//Q91854  
 30 C-PLACE1000014  
 C-PLACE1000078  
 C-PLACE1000492//Rat vacuolar protein sorting homolog r-vps33b mRNA, complete cds.//0//2041bp//87%//  
 U35245  
 C-PLACE1000793//NEUROGENIC PROTEIN BIG BRAIN.//1.70E-07//251aa//24%//P23645  
 35 C-PLACE1000814  
 C-PLACE1000979//ZINC FINGER PROTEIN 135.//2.50E-153//326aa//64%//P52742  
 C-PLACE1001007  
 C-PLACE1001054//Homo sapiens mRNA for RuvB-like DNA helicase TIP49b, complete cds.//4.00E-300//  
 1355bp//100%//AB024301  
 40 C-PLACE1001088  
 C-PLACE1001136  
 C-PLACE1001241  
 C-PLACE1001377//Homo sapiens ADAM10 (ADAM10) mRNA, complete cds.//5.90E-228//827bp//99%//  
 AF009615  
 45 C-PLACE1001395  
 C-PLACE1001740  
 C-PLACE1001746  
 C-PLACE1001983//HYPOTHETICAL 46.4 KD PROTEIN IN FFH-GRPE INTERGENIC REGION.//7.50E-16//  
 319aa//26%//P37908  
 50 C-PLACE1002066  
 C-PLACE1002115  
 C-PLACE1002213  
 C-PLACE1002342//Homo sapiens mRNA for KIAA0728 protein, partial cds.//0//1657bp//98%//AB018271  
 C-PLACE1002450//Human zinc finger protein mRNA, complete cds.//0//2565bp//99%//U69274  
 55 C-PLACE1002474//Mus musculus matrilin-2 precursor mRNA, complete cds.//0//2092bp//84%//U69262  
 C-PLACE1002499  
 C-PLACE1002578  
 C-PLACE1002714

C-PLACE1002772  
 C-PLACE1002775//PEREGRIN (BR140 PROTEIN).//3.80E-13//272aa//28%//P55201  
 C-PLACE1002834//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//5.50E-203//396aa//86%//  
 P51522  
 5 C-PLACE1002993  
 C-PLACE1003030//Homo sapiens snRNA activating protein complex 190kD subunit (SNAP190) mRNA, complete  
 cds.//8.50E-44//225bp//100%//AF032387  
 C-PLACE1003205  
 C-PLACE1003249  
 10 C-PLACE1003493//ENDOTHELIAL CELL MULTIMERIN PRECURSORS.//1.70E-23//594aa//33%//P28481  
 C-PLACE1003553  
 C-PLACE1003592  
 C-PLACE1003596//OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG.//2.60E-93//270aa//66%//  
 P46975  
 15 C-PLACE1003669//TRICHOHYALIN.//5.60E-09//219aa//30%//P22793  
 C-PLACE1003709//Homo sapiens mitotic checkpoint kinase Bub1 (BUB1) mRNA, complete cds.//6.20E-282//  
 1316bp//98%//AF053305  
 C-PLACE1003870  
 20 C-PLACE1003885//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANSFERASE).//3.70E-222//651aa//66%//P25500  
 C-PLACE1003892  
 C-PLACE1003900  
 C-PLACE1004336  
 C-PLACE1004384  
 25 C-PLACE1004425  
 C-PLACE1004471//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//2.90E-56//276aa//41%//  
 P51522  
 C-PLACE1004506//Homo sapiens carboxyl terminal LIM domain protein (CLIM1) mRNA, complete cds.//2.10E-  
 16//402bp//62%//U90878  
 30 C-PLACE1004518  
 C-PLACE1004550//Homo sapiens CGI-20 protein mRNA, complete cds.//3.50E-274//1305bp//97%//AF132954  
 C-PLACE1004681  
 C-PLACE1004693  
 35 C-PLACE1004716//Homo sapiens HSPC038 protein mRNA, complete cds.//2.70E-103//586bp//91%//AF125099  
 C-PLACE1004815  
 C-PLACE1004836  
 C-PLACE1004838  
 C-PLACE1004840  
 C-PLACE1004900  
 40 C-PLACE1004985  
 C-PLACE1005085  
 C-PLACE1005086  
 C-PLACE1005108  
 C-PLACE1005146  
 45 C-PLACE1005409  
 C-PLACE1005453  
 C-PLACE1005477  
 C-PLACE1005557//60S RIBOSOMAL PROTEIN L27.//1.90E-11//60aa//48%//P46288  
 C-PLACE1005595  
 50 C-PLACE1005603  
 C-PLACE1005639  
 C-PLACE1005727//Homo sapiens STRIN protein (STRIN) mRNA, complete cds.//2.00E-118//378bp//98%//  
 AF162680  
 C-PLACE1005799  
 55 C-PLACE1005813//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.//0//2040bp//99%//AF065482  
 C-PLACE1005884  
 C-PLACE1005968  
 C-PLACE1006002

C-PLACE1006003//Homo sapiens CGI-94 protein mRNA, complete cds.//2.40E-177//829bp//99%//AF151852  
 C-PLACE1006017  
 C-PLACE1006037  
 C-PLACE1006076  
 5 C-PLACE1006143  
 C-PLACE1006248//Homo sapiens mRNA for KIAA0648 protein, partial cds.//0//1489bp//100%//AB014548  
 C-PLACE1006288//VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN 1 (VDAC1) (PLASMA-  
 LEMMAL PORIN) (OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN) (PORIN 31HL) (PORIN 31HM).//  
 10 4.60E-117//147aa//80%//P21796  
 C-PLACE1006318//Mus musculus skm-BOP2 (Bop) mRNA, complete cds.//3.00E-07//376bp//59%//U76374  
 C-PLACE1006368//HYALURONAN-MEDIATED MOTILITY RECEPTOR (HYALURONIC ACID RECEPTOR).//  
 1.30E-18//460aa//24%//Q00547  
 C-PLACE1006371  
 C-PLACE1006469//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- AC-  
 15 TIVATING ENZYME).//1.20E-83//313aa//49%//P27550  
 C-PLACE1006506//Homo sapiens anaphase-promoting complex subunit 4 (APC4) mRNA, complete cds.//0//  
 2170bp//99%//AF191338  
 C-PLACE1006521  
 C-PLACE1006534//Homo sapiens mRNA; cDNA DKFZp564G1964 (from clone DKFZp564G1964).//1.70E-192//  
 20 883bp//99%//AL110144  
 C-PLACE1006617  
 C-PLACE1006640  
 C-PLACE1006754//BILARY GLYCOPROTEIN 1 PRECURSOR (BGP-1) (ANTIGEN CD66) (CD66A ANTIGEN).//  
 6.20E-63//191aa//43%//P13688  
 25 C-PLACE1006760  
 C-PLACE1006779  
 C-PLACE1006805  
 C-PLACE1006815  
 C-PLACE1006867  
 30 C-PLACE1007045  
 C-PLACE1007097  
 C-PLACE1007111  
 C-PLACE1007112  
 C-PLACE1007140//Homo sapiens mRNA for KIAA1009 protein, complete cds.//0//3492bp//99%//AB023226  
 35 C-PLACE1007218  
 C-PLACE1007454  
 C-PLACE1007478  
 C-PLACE1007677  
 C-PLACE10077057//Mus musculus mRNA for Ndr1 related protein Ndr3, complete cds.//1.10E-184//1096bp//  
 40 82%//AB033922  
 C-PLACE1007737  
 C-PLACE1007743  
 C-PLACE1007852//Homo sapiens mRNA for KIAA0878 protein, complete cds.//1.00E-232//1174bp//94%//  
 AB020685  
 45 C-PLACE1007877  
 C-PLACE1008045  
 C-PLACE1008080//Homo sapiens mRNA for HEXIM1 protein, complete cds.//0//2152bp//99%//AB021179  
 C-PLACE1008111//PROBABLE OXIDOREDUCTASE (EC 1.---).//3.00E-25//208aa//37%//Q03326  
 C-PLACE1008201//Rattus rattus zinc finger protein, complete cds.//0//2265bp//83%//L23077  
 50 C-PLACE1008231  
 C-PLACE1008244//VEGETATILE INCOMPATIBILITY PROTEIN HET-E-1.//9.50E-21//148aa//38%//Q00808  
 C-PLACE1008330//EOSINOPHIL LYSOPHOSPHOLIPASE (EC 3.1.1.5) (CHARCOT-LEYDEN CRYSTAL PRO-  
 TEIN) (LYSOLECITHIN ACYLHYDROLASE) (CLC) (GALACTIN- 10).//2.20E-23//94aa//47%//Q05315  
 C-PLACE1008331  
 55 C-PLACE1008369  
 C-PLACE1008392  
 C-PLACE1008405  
 C-PLACE1008424

C-PLACE1008584  
 C-PLACE1008625  
 C-PLACE1008630  
 C-PLACE1008643//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN  
 5 H2).//5.20E-90//483aa//38%//002668  
 C-PLACE1008715  
 C-PLACE1008748  
 C-PLACE1008757  
 C-PLACE1008798  
 10 C-PLACE1008851  
 C-PLACE1008947  
 C-PLACE1009039  
 C-PLACE1009048  
 C-PLACE1009050  
 15 C-PLACE10091137//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds.//  
 0//2529bp//99%//AF035586  
 C-PLACE1009150  
 C-PLACE1009200  
 C-PLACE1009246//POLLEN SPECIFIC PROTEIN SF3.//4.40E-16//82aa//43%//P29675  
 20 C-PLACE1009298//Homo sapiens vacuolar sorting protein 35 (VPS35) mRNA, complete cds.//0//2262bp//99%//  
 AF191298  
 C-PLACE1009308//GLUCOSE REPRESSION MEDIATOR PROTEIN.//4.00E-06//439aa//23%//P14922  
 C-PLACE1009398//ZINC FINGER PROTEIN 135.//6.20E-97//361aa//51%//P52742  
 C-PLACE1009410  
 25 C-PLACE1009477//Homo sapiens mRNA for KIAA0684 protein, partial cds.//6.50E-148//592bp//99%//AB014584  
 C-PLACE1009493  
 C-PLACE1009539  
 C-PLACE1009595  
 C-PLACE1009637  
 30 C-PLACE1009639  
 C-PLACE1009798//RLR1 PROTEIN.//1.60E-18//270aa//23%//P53552  
 C-PLACE1009861//CATHEPSIN B-LIKE CYSTEINE PROTEINASE 6 PRECURSOR (EC 3.4.22.-).//6.50E-28//  
 209aa//38%//P43510  
 C-PLACE1009888  
 35 C-PLACE1009925//Homo sapiens RNA helicase (RIG-I) mRNA, complete cds.//0//1730bp//99%//AF038963  
 C-PLACE1009947  
 C-PLACE1010069  
 C-PLACE1010089//Homo sapiens mRNA for KIAA1097 protein, partial cds.//0//1554bp//100%//AB029020  
 C-PLACE1010231//CELL SURFACE GLYCOPROTEIN EMR1 PRECURSOR (EMR1 HORMONE RECEPTOR).//  
 40 5.10E-27//371aa//28%//Q14246  
 C-PLACE1010270  
 C-PLACE1010562  
 C-PLACE1010579//Homo sapiens PTB domain adaptor protein CED-6 mRNA, complete cds.//9.30E-299//  
 1362bp//99%//AF200715  
 45 C-PLACE1010624  
 C-PLACE1010628//Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and  
 S171 gene, partial cds.//7.50E-08//324bp//64%//AF109907  
 C-PLACE1010662//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-)  
 (DUGT).//1.80E-222//808aa//52%//Q09332  
 50 C-PLAC.E1010702//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//5.20E-151//427aa//55%//P28160  
 C-PLACE1010761  
 C-PLACE1010802 C-PLACE1010833//CALTRACTIN (CENTRIN).//0.0000001//154aa//28%//P41209  
 C-PLACE1010896//NUF1 PROTEIN (SPINDLE POLY BODY SPACER PROTEIN SPC110).//1.50E-25//583aa//  
 23%//P35580  
 55 C-PLACE1010916  
 C-PLACE1010947  
 C-PLACE1010965  
 C-PLACE1011032

C-PLACE1011041//Homo sapiens mRNA for BAP2-alpha protein, complete cds.//0//1701bp//97%//AB015019  
 C-PLACE1011056//HISTONE H1, GONADAL.//6.80E-13//154aa//37%//P02256  
 C-PLACE1011090//Homo sapiens mRNA; cDNA DKFZp586A0522 (from clone DKFZp586A0522).//0//880bp//  
 99%//AL050159  
 5 C-PLACE1011160//Homo sapiens HFB30 mRNA, complete cds.//0//1691bp//99%//AB022663  
 C-PLACE1011214  
 C-PLACE1011229//Homo sapiens ubiquitin-specific protease homolog (UPH) mRNA, complete cds.//2.30E-152//  
 701bp//99%//AF153604  
 C-PLACE1011273  
 10 C-PLACE1011291  
 C-PLACE1011310//MYOSIN HEAVY CHAIN, GIZZARD SMOOTH MUSCLE.//3.50E-20//496aa//25%//P10587  
 C-PLACE1011371//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN  
 H2).//1.70E-78//383aa//39%//Q61703  
 C-PLACE1011503  
 15 C-PLACE1011635//Homo sapiens heparan sulfate D-glucosaminyl 3-O-sulfotransferase-3B (30ST3B1) mRNA,  
 complete cds.//0//1559bp//99%//AF105377  
 C-PLACE1011646//Homo sapiens clone 25059 mRNA sequence.//5.00E-223//1035bp//99%//AF131752  
 C-PLACE1011650  
 C-PLACE1011675  
 20 C-PLACE1011725  
 C-PLACE1011749  
 C-PLACE1011922//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN, TYPE  
 B) (NMMHC-B).//1.30E-15//409aa//27%//P35580  
 C-PLACE1012031//Homo sapiens mRNA for KIAA0713 protein, partial cds.//0//1163bp//100%//AB018256  
 25 C-PLACE2000006  
 C-PLACE2000007//Homo sapiens mRNA for KIAA0913 protein, partial cds.//0//1968bp//97%//AB020720  
 C-PLACE2000034//LAR PROTEIN PRECURSOR (LEUKOCYTE ANTIGEN RELATED) (EC 3.1.3.48).//2.20E-29//  
 212aa//35%//P10586  
 C-PLACE2000039//Rattus norvegicus cytoplasmic dynein heavy chain (MAP 1C), mRNA, complete cds.//4.60E-  
 30 291//1167bp//89%//L08505  
 C-PLACE2000061  
 C-PLACE2000072//Homo sapiens ZNF202 beta (ZNF202) mRNA, complete cds.//0//3174bp//99%//AF027219  
 C-PLACE2000097  
 C-PLACE2000103  
 35 C-PLACE2000115  
 C-PLACE2000124  
 C-PLACE2000140  
 C-PLACE2000164//TIPD PROTEIN.//2.10E-59//481aa//33%//O15736  
 C-PLACE2000176  
 40 C-PLACE2000223  
 C-PLACE2000235  
 C-PLACE2000274//DYNEIN BETA CHAIN, CILIARY.//2.20E-167//880aa//37%//P23098  
 C-PLACE2000302  
 C-PLACE2000347  
 45 C-PLACE2000359  
 C-PLACE2000371//TENSIN.//2.90E-78//561aa//37%//Q04205  
 C-PLACE2000379  
 C-PLACE2000399//T-CELL SURFACE GLYCOPROTEIN E2 PRECURSOR (E2 ANTIGEN) (CD99) (MIC2 PRO-  
 TEIN) (12E7).//1.60E-14//180aa//39%//P14209  
 50 C-PLACE2000404//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE-TRNA LIGASE)  
 (LEURS).//9.90E-229//821aa//54%//Q09996  
 C-PLACE2000450  
 C-PLACE2000455  
 C-PLACE3000059//Mus musculus mRNA for ubiquitin conjugating enzyme.//0//1979bp//90%//Y17267  
 55 C-PLACE3000070  
 C-PLACE3000119  
 C-PLACE3000121//VESICULAR TRAFFIC CONTROL PROTEIN SEC15.//1.90E-08//281 aa//22%//P22224  
 C-PLACE3000136

C-PLACE3000147//Homo sapiens metalloproteinase with thrombospondin type 1 motifs ADAMTS1 (ADAMTS1) mRNA, complete cds./0//2043bp//99%//AF170084  
 C-PLACE3000148  
 C-PLACE3000155//Homo sapiens mRNA for KIAA0672 protein, complete cds./2.10E-75//382bp//99%//  
 5 AB014572  
 C-PLACE3000160  
 C-PLACE3000169//ZINC FINGER PROTEIN 135./2.50E-90//358aa//47%//P52742  
 C-PLACE3000194  
 C-PLACE3000199  
 10 C-PLACE3000218//Homo sapiens putative protein O-mannosyltransferase (POMT2) mRNA, complete cds./0//1862bp//98%//AF105020  
 C-PLACE3000230  
 C-PLACE3000244//PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR).//0//1435aa/92%//P53995  
 15 C-PLACE3000254//Homo sapiens transcriptional activator SRCAP (SRCAP) mRNA, complete cds./0//4583bp//83%//AF143946  
 C-PLACE3000276  
 C-PLACE3000310  
 C-PLACE3000320  
 C-PLACE3000331  
 20 C-PLACE3000339//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//9.60E-08//359aa//23 %//P08640  
 C-PLACE3000352  
 C-PLACE3000353//Homo sapiens mRNA; cDNA DKFZp586H0623 (from clone DKFZp586H0623).//0//2456bp//99%//AL096739  
 25 C-PLACE3000362  
 C-PLACE3000365  
 C-PLACE3000388  
 C-PLACE3000413  
 C-PLACE3000425  
 30 C-PLACE4000009//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN, TYPE B) (NMHC-B).//2.90E-54//626aa//29%//P35580  
 C-PLACE4000014//X-LINKED HELICASE II (X-LINKED NUCLEAR PROTEIN) (XNP).//3.10E-111//348aa//41%//P46100  
 C-PLACE4000052//Homo sapiens ATP cassette binding transporter 1 (ABC1) mRNA, complete cds./0//4661bp//99%//AF165281  
 35 C-PLACE4000089  
 C-PLACE4000128//Mus musculus putative transcription factor mRNA, complete cds./1.60E-86//190aa//88%//AF091234  
 C-PLACE4000129  
 40 C-PLACE4000147  
 C-PLACE4000192//ZINC FINGER PROTEIN 142 (KIAA0236) (HA4654).//7.00E-22//369aa//25%//P52746  
 C-PLACE4000211//Homo sapiens TTF-I interacting peptide 5 mRNA, partial cds./1.70E-262//1217bp//98%//AF000422  
 C-PLACE4000222  
 45 C-PLACE4000269//Homo sapiens mRNA for KIAA1067 protein, partial cds./0//3787bp//99%//AB028990  
 C-PLACE4000270  
 C-PLACE4000300  
 C-PLACE4000387  
 C-PLACE4000392  
 50 C-PLACE4000431//H.sapiens gene for U5 snRNP-specific 200kD protein./0//5142bp//90%//Z70200  
 C-PLACE4000450//Homo sapiens TTF-I interacting peptide 5 mRNA, partial cds./2.70E-261//1217b.p//98%//AF000422  
 C-PLACE4000465  
 55 C-PLACE4000489//PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT I-BINDING ACTIVITIY) (TRANSCRIPTION FACTOR NTF-1).//5.70E-60//254aa//44%//P13002  
 C-PLACE4000654//Mus musculus mRNA for ubiquitin conjugating enzyme./0//6340bp//87%//Y17267  
 C-SKNMC1000011//PUTATIVE IMPORTIN BETA-4 SUBUNIT (KARYOPHERIN BETA-4 SUBUNIT).//5.50E-35//431aa//29%//O60100

C-SKNMC1000046//Homo sapiens liprin-alpha3 mRNA, partial cds.//1.90E-162//749bp//99%//AF034800  
 C-SKNMC1000050//CALPAIN 2, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM-ACTIVATED NEUTRAL PROTEINASE) (CANP) (M-TYPE).//3.20E-41//87aa//98%//P17655  
 C-THYRO1000034//TRICHOHYALIN.//9.40E-10//176aa//30%//P37709  
 5 C-THYRO1000070  
 C-THYRO1000072//MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC 2.7.1.117) (MLCK) [CONTAINS: TELOKIN].//3.40E-16//201aa//29%//P11799  
 C-THYRO1000092  
 C-THYRO1000121//Homo sapiens mRNA for KIAA1116 protein, complete cds.//0//2159bp//99%//AB029039  
 10 C-THYRO1000124  
 C-THYRO1000197//Homo sapiens mRNA for poly(A)-specific ribonuclease.//0//2362bp//99%//AJ005698  
 C-THYRO1000199//Homo sapiens mRNA for KIAA0652 protein, complete cds.//0//1409bp//98%//AB014552  
 C-THYRO1000206  
 C-THYRO1000242//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//5.00E-118//239aa//66%//  
 15 P51523  
 C-THYRO1000253  
 C-THYRO1000270  
 C-THYRO1000288//Homo sapiens mRNA for Hs Ste24p, complete cds.//0//2161bp//99%//AB016068  
 C-THYRO1000320  
 20 C-THYRO1000358//SELENIUM-BINDING LIVER PROTEIN.//2.30E-229//237aa//79%//P17563  
 C-THYRO1000368  
 C-THYRO1000381  
 C-THYRO1000387  
 C-THYRO1000394//Homo sapiens peroxisomal membrane protein PMP 24 mRNA, complete cds.//1.20E-299//  
 25 1325bp//99%//AF072864  
 C-THYRO10003957//Homo sapiens actin-binding protein (IPP) mRNA, complete cds.//0//2092bp//99%//AF156857  
 C-THYRO1000401  
 C-THYRO1000488//Homo sapiens HFB30 mRNA, complete cds.//0//2254bp//100%//AB022663  
 C-THYRO1000501//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A))(RO(SS-A)).//  
 30 4.20E-98//408aa//42%//P19474  
 C-THYRO1000558  
 C-THYRO1000570  
 C-THYRO1000605//Homo sapiens histone acetyltransferase (HBOa) mRNA, complete cds.//0//3080bp//99%//  
 AF140360  
 35 C-THYRO1000625  
 C-THYRO1000637  
 C-THYRO1000676  
 C-THYRO1000684//Homo sapiens mRNA for KIAA0872 protein, complete cds.//0//2131bp//99%//AB020679  
 C-THYRO1000712  
 40 C-THYRO1000805  
 C-THYRO1000815  
 C-THYRO1000855  
 C-THYRO1000934//PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2) (P5CR) (P5C REDUCTASE).//  
 7.50E-57//315aa//43%//P32322  
 45 C-THYRO1000988  
 C-THYRO1001033//TRANSFORMATION-SENSITIVE PROTEIN IEF SSP 3521.//8.40E-12//167aa//29%//P31948  
 C-THYRO1001120//Mus musculus FX-induced thymoma transcript (FXI-T1) mRNA, complete cds.//1.90E-92//  
 1479bp//66%//U38252  
 C-THYRO1001204//Homo sapiens cathepsin Z precursor (CTSZ) gene, exons 4, 5, and 6 and complete cds; and  
 50 TH1 gene partial sequence.//3.80E-100//478bp//99%//AF136276  
 C-THYRO1001262  
 C-THYRO1001271  
 C-THYRO1001287//MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE (EC 3.2.1.113) (MAN(9)-  
 ALPHA-MANNOSIDASE) (FRAGMENT).//3.40E-51//429aa//33%//P45701  
 55 C-THYRO1001313//Homo sapiens sorting nexin 11 (SNX11) mRNA, complete cds.//0//2330bp//94%//AF121861  
 C-THYRO1001347  
 C-THYRO1001363//Homo sapiens mRNA; cDNA DKFZp56400423 (from clone DKFZp56400423).//0//2173bp//  
 99%//AL080120

C-THYRO1001374//Homo sapiens mRNA for KIAA0707 protein, partial cds.//0//1700bp//99%//AB014607  
 C-THYRO1001403  
 C-THYRO1001405//PLECTIN.//6.90E-19//450aa//27%//P30427  
 C-THYRO1001406//Homo sapiens steroid dehydrogenase homolog mRNA, complete cds.//0//1676bp//98%//  
 5 AF078850  
 C-THYRO1001426  
 C-THYRO1001458//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN,  
 TYPE B) (NMMHC-B).//2.70E-171//559aa//59%//P35580  
 C-THYRO1001480  
 10 C-THYRO1001487  
 C-THYRO1001584  
 C-THYRO1001661  
 C-THYRO1001746  
 C-THYRO1001772  
 15 C-THYRO1001854  
 C-Y79AA1000013//Mus musculus RING finger protein A07 mRNA, complete cds.//8.90E-205//1435bp//81 %//  
 AF171060  
 C-Y79AA1000033//Homo sapiens CARD4 mRNA, complete cds.//0//2929bp//96%//AF126484  
 C-Y79AA1000231//Homo sapiens nucleolar protein NOP5/NOP58 mRNA, complete cds.//0//1515bp//99%//  
 20 AF123534  
 C-Y79AA1000342//Homo sapiens Ciz1 mRNA, complete cds.//0//2644bp//81%//AB030835  
 C-Y79AA1000349//M.musculus Spnr mRNA for RNA binding protein.//0//2048bp//93%//X84692  
 C-Y79AA1000410  
 C-Y79AA1000539  
 25 C-Y79AA1000589//Homo sapiens clone 614 unknown mRNA, complete sequence.//1.00E-302//1375bp//99%//  
 AF091080  
 C-Y79AA1000802  
 C-Y79AA1000827  
 C-Y79AA1000966//Homo sapiens COP9 complex subunit 4 mRNA, complete cds.//0//1586bp//99%//AF100757  
 30 C-Y79AA1000969  
 C-Y79AA1000985//Human centrosomal protein kendrin mRNA, complete cds.//4.70E-151//985bp//87%//U52962  
 C-Y79AA1001061  
 C-Y79AA1001068  
 C-Y79AA1001216  
 35 C-Y79AA1001299//Homo sapiens mRNA for integrase interactor 1b protein (INI1B).//0//996bp//99%//AJ011738  
 C-Y79AA1001511  
 C-Y79AA1001594//HYALURONAN-MEDIATED MOTILITY RECEPTOR (HYALURONIC ACID RECEPTOR).//  
 2.50E-14//410aa//24%//Q00547  
 C-Y79AA1001692//Mus musculus strain C57BL/J germ cell-less protein (Gcl) mRNA, complete cds.//1.40E-78//  
 40 227aa//40%//Q01820  
 C-Y79AA1001866//Homo sapiens zinc finger protein ZNF180 (ZNF180) mRNA, complete cds.//0//2927bp//97%//  
 AF192913  
 C-Y79AA1001874//OX40L RECEPTOR PRECURSOR (ACT35 ANTIGEN) (TAX-TRANSCRIPTIONALLY ACTI-  
 VATED GLYCOPROTEIN 1 RECEPTOR) (CD134 ANTIGEN).//4.50E-08//135aa//31%//P43489  
 45 C-Y79AA1002139//DNAJ PROTEIN HOMOLOG 1 (DROJ1).//9.00E-17//120aa//45%//Q24133  
 C-Y79AA1002210//YTUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PRO-  
 TEIN).//0.0000018//140aa7//25%//Q13829  
 C-Y79AA1002211//PHOSPHATIDYLETHANOLAMINE-BINDING PROTEIN HOMOLOG F40A3.3.//1.70E-17//  
 146aa//35%//016264  
 50 C-Y79AA1002220  
 C-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds.//0//3168bp//99%//AB014592  
 C-Y79AA1002258//Homo sapiens mRNA for HIP1R, complete cds.//0//2106bp//99%//AB013384  
 C-Y79AA1002361//Rattus norvegicus mRNA for protein phosphatase 1 (GL-subunit).//6.90E-140//966bp//82%//  
 Y18208  
 55 C-Y79AA1002399//Homo sapiens mRNA for sperm protein.//0//1163bp//95%//X91879  
 C-Y79AA1002416//Mus musculus CTP synthetase homolog (CTPsH) mRNA, complete cds.//3.9e-317//1902bp//  
 86%//U49385  
 C-Y79AA1002431//TRANSDUCIN-LIKE ENHANCER PROTEIN 2 (ESG2).//9.80E-62//318aa//35%//Q04725

C-Y79AA1002482//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.70E-137//340aa//51%//Q05481  
 C-Y79AA1002487//Homo sapiens chromosome 5 F-box protein Fbx4 (FBX4) mRNA, complete cds.//7.3e-310//1444bp//98%//AF129534  
 5 C-HEMBA1000290  
 C-HEMBA1000459  
 C-HEMBA1000505  
 C-HEMBA1001196//Human DNA topoisomerase II (top2) mRNA, complete cds.//1.60E-268//1213bp//100%//J04088  
 10 C-HEMBA1002503  
 C-HEMBA1002508  
 C-HEMBA1002513//Homo sapiens mRNA for histone deacetylase-like protein (JM21).//0//2432bp//99%//AJ011972  
 C-HEMBA1003480  
 15 C-HEMBA1003538//COMPLEMENT C1R COMPONENT PRECURSOR (EC 3.4.21.41).//2.40E-110//242aa//58%//P00736  
 C-HEMBA10036451/TTPD PROTEIN.//2.40E-10//289aa//23%//015736  
 C-HEMBA1003646//Homo sapiens mRNA for KIAA1013 protein, partial cds.//0//3049bp//99%//AB023230  
 C-HEMBA1003667  
 20 C-HEMBA1003679//SIALIDASE (EC 3.2.1.18) (NEURAMINIDASE) (NA) (MAJOR SURFACE ANTIGEN).//1.00E-09//611aa//22%//P23253  
 C-HEMBA1003827  
 C-HEMBA1003838  
 C-HEMBA1004055  
 25 C-HEMBA1004056  
 C-HEMBA1004086  
 C-HEMBA1004335  
 C-HEMBA1004353//C-MYC BINDING PROTEIN MM-1.//3.00E-71//89aa//96%//Q99471  
 C-HEMBA1004479//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PRO-  
 30 TEIN).//3.10E-51//152aa//40%//Q61221  
 C-HEMBA1004499//Homo sapiens delta-tubulin mRNA, complete cds.//3.40E-92//483bp//95%//AF201333  
 C-HEMBA1004507  
 C-HEMBA1004638  
 35 C-HEMBA1004669//SON PROTEIN (SON3).//7.30E-17//288aa//36%//P18583  
 C-HEMBA1004709  
 C-HEMBA1004860  
 C-HEMBA1005206//Drosophila simulans anon73B1 gene and Su(P) gene.//1.90E-11//376bp//63%//AJ250308  
 C-HEMBA1005472  
 40 C-HEMBA1005513//MALES-ABSENT ON THE FIRST PROTEIN (EC 2.3.1.-).//1.90E-129//332aa//61%//002193  
 C-HEMBA1005572  
 C-HEMBA1005780  
 C-HEMBA1005990//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//0//2371bp//100%//AF082516  
 C-HEMBA1006038//LAMININ ALPHA-5 CHAIN (FRAGMENT).//3.10E-33//81aa//64%//Q61001  
 45 C-HEMBA1006124  
 C-HEMBA1006461  
 C-HEMBA1006521//3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) (3-KETOACYL-  
 ACYL CARRIER PROTEIN REDUCTASE).//4.00E-33//177aa//42%//P25716  
 C-HEMBA1006617  
 50 C-HEMBA1006650//ARP2/3 COMPLEX 20 KD SUBUNIT (P20-ARC).//9.00E-40//113aa//82%//015509  
 C-HEMBA1006779  
 C-HEMBA1006796  
 C-HEMBA1006812  
 C-HEMBA1006914//Human anthracycline-associated resistance ARX mRNA, complete cds.//0//1837bp//99%//U35832  
 55 C-HEMBA1007174//Homo sapiens mRNA for KIAA1065 protein, complete cds.//0//1079bp//97%//AB028988  
 C-HEMBB1000240  
 C-HEMBB1000264//CHL1 PROTEIN.//9.50E-19//104aa//45%//P22516

C-HEMBB1000335  
 C-HEMBB1000337  
 C-HEMBB1000554  
 C-HEMBB1000573  
 5 C-HEMBB1000749  
 C-HEMBB1000774  
 C-HEMBB1000835  
 C-HEMBB1001197  
 C-HEMBB1001315  
 10 C-HEMBB1001482//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.10E-57//941aa//  
 27%//Q05481  
 C-HEMBB1001500  
 C-HEMBB1001562//CYLICIN II (MULTIPLE-BAND POLYPEPTIDE II).//1.40E-06//373aa//21%//Q28092  
 C-HEMBB1001619  
 15 C-HEMBB1001630  
 C-HEMBB1001665  
 C-HEMBB1001684//Homo sapiens mRNA for KIAA1108 protein, partial cds.//0//2348bp//99%//AB029031  
 C-HEMBB1001812  
 C-HEMBB1001834  
 20 C-HEMBB1001869  
 C-HEMBB1001871//BONE/CARTILAGE PROTEOGLYCAN I PRECURSOR (BIGLYCAN) (PG-S 1).//5.40E-75//  
 241aa//48%//P47853  
 C-HEMBB1001872//CELL SURFACE GLYCOPROTEIN EMR1 PRECURSOR (EMR1 HORMONE RECEPTOR)  
 (CELL SURFACE GLYCOPROTEIN F4/80).//1.90E-22//210aa//27%//Q61549  
 25 C-HEMBB1001905//TRICHOHYALIN./.2.10E-10//268aa//27%//P37709  
 C-HEMBB1001908//Human monocytic leukaemia zinc finger protein (MOZ) mRNA, complete cds.//1.60E-131//  
 874bp//86%//U47742  
 C-HEMBB1001915//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 64E (EC 3.1.2.15) (UBIQUITIN THI-  
 OLESTERASE 64E) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 64E) (DEUBIQUITINATING ENZYME  
 30 64E).//6.90E-132//561aa//50%//Q24574  
 C-HEMBB1001925  
 C-HEMBB1002044//Mus musculus mRNA for vascular cadherin-2.//0//3562bp//81%//Y08715  
 C-HEMBB1002134//ZINC-FINGER PROTEIN NEURO-D4.//8.10E-56//176aa//67%//P56163  
 C-HEMBB1002152  
 35 C-HEMBB1002300  
 C-HEMBB1002381  
 C-HEMBB1002383  
 C-HEMBB1002534  
 C-MAMMA1000143  
 40 C-MAMMA1000183//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3.40E-134//359aa//63%//  
 P51523  
 C-MAMMA1000227  
 C-MAMMA1000257  
 C-MAMMA1000264  
 45 C-MAMMA1000270  
 C-MAMMA1000279  
 C-MAMMA1000372  
 C-MAMMA1000559  
 C-MAMMA1000752  
 50 C-MAMMA1000760  
 C-MAMMA1000778  
 C-MAMMA1000855  
 C-MAMMA1000859  
 C-MAMMA1000897//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITI HEAVY CHAIN  
 55 H3) (SERUM-DERIVED HYALURONAN-ASSOCIATED PROTEIN) (SHAP).//1.00E-141//576aa//37%//Q06033  
 C-MAMMA1000940  
 C-MAMMA1001073  
 C-MAMMA1001080//Homo sapiens SNC73 protein (SNC73) mRNA, complete cds.//1.6e-312//1596bp//94%//

AF067420  
 C-MAMMA10011987//Homo sapiens eps15RmRNA, partial cds./0//2253bp//99%//AB015346  
 C-MAMMA1001202  
 C-MAMMA1001222//EBNA-2 NUCLEAR PROTEIN./.6.60E-09//255aa//29%//P12978  
 5 C-MAMMA1001252  
 C-MAMMA1001296  
 C-MAMMA1001502  
 C-MAMMA1001630  
 C-MAMMA1001633//ZINC FINGER PROTEIN 165./.6.30E-39//160aa//55%//P49910  
 10 C-MAMMA1001683  
 C-MAMMA1001715  
 C-MAMMA1001730//Homo sapiens brain and nasopharyngeal carcinoma susceptibility protein NSG-x mRNA, par-  
 tial cds./0//1603bp//99%//AF095687  
 C-MAMMA1001760  
 15 C-MAMMA1001769  
 C-MAMMA1001785  
 C-MAMMA1001848  
 C-MAMMA1001874  
 C-MAMMA1001956  
 20 C-MAMMA1002009  
 C-MAMMA1002033  
 C-MAMMA1002155  
 C-MAMMA1002498  
 C-MAMMA1002545  
 25 C-MAMMA1002571  
 C-MAMMA1002573//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3)(GLUCAN 1,4-ALPHA- GLUCOSI-  
 DASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//2.60E-19//666aa//23%//P08640  
 C-MAMMA1002590  
 C-MAMMA1002617//ZINC FINGER PROTEIN 135./.7.60E-89//252aa//57%//P52742  
 30 C-MAMMA1002618  
 C-MAMMA1002636  
 C-MAMMA1002646  
 C-MAMMA1002665  
 C-MAMMA1002708  
 35 C-MAMMA1002728  
 C-MAMMA1002744  
 C-MAMMA1002764  
 C-MAMMA1002765  
 C-MAMMA1002830  
 40 C-MAMMA1002844//TRIOSE PHOSPHATE/PHOSPHATE TRANSLOCATOR, NON-GREEN PLASTID PRECUR-  
 SOR (CTPT).//4.90E-10//334aa//22%//P52178  
 C-MAMMA100285 8//Rat cMG1 mRNA./.3.70E-238//1147bp//92%//X52590  
 C-MAMMA1002880  
 C-MAMMA1002892  
 45 C-MAMMA1002909  
 C-MAMMA1002941  
 C-MAMMA1002947  
 C-MAMMA1002972//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS27./.1.10E-05//69aa//42%//  
 P40343  
 50 C-MAMMA1002973  
 C-MAMMA1002987  
 C-MAMMA1003003  
 C-MAMMA1003026//Homo sapiens HSPC057 mRNA, complete cds./0//1773bp//98%//AF161542  
 C-MAMMA1003031  
 55 C-MAMMA1003089  
 C-NT2RM1000092//MULTIDRUG RESISTANCE PROTEIN 2 (MULTIDRUG-EFFLUX TRANSPORTER 2).//  
 1.00E-07//362aa//23%//P39843  
 C-NT2RM1000272

C-NT2RM1000341  
 C-NT2RM1000539//Homo sapiens mRNA for Lsm5 protein./.3.00E-158//733bp//99%//AJ238097  
 C-NT2RM1000553//Homo sapiens putative glycolipid transfer protein mRNA, complete cds./.3.40E-177//814bp//  
 99%//AF103731  
 5 C-NT2RM1000623//RIBONUCLEASE INHIBITOR./.4.40E-21//372aa//30%//P10775  
 C-NT2RM1000702//PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).//5.60E-08//187aa//  
 27%//P49695  
 C-NT2RM1000833//Homo sapiens sec61 homolog mRNA, complete cds./.0//3541bp//99%//AF084458  
 10 C-NT2RM1000883//Homo sapiens I-1 receptor candidate protein mRNA, complete cds./.0//5107bp//99%//  
 AF082516  
 C-NT2RM1001082  
 C-NT2RM1001112  
 C-NT2RM2001105//Drosophila melanogaster eyelid (eld) mRNA, complete cds./.1.20E-28//805bp//61%//  
 AF053091  
 15 C-NT2RM2001360//Homo sapiens clone C40 unknown mRNA./.1.00E-250//1136bp//100%//AF103798  
 C-NT2RM2001797//Homo sapiens mRNA; cDNA DKFZp572C163 (from clone DKFZp572C163); partial cds./.0//  
 2300bp//100%//AL110217  
 C-NT2RM2001803//Homo sapiens IkappaB kinase cbmplex associated protein (IKAP) mRNA, complete cds./.0//  
 2249bp//99%//AF044195  
 20 C-NT2RM4002504  
 C-NT2RP1000409  
 C-NT2RP1000460//Homo sapiens mRNA for KIAA1068 protein, partial cds./.0//3199bp//99%//AB028991  
 C-NT2RP1000746//Homo sapiens 60S acidic ribosomal protein PO mRNA, complete cds./.9.70E-196//901bp//  
 99%//AF173378  
 25 C-NT2RP1000796  
 C-NT2RP1001013//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//7.70E-253//425aa//98%//  
 P51522  
 C-NT2RP2001214  
 C-NT2RP2001233//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.00E-128//409aa//  
 30 45%//Q05481  
 C-NT2RP2001440//Homo sapiens mRNA for 14-3-3gamma, complete cds./.0//3712bp//99%//AB024334  
 C-NT2RP2002056  
 C-NT2RP2002105//H.sapiens MSH-R gene for melanocyte stimulating hormone receptor./.0//1644bp//98%//  
 X65634  
 35 C-NT2RP2002333  
 C-NT2RP2002677  
 C-NT2RP2002755  
 C-NT2RP2002843  
 C-NT2RP2003101  
 40 C-NT2RP2003668  
 C-NT2RP2003799  
 C-NT2RP2004095  
 C-NT2RP2004300  
 C-NT2RP2004675  
 45 C-NT2RP2004920//TRANSCRIPTIONAL REGULATOR ATRX (X-LINKED NUCLEAR PROTEIN) (HETERO-  
 CHROMATIN PROTEIN 2) (HP1 ALPHA-INTERACTING PROTEIN) (HP1-BP38 PROTEIN).//4.20E-09//804aa//  
 22%//Q61687  
 C-NT2RP2005144//Homo sapiens tubby like protein 3 (TULP3) mRNA, complete cds./.2.10E-308//1437bp//98%//  
 AF045583  
 50 C-NT2RP2005719//GPI-ANCHORED PROTEIN P137./.4.00E-14//99aa//43%//Q14444  
 C-NT2RP2005726  
 C-NT2RP2005776//POLY(A) POLYMERASE TYPE 2 (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYL-  
 TRANSFERASE).//4.40E-55//358aa//42%//P51005  
 C-NT2RP2005980  
 55 C-NT2RP2006184//Homo sapiens mRNA for KIAA0918 protein, partial cds./.0//4235bp//99%//AB020725  
 C-NT2RP2006534//5'-AMP-ACTIVATED PROTEIN KINASE, CATALYTIC ALPHA-1 CHAIN (EC 2.7.1.-) (AMPK  
 ALPHA-1 CHAIN) (FRAGMENT).//3.20E-11//32aa//96%//Q13131  
 C-NT2RP2006554

C-NT2RP3000584  
 C-NT2RP3001115  
 C-NT2RP3001723//Homo sapiens cell recognition molecule Caspr2 (CASPR2) mRNA, complete cds.//1.40E-58//  
 1138bp//63%//AF193613  
 5 C-NT2RP3001938//SPORULATION-SPECIFIC PROTEIN 1 (EC 2.7.1.-)//1.30E- 22//227aa//33%//P08458  
 C-NT2RP3002330//Homo sapiens eRFS mRNA, complete cds.//0//2443bp//99%//U87791  
 C-NT2RP3002402  
 C-NT2RP3002484//Homo sapiens mRNA for KIAA0998 protein, partial cds.//1.20E-124//597bp//98%//AB023215  
 C-NT2RP3002512  
 10 C-NT2RP3002713  
 C-NT2RP3002770//MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD116.//1.00E-07//70aa//  
 41%//P17564  
 C-NT2RP3002799  
 C-NT2RP3002810//HISTIDINE-RICH PROTEIN KE4.//2.20E-10//260aa//26%//Q31125  
 15 C-NT2RP3002818//INSERTION ELEMENT IS2A HYPOTHETICAL 48.2 KD PROTEIN.//5.70E-226//303aa//97%//  
 P51026  
 C-NT2RP3002955  
 C-NT2RP3002985  
 C-NT2RP3003059//Rattus norvegicus potassium channel regulator 1 mRNA, complete cds.//3.80E-152//1007bp//  
 20 82%//U78090  
 C-NT2RP3003121  
 C-NT2RP3003133//Homo sapiens ZK1 mRNA for Kruppel-type zinc finger protein, complete cds.//0//1998bp//  
 91%//AB011414  
 C-NT2RP3003138//Homo sapiens kinesin superfamily motor KIF4 mRNA, complete cds.//0//2159bp//98%//  
 25 AF071592  
 C-NT2RP3003155  
 C-NT2RP3003157  
 C-NT2RP3003185//TROPOMYOSIN 1, FUSION PROTEIN 33.//2.80E-06//402aa//23%//P49455  
 C-NT2RP3003264  
 30 C-NT2RP3003346  
 C-NT2RP3003403  
 C-NT2RP3003411//Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds.//6.30E-270//  
 743bp//90%//AF071317  
 C-NT2RP3003500//SCY1 PROTEIN.//9.20E-27//601aa//23%//P53009  
 35 C-NT2RP3003572  
 C-NT2RP3003576  
 C-NT2RP3003665//Homo sapiens mRNA for beta-ureidopropionase, complete cds.//0//1690bp//99%//AB013885  
 C-NT2RP3003672//T-CELL SURFACE GLYCOPROTEIN E2 PRECURSOR (E2 ANTIGEN) (CD99) (MIC2 PRO-  
 TEIN) (12E7).//2.20E-13//146aa//42%//P14209  
 40 C-NT2RP3003680//Homo sapiens mRNA; cDNA DKFZp434J154 (from clone DKFZp434J154); complete cds.//0//  
 2047bp//95%//AL080155  
 C-NT2RP3003799//Rattus norvegicus Srg1 (Sytr1) mRNA, complete cds.//9.00E-238//1529bp//84%//U71294  
 C-NT2RP3003800//Rattus norvegicus tyrosine protein kinase pp60-c-src mRNA, complete cds.//1.90E-163//  
 924bp//89%//AF130457  
 45 C-NT2RP3003828  
 C-NT2RP3003932  
 C-NT2RP3003992//Homo sapiens mRNA; cDNA DKFZp564C186 (from clone DKFZp564Cl 86).//0//2739bp//  
 99%//AL050019  
 C-NT2RP3004013//M.musculus Spnr mRNA for RNA binding protein.//6.50E-240//1215bp//94%//X84692  
 50 C-NT2RP3004028  
 C-NT2RP3004041  
 C-NT2RP3004051  
 C-NT2RP3004078//H.sapiens HRFX2 mRNA.//0//1806bp//99%//X76091  
 C-NT2RP3004093  
 55 C-NT2RP3004095  
 C-NT2RP3004125//Mus musculus zinc finger protein splice variant FIZ1-B (Fiz1) mRNA, complete cds.//4.60E-  
 229//1560bp//78%//AF126747  
 C-NT2RP3004148//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSI-

**EP 1 074 617 A2**

DASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//7.90E-05//271aa//22%//P08640  
C-NT2RP3004155//Homo sapiens COQ7 protein mRNA, complete cds.//1.10E-179//823bp//100%//AF098948  
C-NT2RP3004189//VEGETABLE INCOMPATIBILITY PROTEIN HET-E-1J/1.30E-14//242aa//24%//Q00808  
C-NT2RP3004332  
5 C-NT2RP3004349  
C-NT2RP3004470  
C-NT2RP4000035  
C-NT2RP4000049  
C-NT2RP4000102  
10 C-NT2RP4000167  
C-NT2RP4000515  
C-NT2RP4000517  
C-NT2RP4000519  
C-NT2RP5003512//Homo sapiens mRNA for KIAA1291 protein, partial cds.//0//1980bp//99%//AB033117  
15 C-OVARC1000092  
C-OVARC1000533  
C-OVARC1000678  
C-OVARC1000689//Homo sapiens mRNA; cDNA DKFZp434C1415 (from clone DKFZp434C1415); partial cds.//  
0//2032bp//99%//AL133014  
20 C-OVARC1000802  
C-OVARC1000890  
C-OVARC1000891  
C-OVARC1000945//Rattus norvegicus mRNA for atypical PKC specific binding protein, complete cds.//0//1961bp//  
82%//AB005549  
25 C-OVARC1001072  
C-OVARC1001117  
C-OVARC1001200//Mus musculus mRNA for HS1 binding protein 3.//5.80E-88//658bp//80%//AJ132192  
C-OVARC1001244//H.sapiens mRNA for Drosophila female sterile homeotic (FSH) homologue.//0//1467bp//99%//  
X62083  
30 C-OVARC1001329  
C-OVARC1001341  
C-OVARC1001376  
C-OVARC1001496//Homo sapiens C-terminal binding protein 2 mRNA, complete cds.//0//1876bp//98%//  
AF016507  
35 C-OVARC1001873  
C-PLACE1000007//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE R10E11.3 (EC 3.1.2.15)  
(UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING EN-  
ZYME).//1.60E-81//212aa//70%//P34547  
C-PLACE1000547//Homo sapiens GDP-mannose pyrophosphorylase B (GMPPB) mRNA, complete cds.//3.70E-  
40 241//1124bp//98%//AF135421  
C-PLACE1001036//Homo sapiens mRNA for KIAA1017 protein, complete cds.//0//2117bp//99%//AB023234  
C-PLACE1001076  
C-PLACE1001118//ZINC FINGER PROTEIN 135.//5.40E-147//443aa//57%//P52742  
C-PLACE1001366  
45 C-PLACE1001545  
C-PLACE1001608  
C-PLACE1002004  
C-PLACE1002256  
C-PLACE1002437//ATP-BINDING CASSETTE TRANSPORTER 1.//4.50E-76//180aa//83%//P41233  
50 C-PLACE1002591//CORONIN-LIKE PROTEIN P57.//4.40E-70//208aa//66%//P31146  
C-PLACE1002665//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.//0//2462bp//89%//  
AF079765  
C-PLACE1003383  
C-PLACE1003864  
55 C-PLACE1004793//RETROVIRUS-RELATED ENV POLYPOLYPEPTIDE.//5.20E-47//577aa//25%//P10267  
C-PLACE1004913  
C-PLACE1004979  
C-PLACE1005052//Homo sapiens CGI-16 protein mRNA, complete cds.//6.6e-313//1413bp//99%//AF132950

C-PLACE1005055//Homo sapiens mRNA for KIAA0576 protein, partial cds.//0//2431bp//99%//AB011148  
 C-PLACE1005128  
 C-PLACE1005162  
 5 C-PLACE1005176//Homo sapiens hypothalamus protein HT001 mRNA, complete cds.//3.90E-212//1040bp//  
 96%//AF113539  
 C-PLACE1005467//PENICILLIN-BINDING PROTEIN 4\* (PBP 4\*) (PBP 4A).//1.10E-09//93aa//31%//P32959  
 C-PLACE1005549//Homo sapiens mRNA for Rho guanine nucleotide-exchange factor, splice variant NET1A.//  
 7.60E-97//1287bp//67%//AJ010046  
 10 C-PLACE1005584//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (P135 PROTEIN) (IER 2.9/ER2.6).//  
 6.80E-09//267aa//30%//P29128  
 C-PLACE1005611//Mus musculus mRNA for mDjIO, complete cds.//2.00E-33//379bp//66%//AB028860  
 C-PLACE1005802  
 C-PLACE1005850  
 15 C-PLACE1005898  
 C-PLACE1005932  
 C-PLACE1006129//Homo sapiens HSPC057 mRNA, complete cds.//0//2849bp//98%//AF161542  
 C-PLACE1006360  
 C-PLACE1006795  
 20 C-PLACE1006878//TRNA-SPUCING ENDONUCLEASE SUBUNIT SEN2 (EC 3.1.27.9) (TRNA-INTRON ENDO-  
 NUCLEASE).//1.90E-08//122aa//36%//P16658  
 C-PLACE1007557  
 C-PLACE1007807  
 C-PLACE1008181  
 25 C-PLACE1008426//Homo sapiens mRNA for KIAA1288 protein, partial cds.//0//3311bp//99%//AB033114  
 C-PLACE1008455  
 C-PLACE1008941  
 C-PLACE1009935  
 C-PLACE1010310//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).//1.20E-18//467aa//30%//P46804  
 C-PLACE1011891  
 30 C-PLACE10118967//Mus musculus Wnt10a mRNA, complete cds.//2.60E-287//1820bp//85%//U61969  
 C-PLACE2000003  
 C-PLACE2000132  
 C-PLACE2000170  
 C-PLACE2000335  
 35 C-PLACE3000124  
 C-PLACE3000158  
 C-PLACE3000207  
 C-PLACE3000221  
 C-PLACE3000271  
 40 C-PLACE3000304  
 C-PLACE3000322  
 C-PLACE3000341  
 C-PLACE3000373  
 C-PLACE3000399  
 45 C-PLACE3000401  
 C-PLACE3000402  
 C-PLACE3000406  
 C-PLACE3000475  
 C-PLACE400063//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSI-  
 50 DASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//1.70E-15//740aa//23%//P08640  
 C-PLACE400093  
 C-PLACE400100//Homo sapiens hydroxypyruvate reductase (GRHPR) gene, complete cds.//0//4199bp//97%//  
 AF146689  
 55 C-PLACE4000131//Homo sapiens mRNA; cDNA DKFZp586J0917 (from clone DKFZp586J0917); partial cds.//0//  
 1612bp//97%//AL117455  
 C-PLACE4000247  
 C-PLACE4000250  
 C-PLACE4000252

C-PLACE4000259//H.sapiens gene for U5 snRNP-specific 200kD protein.//0//5143bp//90%//Z70200  
 C-PLACE4000261//PEREGRIN (BR140 PROTEIN).//9.50E-10//128aa//34%//P55201  
 C-PLACE4000320  
 C-PLACE4000344  
 5 C-PLACE4000367  
 C-PLACE4000401//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME).//7.20E-22//54aa//62%//Q01576  
 C-PLACE4000411//Homo sapiens mRNA; cDNA DKFZp586D0624 (from clone DKFZp586D0624); partial cds.//0//2159bp//98%//AL117654  
 10 C-PLACE4000487  
 C-PLACE4000494  
 C-PLACE4000521  
 C-PLACE4000548//Homo sapiens mRNA for KIAA0947 protein, partial cds.//0//4864bp//99%//AB023164  
 C-SKNMC1000013//Homo sapiens ATP-binding cassette protein M-ABC1 mRNA, nuclear gene encoding mitochondrial protein, complete cds.//0//2384bp//99%//AF047690  
 15 C-SKNMC1000091//Homo sapiens mRNA for leucine-zipper protein, complete cds.//6.10E-190//872bp//99%//AB021663  
 C-THYRO1000343//Homo sapiens mRNA for KIAA0790 protein, partial cds.//0//3711bp//99%//AB018333  
 C-THYRO1000569//Mus musculus hematopoietic zinc finger protein mRNA, complete cds.//0//1557bp//91%//  
 20 AF118566  
 C-THYRO1001142  
 C-THYRO1001189//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.10E-200//546aa//62%//005481  
 C-THYRO1001320  
 25 C-THYRO1001537//Homo sapiens mRNA; cDNA DKFZp586A0522 (from clone DKFZp586A0522); partial cds.//0//1010bp//98%//AL050159  
 C-THYRO1001602  
 C-THYRO1001721//RING CANAL PROTEIN (KELCH PROTEIN).//9.30E-34//220aa//38%//Q04652  
 C-THYRO1001828  
 30 C-Y79AA1000346//Homo sapiens nonclathrin coat protein gamma2-COP mRNA, complete cds.//0//2520bp//99%//AF157833  
 C-Y79AA1001167  
 C-Y79AA1001384//Homo sapiens very large G-protein coupled receptor-1 (VLGR1) mRNA, complete cds.//0//4708bp//99%//AF055084  
 35 C-Y79AA1001875//RAS-RELATED PROTEIN RAB-7.//9.40E-12//34aa//97%//P51149  
 C-Y79AA1002103//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//3.00E-257//549aa//76%//P16415  
 C-HEMBA1006092  
 C-HEMBA1006406  
 C-HEMBB1000790  
 40 C-HEMBB1000917  
 C-HEMBB1002280  
 C-MAMMA1000802  
 C-MAMMA1001322//B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).//0.000000017//46aa//60%//P20931  
 C-MAMMA1002597  
 45 C-MAMMA1002868  
 C-NT2RP2003161  
 C-NT2RP2003339  
 C-NT2RP3001282  
 C-PLACE1001761  
 50 C-PLACE1004491  
 C-PLACE1004686  
 C-PLACE1005574  
 C-PLACE1006382  
 55 C-PLACE1006792  
 C-PLACE3000455  
 C-PLACE4000230//Mus musculus semaphorin Vla mRNA, complete cds.//0//2567bp//88%//AF030430  
 C-THYRO1000916

C-HEMBA1000327  
 C-HEMBB1000637  
 C-HEMBB1001967  
 C-MAMMA1000266  
 5 C-NT2RP2002979  
 C-PLACE1007866  
 C-PLACE3000350//SERINE/THREONINE-PROTEIN KINASE PAK-GAMMA (EC 2.7.1.-) (GAMMA-PAK)  
 (P21-ACTIVATED KINASE 2) (PAK-2) (PAK65) (S6/H4 KINASE).//9.80E-25//155aa/45%//Q13177  
 C-PLACE4000156//ZINC FINGER PROTEIN 132.//7.10E-151//476aa/46%//P52740  
 10 C-THYRO1001637  
 C-MAMMA1002215  
 C-MAMMA1002721  
 C-NT2RP2002070

15 Homology search result 14.

[0334] Data obtained by the homology search for full-length nucleotide sequences and deduced amino acid sequences. In the result of the search shown below, both units, aa and bp, are used as length units for the sequences to be compared. Each data includes Clone name, Definition in matching data, P value, Length of sequence to be compared, 20 Homology, and Accession number (No.) of matching data. These items are shown in this order, separated by a double-slash mark, //.

C-HEMBA100005//DNAJ PROTEIN HOMOLOG MTJ1.//1.90E-250//554aa/85%//061712  
 C-HEMBA100012//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--TRNA LIGASE)  
 25 (LEURS).//6.40E-99//457aa/45%//Q09996  
 C-HEMBA100020//Homo sapiens beta 2 gene.//7.50E-264//1194bp/95%//X02344  
 C-HEMBA100030//Homo sapiens ARF GTPase-activating protein GIT1 mRNA, complete cds.//0//1759bp/99%//  
 AF124490  
 C-HEMBA1000129//HYPOTHETICAL HEUCASE C8A4.08C IN CHROMOSOME I.//3.80E-25//166aa/36%//  
 30 Q09884  
 C-HEMBA1000141//Homo sapiens SUMO-1-specific protease (SSP1) mRNA, complete cds.//0//1135bp/100%//  
 AF196304  
 C-HEMBA1000150//Homo sapiens putative RNA helicase mRNA, complete cds.//5.20E-213//525bp/99%//  
 AF085356  
 35 C-HEMBA1000156//NEUROFILAMENT TRIPLET M PROTEIN (160 KD NEUROFILAMENT PROTEIN) (NF-M).//  
 1.90E-12//368aa/24%//P08553  
 C-HEMBA1000158//HEPATOCYTE NUCLEAR FACTOR 3-GAMMA (HNF-3G).//5.00E-16//166aa/36%//P35584  
 C-HEMBA1000168//CYLICIN I (MULTIPLE-BAND POLYPEPTIDE D).//2.90E-14//303aa/25%//P35662  
 C-HEMBA1000185//RAS-RELATED PROTEIN RAL-A.//3.40E-12//125aa/31%//P48555  
 40 C-HEMBA1000201//Homo sapiens mRNA for integrase interactor 1b protein (INI1B).//0//1612bp/99%//AJ011738  
 C-HEMBA1000216//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PRO-  
 TEIN).//1.00E-86//146aa/56%//Q61221  
 C-HEMBA1000303//Mus musculus Plenty of SH3s (POSH) mRNA, complete cds.//7.10E-254//1440bp/87%//  
 AF030131  
 45 C-HEMBA1000304//Rattus norvegicus Ca2+-dependent activator protein (CAPS) mRNA, complete cds.//5.10E-  
 131//712bp/91%//U16802  
 C-HEMBA1000307//CARNITINE DEFICIENCY-ASSOCIATED PROTEIN EXPRESSED IN VENTRICLE 1//5.20E-  
 49//107aa/91%//035594  
 C-HEMBA1000333//Homo sapiens F-box protein Fbx21 (FBX21) mRNA, complete cds.//0//1866bp/100%//  
 50 AF174601  
 C-HEMBA1000369//Homo sapiens mRNA for PICK1, complete cds.//0//1949bp/98%//AB026491  
 C-HEMBA1000411//ANKYRIN.//5.70E-12//127aa/38%//Q02357  
 C-HEMBA1000488//RING CANAL PROTEIN (KELCH PROTEIN).//3.30E-45//481aa/29%//Q04652  
 C-HEMBA1000491//RAS-LIKE PROTEIN 2.//2.00E-22//188aa/31%//P22279  
 55 C-HEMBA1000518//PECANEX PROTEIN.//2.10E-19//227aa/38%//P18490  
 C-HEMBA1000523//TESTIS-SPECIFIC PROTEIN PBS13.//2.40E-44//292aa/36%//Q01755  
 C-HEMBA1000531//HEAT SHOCK 70 KD PROTEIN COGNATE 1 (HEAT SHOCK 70 KD PROTEIN 70C) (FRAG-  
 MENTS).//2.60E-12//73aa/41%//P02826

C-HEMBA1000542//Rattus norvegicus mRNA for dipeptidyl peptidase III, complete cds.//2.20E-194//663bp//83%//D89340  
 5 C-HEMBA1000555//Mus musculus Msx2 interacting nuclear target protein mRNA, complete cds.//7.90E-226//1501bp//83%//AF156529  
 C-HEMBA1000561//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//3.40E-37//674aa//25%//Q05481  
 C-HEMBA1000569//GPI-ANCHORED PROTEIN P137.//6.50E-19//265aabp//32%//Q60865  
 C-HEMBA1000588//Mus musculus FLI-LRR associated protein-1 mRNA, complete cds.//2.10E-144//602bp//77%//AF045573  
 10 C-HEMBA1000591//PTB-ASSOCIATED SPLICING FACTOR (PSF).//2.20E-17//198aa//40%//P23246  
 C-HEMBA1000592//Homo sapiens sorting nexin 6 (SNX6) mRNA, complete cds.//0//1465bp//99%//AF121856  
 C-HEMBA1000608//HYPOTHETICAL PROTEIN KIAA0411 (FRAGMENT).//1.80E-55//179aa//61%//O43295  
 C-HEMBA1000657//Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds.//7.20E-156//1366bp//76%//U35776  
 15 C-HEMBA1000851//Homo sapiens DNA binding protein p96PIF mRNA, complete cds.//0//1862bp//99%//AF173868  
 C-HEMBA1000852//ARYLSULFATASE D PRECURSOR (EC 3.1.6.-) (ASD).//1.00E-78//119aa//87%//P51689  
 C-HEMBA1000910//MELANOMA-ASSOCIATED ANTIGEN B1 (MAGE-B1 ANTIGEN) (MAGE-XP ANTIGEN)//1.60E-30//127aa//40%//P43366  
 20 C-HEMBA1000919//HYPOTHETICAL 65.5 KD TRP-ASP REPEATS CONTAINING PROTEIN F02E8.5 IN CHROMOSOME X.//1.00E-10//288aa//23%//Q19124  
 C-HEMBA1001019//CELL DIVISION CONTROL PROTEIN 2 HOMOLOG (EC 2.7.1.-) (P34 PROTEIN KINASE) (CYCLIN-DEPENDENT KINASE 1) (CDK1).//3.10E-10//70aa//58%//P06493  
 25 C-HEMBA1001043//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID)(FRAGMENT).//1.40E-12//131aa//38%//Q01485  
 C-HEMBA1001059//Human N-acetylgalactosamine 6-sulphatase (GALNS) gene, exon 14.//4.80E-169//786bp//99%//U06088  
 C-HEMBA1001071//PROCOLLAGEN ALPHA 1(III) CHAIN PRECURSOR.//1.50E-92//82aa//100%//P02461  
 30 C-HEMBA1001077//Homo sapiens transcriptional intermediary factor 1 gamma mRNA, complete cds.//2.00E-80//432bp//94%//AF119043  
 C-HEMBA1001088//PINCH PROTEIN (PARTICULARLY INTERESTING NEW CYS-HIS PROTEIN).//3.50E-50//176aa//57%//P48059  
 C-HEMBA1001137//ZINC FINGER PROTEIN 33A (ZINC FINGER PROTEIN KOX31) (KIAA0065)(HA0946) (FRAGMENT).//1.50E-116//197aa//58%//Q06730  
 35 C-HEMBA1001174//ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 5.//6.80E-79//179aa//80%//P51646  
 C-HEMBA1001197//Homo sapiens rap2 interacting protein x mRNA, complete cds.//0//1511bp//99%//AF112221  
 C-HEMBA1001257//Homo sapiens mRNA 2-methylacyl-CoA racemase.//0//1672bp//99%//AJ130733  
 C-HEMBA1001286//COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR.//0.00000002//198aa//29%//Q60401  
 40 C-HEMBA1001302//Homo sapiens calcium binding protein precursor, mRNA, complete cds.//9.60E-258//682bp//94%//AF153686  
 C-HEMBA1001351//Homo sapiens VAMP-associated protein of 33 kDa (VAP-33) mRNA, complete cds.//1.40E-133//614bp//99%//AF057358  
 C-HEMBA1001387//GTP-BINDING PROTEIN TC10.//2.90E-64//104aa//82%//P17081  
 45 C-HEMBA1001405//Drosophila melanogaster eyelid (eld) mRNA, complete cds.//5.60E-25//863bp//60%//AF053091  
 C-HEMBA1001446//Homo sapiens rap2 interacting protein x mRNA, complete cds.//9.20E-55//719bp//68%//AF112221  
 C-HEMBA1001455//Mus musculus transposon-derived Buster2 transposase-like protein gene, partial cds.//4.20E-290//2008bp//81%//AF205599  
 50 C-HEMBA1001476//Human DNA topoisomerase II (top2) mRNA, complete cds.//1.60E-268//1213bp//100%//J04088  
 C-HEMBA1001510//CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-6 (FRAGMENT).//1.70E-16//63aa//61%//P18850  
 55 C-HEMBA1001526//PERIPLASMIC [FE] HYDROGENASE 1 (EC 1.18.99.1).//4.90E-37//399aa//29%//P29166  
 C-HEMBA1001569//SYNAPTOBREVIN 2 (VESICLE ASSOCIATED MEMBRANE PROTEIN 2) (VAMP-2).//2.30E-53//110aa//100%//P19065  
 C-HEMBA1001579//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//0//808bp//97%//AJ012449

C-HEMBA1001595//SEPTIN 2 HOMOLOG (FRAGMENT).//4.90E-156//348aa//83%//Q14141  
C-HEMBA1001620//MYO-INOSITOL-1-PHOSPHATE SYNTHASE (EC 5.5.1.4) (IPS).//1.60E-166//506aa//60%//  
P42803  
5 C-HEMBA1001635//TESTIS SPECIFIC PROTEIN A (ZINC FINGER PROTEIN TSGA).//1.60E-10//155aa//28%//  
Q63679  
C-HEMBA1001651//CYTADHERENCE HIGH MOLECULAR WEIGHT PROTEIN 1 (CYTADHERENCE ACCES-  
SORY PROTEIN 1).//6.20E-07//362aa//24%//Q50365  
C-HEMBA1001661//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//4.60E-36//  
365aa//33%//P33450  
10 C-HEMBA1001672//Homo sapiens methyl-CpG binding domain-containing protein MBD3 (MBD3) mRNA, com-  
plete cds.//0//1707bp//98%//AF072247  
C-HEMBA1001675//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS9.//5.40E-09//101aa//35%//  
P54787  
C-HEMBA1001714//Homo sapiens mRNA for ATPase inhibitor precursor, complete cds.//3.70E-78//200bp//  
15 100%//AB029042  
C-HEMBA1001723//Homo sapiens G protein beta subunit mRNA, partial cds.//3.10E-267//1212bp//99%//  
AF195883  
C-HEMBA1001734//CADHERIN-11 PRECURSOR (OSTEOBLAST-CADHERIN) (OBCADHERIN) (OSF-4).//  
1.10E-38//87aa//96%//P55288  
20 C-HEMBA1001744//SCY1 PROTEIN.//9.90E-32//481aa//25%//P53009  
C-HEMBA1001746//Homo sapiens squamous cell carcinoma antigen recognized by T cell (SART-2) mRNA, com-  
plete cds.//7.60E-59//998bp//64%//AF098066  
C-HEMBA1001804//Homo sapiens zinc finger DNA binding protein 99 (ZNF281) mRNA, complete cds.//0//  
1637bp//99%//AF125158  
25 C-HEMBA1001809//IMMEDIATE-EARLY PROTEIN IE180.//3.80E-11//206aa//36%//P11675  
C-HEMBA1001819//ZINC FINGER PROTEIN 184 (FRAGMENT).//2.90E-135//459aa//52%//Q99676  
C-HEMBA1001822//Mus musculus Ese2L protein mRNA, complete cds.//1.90E-235//1329bp//89%//AF132479  
C-HEMBA1001824//Homo sapiens nuclear protein NP94 mRNA, complete cds.//1.40E-199//1180bp//89%//  
AF159025  
30 C-HEMBA1001847//ZINC FINGER PROTEIN 29 (ZFP-29).//7.60E-64//221aa//55%//Q07230  
C-HEMBA1001866//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-)  
(DUGT).//5.70E-51//234aa//41%//Q09332  
C-HEMBA1001869//TRITHORAX PROTEIN.//9.60E-05//166aa//27%//P20659  
C-HEMBA1001896//DIMETHYLGLYCINE DEHYDROGENASE PRECURSOR (EC 1.5.99.2) (ME2GLYDH).//  
35 9.30E-36//395aa//26%//Q63342  
C-HEMBA1001913//GCN20 PROTEIN.//2.30E-81//158aa//50%//P43535  
C-HEMBA1001921//Homo sapiens germinal center kinase related protein kinase mRNA, complete cds.//0//  
1850bp//99%//AF000145  
C-HEMBA1001967//Homo sapiens NY-REN-57 antigen mRNA, partial cds.//0//1721bp//99%//AF155114  
40 C-HEMBA1002035//Homo sapiens BAZ1A mRNA for bromodomain adjacent to zinc finger domain 1A, complete  
cds.//0//2149bp//99%//AB032252  
C-HEMBA1002092//Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-3) mRNA, complete cds.//1.30E-  
271//1583bp//88%//U92703  
C-HEMBA1002102//ANKYRIN.//4.40E-10//106aa//35%//Q02357  
45 C-HEMBA1002139//LIM AND SH3 DOMAIN PROTEIN LASP-1 (MLN 50).//7.10E-05//51aa//49%//Q14847  
C-HEMBA1002151//Rattus norvegicus p34 mRNA, complete cds.//1.10E-153//1059bp//82%//AF178669  
C-HEMBA1002161//MYOSIN HEAVY CHAIN, CARDIAC MUSCLE BETA ISOFORM.//1.40E-51//180aa//56%//  
P79293  
C-HEMBA1002177//TRANSCRIPTION FACTOR GATA-4 (GATA BINDING FACTOR-4).//6.00E-13//190aa//36%//  
50 P43694  
C-HEMBA1002212//TYROSINE-PROTEIN KINASE-2 (EC 2.7.1.112) (FRAGMENT).//3.00E-17//267aa//29%//  
P18161  
C-HEMBA1002215//TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)].//2.20E-199//392aa//89%//P47226  
C-HEMBA1002241//PROLIFERATING-CELL NUCLEOLAR ANTIGEN P120 (PROLIFERATION-ASSOCIATED  
55 NUCLEOLAR PROTEIN P120).//3.70E-06//95aa//33%//P46087  
C-HEMBA1002267//Sus scrofa decorin mRNA, complete cds.//1.10E-46//302bp//90%//AF125537  
C-HEMBA1002341//P53-BINDING PROTEIN 2 (53BP2) (FRAGMENT).//3.80E-55//109aa//96%//Q62415  
C-HEMBA1002363//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//0//

1847bp//99%//AF092563  
C-HEMBA1002417/mGHT JUNCTION PROTEIN ZO-1 (TIGHT JUNCTION PROTEIN 1).//1.00E-121//489aa//  
52%//P39447  
C-HEMBA1002419//TRICHOHYALIN.//1.90E-09//299aa//24%//P22793  
C-HEMBA1002458//OVARIAN GRANULOSA CELL 13.0 KD PROTEIN HGR74.//4.20E-24//109aa//55%//Q00994  
C-HEMBA1002469//DXS8237E PROTEIN (FRAGMENT).//3.50E-50//199aa//61%//P98175  
C-HEMBA1002475//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//1.10E-12//285aa//  
31%//P17437  
C-HEMBA1002495//LIGHT-MEDIATED DEVELOPMENT PROTEIN DET1.//6.80E-53//257aa//36%//P48732  
10 C-HEMBA1002513//Homo sapiens mRNA for histone deacetylase-like protein (JM21).//0//2432bp//99%//  
AJ011972  
C-HEMBA1002547//Homo sapiens agrin precursor mRNA, partial cds.//0//1605bp//97%//AF016903  
C-HEMBA1002555//Homo sapiens mSin3A associated polypeptide p30 mRNA, complete cds.//5.30E-51//768bp//  
68%//AF055993  
15 C-HEMBA1002569//Homo sapiens protein associated with Myc mRNA, complete cds.//6.80E-305//951bp//99%//  
AF075587  
C-HEMBA1002746//DNA POLYMERASE BETA (EC 2.7.7.7).//5.00E-37//268aa//34%//P06746  
C-HEMBA1002768//Mus musculus formin binding protein 17 mRNA, partial cds.//7.80E-237//1522bp//85%//  
AB011126  
20 C-HEMBA1002770//Rattus norvegicus mRNA for TIP120, complete cds.//2.90E-176//1024bp//88%//D87671  
C-HEMBA1002777//Fugu rubripes BAW (BAW) mRNA, complete cds.//3.40E-54//319bp//76%//AF153879  
C-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cds.//8.2e-314//1437bp//99%//  
AF071185  
25 C-HEMBA1002818//Homo sapiens mRNA for fibulin-4.//2.00E-304//1383bp//99%//AJ132819  
C-HEMBA1002876//HYPOTHETICAL 26.4 KD PROTEIN EED8.8 IN CHROMOSOME n.//1.50E-44//188aa//  
52%//Q09297  
C-HEMBA1002935//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.30E-15//371aa//  
25%//Q05481  
C-HEMBA1002939//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).//2.00E-34//300aa//  
30 34%//P16157  
C-HEMBA1002951//NUF1 PROTEIN (SPINDLE POLY BODY SPACER PROTEIN SPC110).//4.40E-06//324aa//  
24%//P32380  
C-HEMBA1002973//CAMP-DEPENDENT 3',5'-CYCLIC PHOSPHODIESTERASE 4B (EC 3.1.4.17) (DPDE4).//  
1.20E-27//63aa//100%//P14646  
35 C-HEMBA1002997//CENTROMERIC PROTEIN E (CENP-E PROTEIN).//3.80E-25//534aa//24%//Q02224  
C-HEMBA1002999//Rattus norvegicus lamina associated polypeptide 1C (LAP1C) mRNA, complete cds.//1.40E-  
171//1552bp//75%//U20286  
C-HEMBA1003046//Homo sapiens mitochondrial processing peptidase beta-subunit mRNA.//0//1558bp//99%//  
AF054182  
40 C-HEMBA1003071//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COMPLEX ACID LABILE CHAIN  
PRECURSOR (ALS).//1.30E-09//121aa//40%//P35858  
C-HEMBA1003077//SLIT PROTEIN PRECURSOR.//2.60E-15//199aa//31%//P24014  
C-HEMBA1003096//Mouse 19.5 mRNA, complete cds.//5.60E-11//1139bp//72%//M32486  
45 C-HEMBA1003098//Homo sapiens NY-REN-6 antigen mRNA, partial cds.//6.20E-273//1253bp//99%//AF155096  
C-HEMBA1003136//MANNOSE-1-PHOSPHATE GUANYLTRANSFERASE (EC 2.7.7.13) (ATP-MANNOSE-  
1-PHOSPHATE GUANYLYLTRANSFERASE) (NDP-HEXOSE PYROPHOSPHORYLASE).//8.50E-51//221aa//  
33%//P41940  
C-HEMBA1003148//Homo sapiens mRNA for dachshund protein.//0//1583bp//99%//AJ005670  
50 C-HEMBA1003179//PROBABLE TRNA (5-METHYLAMINOMETHYL-2-THIOURIDYLATE)-METHYLTRANS-  
FERASE (EC 2.1.1.61).//5.90E-74//134aa//53%//P44551  
C-HEMBA1003199//Homo sapiens chromosome 5 F-box protein Fbx4 (FBX4) mRNA, complete cds.//8.50E-87//  
285bp//90%//AF129534  
C-HEMBA1003235//TROPOMYOSIN.//2.30E-06//109aa//33%//Q02088  
C-HEMBA1003250//PROTEIN KINASE APK1A (EC 2.7.1.-).//7.20E-41//245aa//42%//Q06548  
55 C-HEMBA1003281//POLIOVIRUS RECEPTOR PRECURSOR.//6.00E-11//239aa//32%//P32506  
C-HEMBA1003286//Homo sapiens mRNA for beta-1,4-galactosyltransferase IV, complete cds.//5.40E-229//  
1043bp//99%//AB024436  
C-HEMBA1003291//SNF1-RELATED PROTEIN KINASE KIN10 (EC 2.7.1.-) (AKIN10).//6.20E-28//126aa//51%//

Q38997  
C-HEMBA1003369//CENTROMERIC PROTEIN E (CENP-E PROTEIN).//2.00E-08//248aa//23%//Q02224  
C-HEMBA1003408//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (VERSION 1).//  
7.80E-13//297aa//30%//P18616  
5 C-HEMBA1003417//Homo sapiens BAG-family molecular chaperone regulator-2 mRNA, complete cds.//1.50E-  
255//1179bp//99%//AF095192  
C-HEMBA1003418//TRICHOHYALIN.//8.70E-19//281aa//31%//P37709  
C-HEMBA1003433//Homo sapiens gene for NBS1, complete cds.//0//511bp//94%//AB013139  
C-HEMBA1003538//COMPLEMENT C1R COMPONENT PRECURSOR (EC 3.4.21.41).//2.40E-110//242aa/  
10 58%//P00736  
C-HEMBA1003545//INSULIN GENE ENHANCER PROTEIN ISL-2 (TSLET-2).//8.80E-189//360aa//96%//P50480  
C-HEMBA1003555//NUCLEOTIDE-BINDING PROTEIN (NBP).//2.10E-68//251aa//52%//P53384  
C-HEMBA1003560//GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(O) GAMMA-2 SUBUNIT (G GAM-  
MA-I).//1.20E-31//71aa//100%//P16874  
15 C-HEMBA1003568//52 KD RO PROTEIN (SJOGEN SYNDROME TYPE A ANTIGEN (SS-A))(RO(SS-A)).//  
7.90E-49//279aa//32%//P19474  
C-HEMBA1003569//METASTASIS-ASSOCIATED PROTEIN MTA1.//6.90E-206//445aa//74%//Q13330  
C-HEMBA1003581//TALIN.//4.40E-45//52aa//98%//P26039  
C-HEMBA1003591//CHLOROPLAST 28 KD RIBONUCLEOPROTEIN PRECURSOR (28RNP).//4.40E-10//  
20 118aa//35%//P19682  
C-HEMBA1003615//Homo sapiens ART-4 mRNA, complete cds.//0//1713bp//99%//AB026125  
C-HEMBA1003617//Homo sapiens ubiquitin-like product Chap1/Dsk2 mRNA, complete cds.//6.90E-178//501bp//  
97%//AB015344  
C-HEMBA1003645//TIPD PROTEIN.//2.40E-10//289aa//23%//O15736  
25 C-HEMBA1003662//TBX2 PROTEIN (T-BOX PROTEIN 2).//1.20E-75//151aa//99%//Q13207  
C-HEMBA1003679//SIALIDASE (EC 3.2.1.18) (NEURAMINIDASE) (NA) (MAJOR SURFACE ANTIGEN).//1.00E-  
09//611aa//22%//P23253  
C-HEMBA1003680//PUTATIVE AMINOPEPTIDASE ZK353.6 IN CHROMOSOME III (EC 3.4.11.-).//2.40E-92//  
423aa//47%//P34629  
30 C-HEMBA1003684//ZINC FINGER PROTEIN 151 (MIZ-1 PROTEIN).//2.00E-73//526aa//32%//Q13105  
C-HEMBA1003690//HISTONE DEACETYLASE HDA1.//2.10E-59//249aa//47%//P53973  
C-HEMBA1003742//Homo sapiens cleft lip and palate transmembrane protein 1 (CLPTM1) mRNA, complete cds.//  
1.70E-44//501bp//67%//AF037339  
C-HEMBA1003760//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN)  
35 (MEMBER OF PAS PROTEIN 1) (MOP1) (HIF1 ALPHA).//3.70E-124//347aa//55%//Q16665  
C-HEMBA1003773//Mus musculus signal recognition particle receptor beta subunit mRNA, complete cds.//5.80E-  
81//511bp//86%//U17343  
C-HEMBA1003783//Mus musculus bromodomain-containing protein BP75 mRNA, complete cds.//1.10E-190//  
1204bp//84%//AF084259  
40 C-HEMBA1003805//Mus musculus KH domain RNA binding protein QKI-5A mRNA, complete cds.//0//988bp//  
95%//AF090402  
C-HEMBA1003836//MOB1 PROTEIN (MPS1 BINDER 1).//8.10E-31//134aa//52%//P40484  
C-HEMBA1003866//Mus musculus semaphorin Vla mRNA, complete cds.//1.20E-105//1192bp//70%//AF030430  
C-HEMBA1003953//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAGMENT).//3.80E-16//  
45 89aa//46%//P16372  
C-HEMBA1004097//Mus musculus putative transcription factor mRNA, complete cds.//8.50E-221//1188bp//78%//  
AF091234  
C-HEMBA1004131//SEPTIN 2 HOMOLOG (FRAGMENT).//1.60E-166//416aa//72%//Q14141  
C-HEMBA1004168//Homo sapiens geminin mRNA, complete cds.//3.90E-208//951 bp//99%//AF067855  
50 C-HEMBA1004199//HYPOTHETICAL HELICASE K12H4.8 IN CHROMOSOME III.//8.40E-60//243aa//39%//  
P34529  
C-HEMBA1004202//RAS-RELATED PROTEIN RAB-13.//6.20E-30//208aa//37%//P51153  
C-HEMBA1004203//NUCLEOLAR PROTEIN NOP2.//1.50E-12//258aa//29%//P40991  
C-HEMBA1004207//Homo sapiens leptin receptor short form (db) mRNA, complete cds.//0//1892bp//99%//U50748  
55 C-HEMBA1004227//Rattus norvegicus protein phosphatase 2C mRNA, complete cds.//5.70E-217//1217bp//88%//  
AF095927  
C-HEMBA1004248//INSULIN-INDUCED GROWTH RESPONSE PROTEIN CL-6 (IMMEDIATE-EARLY PROTEIN  
CL-6).//2.00E-43//98aa//84%//Q08755

C-HEMBA1004275//Homo sapiens PHD-finger protein (GRC5) mRNA, complete cds./.1.10E-152//1403bp//69%//AF043725  
 C-HEMBA1004276//Homo sapiens AP-4 adaptor complex beta4 subunit mRNA, complete cds./.4.80E-257//738bp//99%//AF092094  
 5 C-HEMBA1004286//Homo sapiens TGF beta receptor associated protein-1 mRNA, complete cds./.0//1982bp//99%//AF022795  
 C-HEMBA1004295//Homo sapiens NY-REN-25 antigen mRNA, partial cds./.9.40E-31//381bp//65%//AF155103  
 C-HEMBA1004321//ZINC FINGER PROTEIN 184 (FRAGMENT).//2.30E-93//357aa/42%//Q99676  
 C-HEMBA1004353//C-MYC BINDING PROTEIN MM-1.//3.00E-71//89aa/96%//Q99471  
 10 C-HEMBA1004354//CHL1 PROTEIN.//9.90E-26//130aa/42%//P22516  
 C-HEMBA1004356//H.sapiens MSSP-2 mRNA.//3.00E-243//573bp//98%//X77494  
 C-HEMBA1004389//Homo sapiens zinc finger DNA binding protein 99 (ZNF281) mRNA, complete cds./.0//1437bp//99%//AF125158  
 C-HEMBA1004408//PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 10 (EC 5.2.1.8) (PPIASE) (ROTAMASE) (CY-  
 15 CLOPHILIN-10).//3.20E-32//148aa/52%//P52017  
 C-HEMBA1004479//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PRO-  
 TEIN).//3.10E-51//152aa/40%//Q61221  
 C-HEMBA1004499//Homo sapiens delta-tubulin mRNA, complete cds./.3.40E-92//483bp//95%//AF201333  
 C-HEMBA1004509//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THI-  
 20 OLESTERASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME ,4)  
 (UBIQUITOUS NUCLEAR PROTEIN HOMOLOG).//2.70E-12//200aa/28%//Q13107  
 C-HEMBA1004534//Homo sapiens gamma-filamin (ABPL) mRNA, complete cds./.1.2e-316//1445bp//99%//  
 AF089841  
 C-HEMBA1004573//Homo sapiens mRNA for HELG protein.//2.00E-59//483bp//68%//AJ277291  
 25 C-HEMBA1004604//Homo sapiens COP9 complex subunit 7a mRNA, complete cds./.0//1612bp//99%//AF193844  
 C-HEMBA1004669//SON PROTEIN (SON3).//7.30E-17//288aa/36%//P18583  
 C-HEMBA1004697//MYOSIN HEAVY CHAIN, SMOOTH MUSCLE ISOFORM (SMMHC) (FRAGMENT).//2.90E-  
 05//303aa/21%//P35749  
 C-HEMBA1004734//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN  
 30 LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42).//9.90E-39//143aa/52%//P42743  
 C-HEMBA1004752//Homo sapiens mRNA for LAK-4p, complete cds./.4.60E-109//650bp//89%//AB002405  
 C-HEMBA1004756//Human transporter protein (g17) mRNA, complete cds./.9.10E-34//515bp//66%//U49082  
 C-HEMBA1004758//Homo sapiens transcription factor SL1 mRNA, complete cds./.2.60E-246//1249bp//94%//  
 L39060  
 35 C-HEMBA1004768//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//5.40E-111//314aa/58%//P08547  
 C-HEMBA1004795//CDC4-UKE PROTEIN (FRAGMENT).//3.80E-69//198aa/66%//P50851  
 C-HEMBA1004847//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//8.20E-154//317aa/94%//  
 Q00004  
 C-HEMBA1004889//Human C3f mRNA, complete cds./.6.70E-24//341aabp//26%//U72515  
 40 C-HEMBA1004929//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//2.50E-05//148aa/24%//  
 P25386  
 C-HEMBA1004930//26S PROTEASOME SUBUNIT S5B (KIAA0072) (HA1357).//3.30E-27//65aa/100%//Q16401  
 C-HEMBA1004972//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEURO FILAMENT PROTEIN) (NF-H).//  
 45 0.00000096//286aa/23%//P12036  
 C-HEMBA1004973//ZINC-BINDING PROTEIN A3374.10E-08//121aa/33%//Q02084  
 C-HEMBA1005009//Homo sapiens BAF53a (BAF53a) mRNA, complete cds./.0//1813bp//99%//AF041474  
 C-HEMBA1005029//Homo sapiens CGI-13 protein mRNA, complete cds./.0//1487bp//99%//AF132947  
 C-HEMBA1005047//RAS-RELATED PROTEIN RAB-24 (RAB-16).//3.40E-101//106aa/98%//P35290  
 50 C-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete cds./.0//2762bp//99%//  
 AF080561  
 C-HEMBA1005201//Homo sapiens CGI-07 protein mRNA, complete cds./.0//1608bp//99%//AF132941  
 C-HEMBA1005202//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//1.90E-179//361aa/95%//  
 Q00004  
 C-HEMBA1005206//Drosophila simulans anon73B1 gene and Su(P) gene.//1.90E-11//376bp//63%//AJ250308  
 55 C-HEMBA1005219//NUCLEAR PROTEIN SNF7.//5.30E-10//189aa/25%//P39929  
 C-HEMBA1005338//Homo sapiens mRNA for matrilin-4, partial.//3.90E-241//1095bp//99%//AJ007581  
 C-HEMBA1005359//ZINC FINGER PROTEIN 137.//3.90E-85//206aa/69%//P52743  
 C-HEMBA1005367//Homo sapiens melastatin 1 (MLSN1) mRNA, complete cds./.9.00E-77//620bp//74%//

AF071787  
C-HEMBA1005394//Mus musculus pantothenate kinase 1 beta (panKbeta) mRNA, complete cds./.3.90E-126//  
1097bp//75%//AF200357

5 C-HEMBA1005423//Homo sapiens cyclin-dependent kinase inhibitor (CDKN2C) mRNA, complete cds./.2.00E-  
213//537bp//99%//AF041248

C-HEMBA1005513//MALES-ABSENT ON THE FIRST PROTEIN (EC 2.3.1.-).//1.90E-129//332aa//61%//O02193

C-HEMBA1005528//CCR4-ASSOCIATED FACTOR 1 (CAF1).//3.10E-154//285aa//99%//Q60809

C-HEMBA1005530//Homo sapiens anaphase-promoting complex subunit 7 (APC7) mRNA, complete cds./.0//  
1578bp//98%//AF191340

10 C-HEMBA1005548//Homo sapiens MAFB/Kreisler basic region/leucine zipper transcription factor (MAFB) mRNA,  
complete cds./.1.00E-220//1014bp//99%//AF134157

C-HEMBA1005558//NUCLEAR PROTEIN SNF7./.6.40E-16//170aa//31%//P39929

C-HEMBA1005576//Mus musculus mRNA for plexin 2, complete cds./.1.20E-122//870bp//82%//D86949

C-HEMBA1005581//Homo sapiens SLT2 (SLIL2) mRNA, complete cds./.0//1721bp//100%//AF133270

15 C-HEMBA1005582//TROPOMYOSIN 1, NON-MUSCLE ISOFORM (TROPOMYOSIN II) (CYTOSKELETAL TRO-  
POMYOSIN).//0.00000009//213aa//27%//P09492

C-HEMBA1005595//DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC).//2.30E-54//562aa//29%//P34036

C-HEMBA1005621//Homo sapiens Mad2-like protein mRNA, complete cds./.8.00E-211//962bp//99%//AF072933

C-HEMBA1005666//Homo sapiens mRNA for DIPB protein./.8.60E-147//685bp//99%//AJ249128

20 C-HEMBA1005699//EPHRIN-B3 PRECURSOR (EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 8)  
(LERK-8) (EPH-RELATED RECEPTOR TRANSMEMBRANE LIGAND ELK-L3).//2.10E-37//98aa//81 %//Q15768

C-HEMBA1005737//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT).//  
4.40E-17//167aa//34%//P25296

C-HEMBA1005815//CALPAIN, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM- ACTIVATED NEU-  
25 TRAL PROTEINASE) (CANP) (MU/M-TYPE).//2.00E-36//342aa//33%//P00789

C-HEMBA1005931//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//5.60E-15//76aa//51%//  
P51522

C-HEMBA1005990//Homo sapiens I-1 receptor candidate protein mRNA, complete cds./.0//2371bp//100%//  
AF082516

30 C-HEMBA1006031//Homo sapiens mRNA for putative phospholipase, complete cds./.0//1413bp//99%//AB019435

C-HEMBA1006038//LAMININ ALPHA-5 CHAIN (FRAGMENT).//3.10E-33//81aa//64%//Q61001

C-HEMBA1006067//Homo sapiens squamous cell carcinoma antigen recognized by T cell (SART-2) mRNA, com-  
plete cds./.8.20E-12//297bp//64%//AF098066

C-HEMBA1006130//SEL-10 PROTEIN./.0.000000043//219aa//25 %//Q93794

35 C-HEMBA1006158//Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene, complete cds./.0//155 lbp//  
99%//AF048693

C-HEMBA1006198//PROLINE-RICH PROTEIN MP-2 PRECURSOR./.1.90E-19//215aa//39%//P05142

C-HEMBA1006248//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAGMENT).//8.60E-23//  
151aa//37%//P16372

40 C-HEMBA1006253//DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT111 PRECURSOR./.0.00000002//  
62aa//53%//P42698

C-HEMBA1006268//Homo sapiens HQ0024c mRNA, complete cds./.3.50E-157//845bp//92%//AF073836

C-HEMBA1006272//RETROVIRUS-RELATED PROTEASE (EC 3.4.23.-).//1.30E-123//200aa//73%//P10265

45 C-HEMBA1006278//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANS-  
FERASE).//1.00E-210//490aa//77%//P25500

C-HEMBA1006283//NUCLEAR POLYADENYLATED RNA-BINDING PROTEIN NAB2./.0.000000012//176aa//  
30%//P32505

C-HEMBA1006291//2-ARYLPROPIONYL-COA EPIMERASE (EC 5.--).//4.20E-12//215aa//23%//P70473

50 C-HEMBA1006309//Homo sapiens aspartyl aminopeptidase mRNA, complete cds./.5.30E-169//774bp//100%//  
AF005050

C-HEMBA1006310//Rattus norvegicus cytosolic sorting protein PACS-1a (PACS-1) mRNA, complete cds./.3.70E-  
225//1189bp//88%//AF076183

C-HEMBA1006344//RADIXIN./.1.50E-31//333aa//28%//P26043

55 C-HEMBA1006347//MALES-ABSENT ON THE FIRST PROTEIN (EC 2.3.1.-).//1.60E-130//332aa//62%//O02193

C-HEMBA1006359//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//3.50E-105//381aa//54%//P28160

C-HEMBA1006398//Human L1 element L1.6 putative pi 50 gene, complete cds./.2.00E-277//1729bp//85%//  
U93563

C-HEMBA1006445//Homo sapiens putative tumor suppressor NOEY2 mRNA, complete cds./.1.40E-270//1224bp//

100%//U96750  
C-HEMBA1006474//40 KD PROTEIN././/1.40E-39//292aa//34%//Q01552  
C-HEMBA1006485//PUROMYCIN-SENSITIVE AMINOPEPTIDASE (EC 3.4.11.-) (PSA).//1.90E-81//153aa//  
97%//P55786  
5 C-HEMBA1006507//DIAPHANOUS PROTEIN HOMOLOG 2././/1.40E-46//316aa//32%//O60879  
C-HEMBA1006521//3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) (3-KETOACYL-  
ACYL CARRIER PROTEIN REDUCTASE).//4.00E-33//177aa//42%//P25716  
C-HEMBA1006559//Mus musculus PRAJA1 (Praja1) mRNA, complete cds././/2.80E-206//1107bp//83%//U06944  
C-HEMBA1006583//Drosophila melanogaster Scribble (scrib) mRNA, complete cds././/1.70E-63//1002bp//65%//  
10 AF190774  
C-HEMBA1006624//DNA/PANTOTHENATE METABOLISM FLAVOPROTEIN HOMOLOG././/0.00000069//109aa//  
38%//Q58323  
C-HEMBA1006650//ARP2/3 COMPLEX 20 KD SUBUNIT (P20-ARC).//9.00E-40//113aa//82%//O15509  
C-HEMBA1006652//60S RIBOSOMAL PROTEIN L7././/2.40E-44//206aa//47%//P14148  
15 C-HEMBA1006708//HYPOTHETICAL 46.4 KD TRP-ASP REPEATS CONTAINING PROTEIN IN PMC1-TFG2  
INTERGENIC REGION././/3.30E-22//241aa//31%//P53196  
C-HEMBA1006737//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID)(FRAGMENT).//  
0.00000043//111aa//40%//Q01485  
C-HEMBA1006758//Homo sapiens protocadherin beta 13 (PCDH-beta13) mRNA, complete cds././/1832bp//  
20 91%//AF152492  
C-HEMBA1006807//Homo sapiens mRNA for SPOP././/5.70E-125//1109bp//75%//AJ000644  
C-HEMBA1006877//OXYSTEROL-BINDINGPROTEIN././/2.00E-59//378aa//39%//P16258  
C-HEMBA1006885//Homo sapiens gene for Proline synthetase associated, complete cds././/0//1467bp//96%//  
AB018566  
25 C-HEMBA1006914//Human anthracycline-associated resistance ARX mRNA, complete cds././/1837bp//99%//  
U35832  
C-HEMBA1006941//Homo sapiens PKC $\zeta$ -interacting protein PICOT (PICOT) mRNA, complete cds././/2.10E-271//  
1234bp//99%//AF118649  
C-HEMBA1006973//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds././/5.60E-143//740bp//94%//  
30 AF004828  
C-HEMBA1006976//H.sapiens mRNA for Gal-beta(1-3/I-4)GlcNAc alpha-2.3-sialyltransferase././/1.90E-80//  
447bp//89%//X74570  
C-HEMBA1007018//DYNEIN LIGHT INTERMEDIATE CHAIN 1, CYTOSOLIC (UC57/59) (DYNEIN LIGHT CHAIN  
A) (DLC-A).//2.40E-188//391aa//89%//Q90828  
35 C-HEMBA1007087//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF  
100 KD SUBUNIT).//8.30E-27//253aa//30%//Q10568  
C-HEMBA1007121//Homo sapiens bisphosphate 3'-nucleotidase mRNA, complete cds././/1.70E-252//1118bp//  
92%//AF125042  
C-HEMBA1007151//Homo sapiens synphilin 1 mRNA, complete cds././/1900bp//99%//AF076929  
40 C-HEMBA1007174//Homo sapiens epsin 2b mRNA, complete cds././/3.80E-271//642bp//99%//AF062085  
C-HEMBA1007194//Homo sapiens origin recognition complex subunit 6 (ORC6) mRNA, complete cds././/0//  
1588bp//99%//AF139658  
C-HEMBA1007224//Homo sapiens SUMO-1-specific protease (SSP1) mRNA, complete cds././/0//1590bp//99%//  
AF196304  
45 C-HEMBA1007243//Chinese hamster hprt mRNA, complete cds././/2.00E-58//650bp//70%//J00060  
C-HEMBA1007251//Homo sapiens F-box protein FBX29 (FBX29) mRNA, partial cds././/5.00E-58//330bp//95%//  
AF176707  
C-HEMBA1007300//Homo sapiens 3',5'-cyclic nucleotide phosphodiesterase 10A1 (PDE10A) mRNA, splice variant 1, complete cds././/1519bp//99%//AF127479  
50 C-HEMBA1007301//COLLAGEN ALPHA 1(III) CHAIN (FRAGMENT).//6.20E-18//115aa//33%//P13941  
C-HEMBB1000036//Homo sapiens CGI-51 protein mRNA, complete cds././/0//1665bp//99%//AF151809  
C-HEMBB1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds././/2.80E-187//  
1582bp//80%//AF084928  
C-HEMBB1000083//MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC  
2.7.1.117) (MLCK) [CONTAINS: TELOKIN].//1.90E-22//426aa//25%//P11799  
55 C-HEMBB1000119//Homo sapiens ASMTL gene././/0//1891bp//99%//Y15521  
C-HEMBB1000144//GUANYLATE CYCLASE ACTIVATING PROTEIN 2(GCAP 2)(RETINAL GUANYLYL CYCLASE ACTIVATOR PROTEIN P24).//1.40E-24//71aa//77%//P51177

C-HEMBB1000217//Homo sapiens SUMO-1-activating enzyme E1 N subunit (SUA1) mRNA, complete cds.//0//1038bp//99%//AF090385  
 C-HEMBB1000226//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE EEDB.5.//2.70E-12//112aa//47%//Q09530  
 5 C-HEMBB1000264//CHL1 PROTEIN.//9.50E-19//104aa//45%//P22516  
 C-HEMBB1000266//HYPOTHETICAL 54.5 KD TRP-ASP REPEATS CONTAINING PROTEIN ZC302.2 IN CHROMOSOME V.//6.10E-09//242aa//26%//Q23256  
 C-HEMBB1000317//FIBULIN-1, ISOFORM D PRECURSOR.//7.10E-62//458aa//35%//P37888  
 C-HEMBB1000593//Homo sapiens transmembrane receptor 2 alpha (TFR2) mRNA, complete cds.//1.30E-107//503bp//99%//AF067864  
 10 C-HEMBB1000631//LONGEVITY-ASSURANCE PROTEIN 1 (LONGEVITY ASSURANCE FACTOR 1).//4.10E-19//232aa//28%//P78970  
 C-HEMBB1000632//GUANINE NUCLEOTIDE RELEASING PROTEIN (GNRP).//2.20E-28//273aa//31%//P27671  
 C-HEMBB1000693//Homo sapiens neurogranin mRNA, complete cds.//0//2952bp//94%//AF040723  
 15 C-HEMBB1000725//Rattus norvegicus GTPase Rab8b (Rab8b) mRNA, complete cds.//6.20E-130//692bp//93%//U53475  
 C-HEMBB1000763//Homo sapiens CGI-89 protein mRNA, complete cds.//0//1676bp//96%//AF151847  
 C-HEMBB1000781//Homo sapiens mitogen-activated protein kinase kinase kinase MEKK2 mRNA, complete cds.//1.20E-126//613bp//97%//AF111105  
 20 C-HEMBB1000789//PUTATIVE 90.2 KD ZINC FINGER PROTEIN IN CCA1-ADK2 INTERGENIC REGION.//5.10E-54//232aa//43%//P39956  
 C-HEMBB1000831//Homo sapiens breast cancer nuclear receptor-binding auxiliary protein (BRX) mRNA, complete cds.//5.80E-60//301bp//99%//AF126008  
 C-HEMBB1000915//SUBTILISIN-LIKE PROTEASE PACE4 PRECURSOR (EC 3.4.21.-).//1.10E-08//129aa//31%//P29122  
 25 C-HEMBB1000927//Homo sapiens A-type potassium channel modulatory protein 2 (KCHIP2) mRNA, complete cds.//1.30E-126//592bp//99%//AF199598  
 C-HEMBB1000947//Homo sapiens clone HAW100 putative ribonuclease III mRNA, complete cds.//0//2292bp//99%//AF116910  
 30 C-HEMBB1000973//Mus musculus schlafen3 (Slfn3) mRNA, complete cds.//3.40E-120//580bp//67%//AF099974  
 C-HEMBB1000985//MIPP PROTEIN (MURINE IAP-PROMOTED PLACENTA-EXPRESSED PROTEIN).//8.60E-18//178aa//30%//P28575  
 C-HEMBB1001011//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.40E-73//230aa//45%//P51523  
 35 C-HEMBB1001056//PROLIFERATING-CELL NUCLEOLAR ANTIGEN P120 (PROLIFERATION-ASSOCIATED NUCLEOLAR PROTEIN P120).//2.90E-19//264aa//34%//P46087  
 C-HEMBB1001058//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//3.60E-52//331bp//80%//AF010144  
 C-HEMBB1001068//Homo sapiens liprin-beta2 mRNA, partial cds.//2.40E-30//1447bp//97%//AF034803  
 40 C-HEMBB1001112//Homo sapiens sec61 homolog mRNA, complete cds.//6.00E-145//961 bp//83 %//AF077032  
 C-HEMBB1001137//Homo sapiens mRNA for putative phospholipase, complete cds.//0//3069bp//99%//AB019435  
 C-HEMBB1001151//Rattus norvegicus golgi stacking protein homolog GRASP55 mRNA, complete cds.//4.20E-210//1835bp//76%//AF110267  
 C-HEMBB1001175//ANKYRIN.//7.00E-11//169aa//31%//Q02357  
 45 C-HEMBB1001234//65 KD YES-ASSOCIATED PROTEIN (YAP65).//5.40E-93//196aa//54%//P46938  
 C-HEMBB1001242//Homo sapiens topoisomerase-related function protein (TRF4-2) mRNA, partial cds.//1.80E-284//713bp//100%//AF089897  
 C-HEMBB1001282//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).//7.00E-43//394aa//34%//P16157  
 50 C-HEMBB1001288//COPPER HOMEOSTASIS PROTEIN CUTC.//7.80E-46//163aa//51%//P46719  
 C-HEMBB1001294//GTP-BINDING PROTEIN TC10.//1.20E-79//196aa//80%//P17081  
 C-HEMBB1001314//Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-3) mRNA, complete cds.//1.30E-129//724bp//86%//U92703  
 C-HEMBB1001331//Mus musculus mRNA for hepatoma-derived growth factor, complete cds, strain:BALB/c.//2.10E-65//458bp//79%//D63850  
 55 C-HEMBB1001339//DXS8237E PROTEIN (FRAGMENT).//4.60E-06//124aa//37%//P98175  
 C-HEMBB1001346//Homo sapiens phenylalanine-tRNA synthetase (FARS1) mRNA, nuclear gene encoding mitochondrial protein, complete cds.//1.10E-58//292bp//99%//AF097441

C-HEMBB1001384//Homo sapiens COP9 complex subunit 4 mRNA, complete cds.//0//1586bp//99%//AF100757  
 C-HEMBB1001429//Homo sapiens leucine aminopeptidase mRNA, complete cds.//0//1933bp//99%//AF061738  
 C-HEMBB1001443//Rattus norvegicus pyruvate dehydrogenase phosphatase isoenzyme 1 mRNA, complete  
 cds.//3.00E-130//553bp//86%//AF062740  
 5 C-HEMBB1001482//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.10E-57//941aa//  
 27%//Q05481  
 C-HEMBB1001562//CYLICIN II (MULTIPLE-BAND POLYPEPTIDE II).//1.40E-06//373aa//21%//Q28092  
 C-HEMBB1001564//VACUOLAR ATP SYNTHASE SUBUNIT H (EC 3.6.1.34) (V-ATPASE H SUBUNIT) (V-AT-  
 PASE M9.2 SUBUNIT) (9.2 KD MEMBRANE ACCESSORY PROTEIN).//9.60E-32//80aa//78%//O15342  
 10 C-HEMBB1001673//Homo sapiens gene for new zinc finger protein, complete cds.//0//1919bp//99%//AB012770  
 C-HEMBB1001736//EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 9 (EIF3 P116) (EIF3  
 P110).//4.60E-15//391aa//25%//P55884  
 C-HEMBB1001749//TRANSCRIPTIONAL ACTIVATOR GCN5.//1.70E-16//84aa//47%//Q03330  
 C-HEMBB1001802//Human desmin mRNA, complete cds.//0//1523bp//98%//U59167  
 15 C-HEMBB1001831//Homo sapiens PAM COOH-terminal interactor protein 1 (PCIP1) mRNA, complete cds.//0//  
 1514bp//99%//AF056209  
 C-HEMBB1001839//GASTRULA ZINC FINGER PROTEIN XLCGF42.1 (FRAGMENT).//6.90E-11//87aa//35%//  
 P18720  
 C-HEMBB1001871//BONE/CARTILAGE PROTEOGLYCAN I PRECURSOR (BIGLYCAN) (PG-S1).//5.40E-75//  
 20 241aa//48%//P47853  
 C-HEMBB1001872//CELL SURFACE GLYCOPROTEIN EMR1 PRECURSOR (EMR1 HORMONE RECEPTOR)  
 (CELL SURFACE GLYCOPROTEIN F4/80).//1.90E-22//210aa//27%//Q61549  
 C-HEMBB1001905//TRICHOHYALIN.//2.10E-10//268aa//27%//P37709  
 C-HEMBB1001908//Human monocytic leukaemia zinc finger protein (MOZ) mRNA, complete cds.//1.60E-131//  
 25 874bp//86%//U47742  
 C-HEMBB1001915//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 64E (EC 3.1.2.15) (UBIQUITIN THI-  
 OLESTERASE 64E) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 64E) (DEUBIQUITINATING ENZYME  
 64E).//6.90E-132//561aa//50%//Q24574  
 C-HEMBB1001950//PROBABLE OXYGEN-INDEPENDENT COPROPORPHYRINOGEN III OXIDASE (EC 1.----)  
 30 (COPROPORPHYRINOGENASE) (COPROGEN OXIDASE).//1.60E-41//370aa//31%//P54304  
 C-HEMBB1002042//CYTOCHROME P450 4C1 (EC 1.14.14.1) (CYPIVC1).//2.70E-49//139aa//55%//P29981  
 C-HEMBB1002044//Mus musculus mRNA for vascular cadherin-2.//0//3562bp//81%//Y08715  
 C-HEMBB1002134//ZINC-FINGER PROTEIN NEURO-D4.//8.10E-56//176aa//67%//P56163  
 C-HEMBB1002193//TYROSINE-PROTEIN KINASE RECEPTOR TYRO3 PRECURSOR (TYROSINE-PROTEIN  
 35 KINASE RSE) (TYROSINE-PROTEIN KINASE DTK) (TK19-2).//8.70E-61//77aa//74%//P55144  
 C-HEMBB1002217//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.10E-132//399aa//  
 44%//Q05481  
 C-HEMBB1002266//NEURONAL PROTEIN.//2.10E-46//121aa//76%//P41737  
 C-HEMBB1002342//Homo sapiens PKC $\zeta$ -interacting protein PICOT (PICOT) mRNA, complete cds.//1.50E-229//  
 40 1045bp//99%//AF118649  
 C-HEMBB1002442//LIN-10 PROTEIN.//9.70E-14//121aa//31%//P34692  
 C-HEMBB1002477//Human Grb2-associated binder-1 mRNA, complete cds.//7.70E-258//774bp//99%//U43885  
 C-HEMBB1002510//GYP7 PROTEIN.//3.10E-50//192aa//42%//P48365  
 C-HEMBB1002550//HYPOTHETICAL UOG-1 PROTEIN.//5.00E-28//266aa//33%//P27544  
 45 C-HEMBB1002600//Homo sapiens tetraspan NET-5 mRNA, complete cds.//0//1417bp//99%//AF089749  
 C-HEMBB1002607//Homo sapiens vitamin D3 receptor interacting protein (DRIP80) mRNA, complete cds.//2.00E-  
 136//660bp//98%//AF105421  
 C-HEMBB1002705//Homo sapiens CGI-27 protein mRNA, complete cds.//7.80E-285//841bp//96%//AF132961  
 C-MAMMA1000020//H.sapiens mRNA for flavin-containing monooxygenase 5 (FMO5).//8.20E-198//868bp//99%//  
 50 Z47553  
 C-MAMMA1000045//ENV POLYPROTEIN [CONTAINS: SURFACE PROTEIN GP85; MEMBRANE PROTEIN  
 GP37].//1.90E-07//249aa//27%//P03396  
 C-MAMMA1000055//TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)].//1.50E-90//323aa//48%//P47226  
 C-MAMMA1000085//PUTATIVE CYSTEINYLY-TRNA SYNTHETASE C29E6.06C (EC 6.1.1.16) (CYSTEINE--  
 55 TRNA LIGASE) (CYSRS).//2.10E-90//427aa//39%//Q09860  
 C-MAMMA1000173//Homo sapiens src homology 3 domain-containing protein HIP-55 mRNA, complete cds.//  
 2.60E-164//1044bp//87%//AF197060  
 C-MAMMA1000183//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3.40E-134//359aa//63%//

P51523  
C-MAMMA1000284//P.walti mRNA for rnp associated protein 55./.2.20E-109//864bp//76%//X99836  
C-MAMMA1000388//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds./.0//1466bp//  
99%//AB015132  
5 C-MAMMA1000416//HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III./.2.00E-30//119aa//  
53%//Q09232  
C-MAMMA1000612//Homo sapiens G protein beta subunit mRNA, partial cds./.8.30E-178//1992bp//84%//  
AF195883  
C-MAMMA1000625//GYP7 PROTEIN./.2.10E-41//198aa//40%//P48365  
10 C-MAMMA1000672//VITELLOGENIC CARBOXYPEPTIDASE PRECURSOR (EC 3.4.16.).//4.40E-33//250aa//  
33%//P42660  
C-MAMMA1000684//Homo sapiens opioid growth factor receptor mRNA, complete cds./.0//2391bp//99%//  
AF172451  
C-MAMMA1000713//L-RBULOKINASE (EC 2.7.1.16.).//7.70E-17//246aa//29%//P94524  
15 C-MAMMA1000731//CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 1 (CHD-1).//1.00E-77//395aa//  
45%//O14646  
C-MAMMA1000734//Homo sapiens mRNA for SEC63 protein./.0//1587bp//99%//AJ011779  
C-MAMMA1000738//HYPOTHETICAL 116.5 KD PROTEIN C20G8.09C IN CHROMOSOME I./.9.00E-299//  
1033aa//55%//P87115  
20 C-MAMMA1000824//ACTIN./.6.20E-20//284aa//28%//P53500  
C-MAMMA1000841//PUTATIVE AMIDASE (EC 3.5.1.4).//7.80E-40//101aa//54%//O27540  
C-MAMMA1000897//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H3 PRECURSOR (TTI HEAVY CHAIN  
H3) (SERUM-DERIVED HYALURONAN-ASSOCIATED PROTEIN) (SHAP).//1.00E-141//576aa//37%//Q06033  
C-MAMMA1000956//Homo sapiens CLDN8 gene for claudin-8./.0//1767bp//99%//AJ250711  
25 C-MAMMA1001008//Homo sapiens aspartic-like protease mRNA, complete cds./.2.50E-276//1263bp//99%//  
AF117892  
C-MAMMA1001030//LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR (LH/CG-R) (LSH-R)  
(LUTEINIZING HOROMINE RECEPTOR) (FRAGMENT).//1.20E-26//276aa//28%//Q90674  
C-MAMMA1001038//MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC  
30 2.7.1.117) (MLCK) [CONTAINS: TELOKIN].//2.60E-107//190aa//95%//Q15746  
C-MAMMA1001041//SPECTRIN BETA CHAIN, BRAIN (SPECTRIN, NON-ERYTHROID BETA CHAIN) (FODRIN  
BETA CHAIN) (SPTBN1).//1.60E-16//113aa//41%//Q01082  
C-MAMMA1001059//Homo sapiens mRNA for DEAD Box Protein 5./.0//1440bp//99%//AJ237946  
C-MAMMA1001075//Homo sapiens CGI-72 protein mRNA, complete cds./.1.30E-181//397bp//98%//AF151830  
35 C-MAMMA1001080//Homo sapiens SNC73 protein (SNC73) mRNA, complete cds./.1.6e-312//1596bp//94%//  
AF067420  
C-MAMMA1001105//OVO PROTEIN (SHAVEN BABY PROTEIN).//4.00E-49//125aa//68%//P51521  
C-MAMMA1001139//SRE-2 PROTEIN./.5.80E-35//239aa//38%//Q09273  
C-MAMMA1001181//ABC1 PROTEIN HOMOLOG PRECURSOR./.1.30E-07//81aa//45%//Q92338  
40 C-MAMMA1001198//Homo sapiens eps15R mRNA, partial cds./.0//2253bp//99%//AB015346  
C-MAMMA1001222//EBNA-2 NUCLEAR PROTEIN./.6.60E-09//255aa//29%//P12978  
C-MAMMA1001259//Mus musculus F-box protein FBX18 mRNA, partial cds./.2.30E-271//1414bp//89%//  
AF184275  
C-MAMMA1001260//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME III./.2.10E-52//630aa//  
45 30%//P34537  
C-MAMMA1001305//RHO-GTPASE-ACTIVATING PROTEIN 1 (GTPASE-ACTIVATING PROTEIN RHOGAP)  
(RHO-RELATED SMALL GTPASE PROTEIN ACTIVATOR) (CDC42 GTPASE-ACTIVATING PROTEIN)  
(P50-RHOGAP).//2.20E-98//283aa//63%//Q07960  
C-MAMMA1001322//B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).//0.000000017//46aa//60%//  
50 P20931  
C-MAMMA1001388//LEUCINE-RICH ALPHA-2-GLYCOPROTEIN (LRG).//1.40E-165//312aa//99%//P02750  
C-MAMMA1001476//URIDINE KINASE (EC 2.7.1.48) (URIDINE MONOPHOSPHOKINASE) (FRAGMENT).//  
6.50E-129//260aa//92%//P52623  
C-MAMMA1001501//CALPAIN 1, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM-ACTIVATED NEU-  
55 TRAL PROTEINASE) (CANP) (MU-TYPE).//5.70E-55//86aa//97%//P07384  
C-MAMMA1001576//Human gamma-tubulin mRNA, complete cds./.7.50E-276//1561bp//90%//M61764  
C-MAMMA1001627//Homo sapiens mRNA for transcription factor TBX6./.5.20E-189//871bp//99%//AJ007989  
C-MAMMA1001633//ZINC FINGER PROTEIN 165./.6.30E-39//160aa//55%//P49910

C-MAMMA1001679//F-ACTIN CAPPING PROTEIN BETA SUBUNIT (CAPZ).//0.00000058//29aa//100%//P47756  
 C-MAMMA1001730//Homo sapiens brain and nasopharyngeal carcinoma susceptibility protein NSG-x mRNA, partial cds.//0//1603bp//99%//AF095687  
 5 C-MAMMA1001735//TUBULIN BETA-5 CHAIN (BETA-TUBULIN CLASS-V).//5.90E-240//445aa//97%//P09653  
 C-MAMMA1001743//Y BOX BINDING PROTEIN-1 (Y-BOX TRANSCRIPTION FACTOR).//8.50E-32//171aa//  
 10 36%//P21573  
 C-MAMMA1001751//Homo sapiens tandem pore domain potassium channel TWIK-2 (KCNK6) mRNA, complete cds.//0//2332bp//99%//AF117708  
 C-MAMMA1001754//Homo sapiens Vacuolar proton pump subunit SFD alpha isoform mRNA complete cds.//0//  
 15 1987bp//99%//AF112204  
 C-MAMMA1001768//CELL DIVISION CYCLE PROTEIN 48 HOMOLOG MJ1156.//3.80E-45//351aa//38%//  
 Q58556  
 C-MAMMA1001771//M.musculus mRNA for semaphorin B.//2.60E-200//1272bp//79%//X85991  
 C-MAMMA1001820//Rattus norvegicus mRNA for PAG608 gene.//1.30E-198//1157bp//80%//Y13148  
 15 C-MAMMA1001837//ZINC FINGER PROTEIN 29 (ZFP-29).//2.60E-77//507aa//38%//Q07230  
 C-MAMMA1001868//TRICHOHYALIN.//2.70E-19//359aa//25%//P22793  
 C-MAMMA1002143//Homo sapiens Cdc42 effector protein 4 mRNA, complete cds.//1.70E-252//1170bp//99%//  
 AF099664  
 20 C-MAMMA1002170//40S RIBOSOMAL PROTEIN S2 (S4) (LLREP3 PROTEIN).//6.00E-66//157aa//70%//P15880  
 C-MAMMA1002198//THIOREDOXIN PEROXIDASE 1 (THIOREDOXIN-DEPENDENT PEROXIDE REDUCTASE  
 1) (THIOL-SPECIFIC ANTIOXIDANT PROTEIN) (TSA) (PRP) (NATURAL KILLER CELL ENHANCING FACTOR  
 B) (NKEF-B).//5.20E-61//60aa//90%//P32119  
 C-MAMMA1002219//Rattus norvegicus rexo70 mRNA, complete cds.//1.30E-181//861bp//98%//AF032667  
 25 C-MAMMA1002236//TRANSLATION INITIATION FACTOR EIF-2B GAMMA SUBUNIT (EIF-2B GDP-GTP EX-  
 CHANGE FACTOR).//8.80E-217//310aa//86%//PP70541  
 C-MAMMA1002268//Mus musculus sphingosine kinase (SPHK1a) mRNA, partial cds.//1.00E-190//1624bp//76%//  
 AF068748  
 C-MAMMA1002297//Homo sapiens mRNA for Rab6 GTPase activating protein.//1.10E-214//881bp//97%//  
 AJ011679  
 30 C-MAMMA1002329//M.musculus mRNA for semaphorin B.//3.80E-45//332bp//84%//X85991  
 C-MAMMA1002351//Mus musculus dynein subunit p25 (p25) mRNA, complete cds.//4.30E-119//773bp//86%//  
 AF190795  
 C-MAMMA1002385//RIBONUCLEOPROTEIN RB97D.//1.50E-07//206aa//29%//Q02926  
 C-MAMMA1002428//LYSOSOME MEMBRANE PROTEIN II (LIMP II) (85 KD LYSOSOMAL MEMBRANE  
 35 SIALOGLYCOPROTEIN) (LGP85) (CD36 ANTIGEN-LIKE 2).//1.10E-24//96aa//68%//Q14108  
 C-MAMMA1002470//PROBABLE NH(3)-DEPENDENT NAD(+) SYNTHETASE (EC 6.3.5.1).//1.00E-11//128aa//  
 36%//P47623  
 C-MAMMA1002485//Homo sapiens stanniocalcin-related protein mRNA, complete cds.//0//1822bp//99%//  
 AF098462  
 40 C-MAMMA1002524//HYPOTHETICAL 117.8 KD PROTEIN IN STE2-FRS2 INTERGENIC REGION.//1.20E-34//  
 337aa//31%//P43571  
 C-MAMMA1002530//Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 gamma) mRNA, complete cds.//  
 0//1910bp//99%//AF065214  
 C-MAMMA1002573//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSI-  
 45 DASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//2.60E-19//666aa//23%//P08640  
 C-MAMMA1002617//ZINC FINGER PROTEIN 135.//7.60E-89//252aa7//57%//P52742  
 C-MAMMA1002619//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE K02C4.3 (EC 3.1.2.15)  
 (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING  
 50 ENZYME).//9.50E-16//159aa//37%//Q09931  
 C-MAMMA1002622//VILLIN.//7.20E-35//53aa//64%//P02640  
 C-MAMMA1002637//KINESIN LIGHT CHAIN (KLC).//1.30E-198//550aa//70%//Q07866  
 C-MAMMA1002650//Mus musculus ODA-8S protein mRNA, complete cds.//5.40E-57//480bp//68%//AF194030  
 C-MAMMA1002655//Homo sapiens mRNA for ganglioside sialidase, complete cds.//0//1515bp//99%//AB008185  
 C-MAMMA1002671//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1)(ACETATE--COA LIGASE)(ACYL-AC-  
 55 TIVATING ENZYME).//1.10E-45//618aa//26%//P27550  
 C-MAMMA1002699//Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds.//4.3e-317//  
 1942bp//85%//AF018261  
 C-MAMMA1002769//Homo sapiens cell cycle progression restoration 8 protein (CPR8) mRNA, complete cds.//

2.20E-25//330bp//77%//AF011794  
C-MAMMA1002842//Mus musculus c-Cbl associated protein CAP mRNA, complete cds.//2.60E-58//373bp//81%//  
U58883  
C-MAMMA1002844//TRIOSE PHOSPHATE/PHOSPHATE TRANSLOCATOR, NON-GREEN PLASTID PRECUR-  
SOR (CTPT).//4.90E-10//334aa//22%//P52178  
C-MAMMA1002858//Rat cMG1 mRNA.//3.70E-238//1147bp//92%//X52590  
C-MAMMA1002869//PINCH PROTEIN (PARTICULARLY INTERESTING NEW CYS-HIS PROTEIN).//1.40E-160//  
305aa//85%//P48059  
C-MAMMA1002881//GLIOMA PATHOGENESIS-RELATED PROTEIN (RTVP-1 PROTEIN).//5.70E-30//214aa//  
35%//P48060  
C-MAMMA1002937//ZINC FINGER PROTEIN 135.//8.30E-99//393aa//43%//P52742  
C-MAMMA1002972//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS27.//1.10E-05//69aa//42%//  
P40343  
C-MAMMA1003011//HISTONE MACRO-H2A.1.//2.70E-123//370aa//66%//Q02874  
C-MAMMA1003013//DNA POLYMERASE BETA (EC 2.7.7.7).//7.40E-46//332aa//36%//P06746  
C-MAMMA1003035//RIBOSOMAL LARGE SUBUNIT PSEUDOURIDINE SYNTHASE C (EC 4.2.1.70) (PSEU-  
DOURIDYLATE SYNTHASE) (URACIL HYDROLYASE).//1.90E-13//108aa//33%//P23851  
C-MAMMA1003047//Homo sapiens protein inhibitor of activated STAT protein PIASy mRNA, complete cds.//0//  
1533bp//99%//AF077952  
C-MAMMA1003057//MD6 PROTEIN.//3.10E-225//419aa//97%//Q60584  
C-MAMMA1003113//Mus musculus COP9 complex subunit 7a (COPS7a) mRNA, complete cds.//1.10E-234//  
1178bp//86%//AF071316  
C-MAMMA1003127//MYOSIN I ALPHA (MMI-ALPHA).//2.20E-105//217aa//89%//P46735  
C-MAMMA1003146//Homo sapiens mRNA for GalT3 protein.//4.30E-218//996bp//99%//Y15062  
C-MAMMA1003150//HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECUR-  
SOR.//5.00E-13//592aa//24%//P47179  
C-MAMMA1003166//Homo sapiens MLL septin-like fusion protein (MSF) mRNA, complete cds.//3.10E-158//  
592bp//97%//AF123052  
C-NT2RM1000001//D.melanogaster sap47-2 mRNA.//1.50E-10//417bp//62%//X80110  
C-NT2RM1000039//HYPOTHETICAL 41.4 KD PROTEIN IN SRLQ-HYPF INTERGENIC REGION (EC 1.18.1.-)  
(ORF4).//2.90E-14//299aa//25%//P37596  
C-NT2RM1000055//Rattus norvegicus mRNA for TIP120, complete cds.//0//3106bp//89%//D87671  
C-NT2RM1000080//UNC-1 PROTEIN.//5.90E-25//211aa//31%//Q21190  
C-NT2RM1000086//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME III.//8.40E-52//364aa//  
32%//P34537  
C-NT2RM1000092//MULTIDRUG RESISTANCE PROTEIN 2 (MULTIDRUG-EFFLUX TRANSPORTER 2).//  
1.00E-07//362aa//23%//P39843  
C-NT2RM1000118//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) (CAL-  
CINEURIN REGULATORY SUBUNIT).//1.20E-10//150aa//28%//P87072  
C-NT2RM1000132//Homo sapiens NADH:ubiquinone oxidoreductase NDUFS6 subunit mRNA, nuclear gene en-  
coding mitochondrial protein, complete cds.//7.80E-110//516bp//99%//AF044959  
C-NT2RM1000153//CYTOSOLIC PURINE 5'-NUCLEOTIDASE (EC 3.1.3.5).//3.30E-38//469aa//27%//P49902  
C-NT2RM1000186//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) (CAL-  
CINEURIN REGULATORY SUBUNIT).//1.20E-10//150aa//28%//P87072  
C-NT2RM1000187//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE  
SPAC10F6.02C.//1.10E-10//94aa//47%//O42643  
C-NT2RM1000199//Homo sapiens mRNA for type I transmembrane receptor (psk-1 gene).//0//2476bp//99%//  
AJ245820  
C-NT2RM1000244//Homo sapiens TRAF4 associated factor 1 mRNA, partial cds.//2.00E-126//592bp//99%//  
U81002  
C-NT2RM1000252//H.sapiens E-MAP-115 mRNA.//9.70E-35//569bp//64%//X73882  
C-NT2RM1000256//Homo sapiens mRNA for Glutamine:fructose-6-phosphate amidotransferase, complete cds.//  
0//3012bp//99%//AB016789  
C-NT2RM1000257//MAGO NASHI PROTEIN.//7.90E-69//143aa//91%//P49028  
C-NT2RM1000260//Homo sapiens thyroid hormone receptor-associated protein complex component TRAP100  
mRNA, complete cds.//0//2766bp//99%//AF055995  
C-NT2RM1000280//VACUOLAR ATP SYNTHASE SUBUNIT D (EC 3.6.1.34) (V-ATPASE D SUBUNIT) (V- AT-  
PASE 28 KD ACCESSORY PROTEIN).//1.50E-106//118aa//97%//P39942

C-NT2RM1000354//Xenopus laevis chromosome condensation protein XCAP-G mRNA, complete cds././/7.40E-245//2101bp//68%//AF111423  
 C-NT2RM1000355//Homo sapiens transmembrane protein BRI (BRI) mRNA, complete cds.7/0//1599bp//99%//AF152462  
 5 C-NT2RM1000377//Homo sapiens dual specificity phosphatase MKP5 (MKP5) mRNA, complete cds././/3.20E-196//1016bp//94%//AF179212  
 C-NT2RM1000388//HYPOTHETICAL 27.7 KD PROTEIN IN CPT1-SPC98 INTERGENIC REGION././/0.00000019//67aa//31%//P53915  
 C-NT2RM1000421//RIBONUCLEASE INHIBITOR././/4.40E-21//372aa//30%//P10775  
 10 C-NT2RM1000430//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds././/1.40E-185//1486bp//81%//AF084928  
 C-NT2RM1000499//Caenorhabditis elegans mRNA for centaurin gamma 1A././/3.00E-17//927bp//58%//AJ132700  
 C-NT2RM1000539//Homo sapiens mRNA for Lsm5 protein././/3.00E-158//733bp//99%//AJ238097  
 C-NT2RM1000553//Homo sapiens putative glycolipid transfer protein mRNA, complete cds././/3.40E-177//814bp//  
 15 99%//AF103731  
 C-NT2RM1000555//UNR PROTEIN././/0//678aa//98%//P18395  
 C-NT2RM1000563//TRANSMISSION-B LOCKING TARGET ANTIGEN S230 PRECURSOR././/0.0000068//199aa//30%//Q08372  
 C-NT2RM1000623//RIBONUCLEASE INHIBITOR././/4.40E-21//372aa//30%//P10775  
 20 C-NT2RM1000648//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//8.50E-75//301aa//39%//P43636  
 C-NT2RM1000661//Homo sapiens translation initiation factor 4e mRNA, complete cds././/5.70E-210//960bp//99%//AF038957  
 C-NT2RM1000666//DNA-BINDING PROTEIN A././/2.20E-09//165aa//34%//P16989  
 C-NT2RM1000691//Homo sapiens mRNA for PLU-1 protein././/0//3104bp//99%//AJ132440  
 25 C-NT2RM1000702//PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).//5.60E-08//187aa//27%//P49695  
 C-NT2RM1000742//Homo sapiens AC133 antigen mRNA, complete cds././/0//3524bp//99%//AF027208  
 C-NT2RM1000746//Homo sapiens polyamine modulated factor-1 (PMF1) mRNA, complete cds././/6.70E-227//1043bp//99%//AF141310  
 30 C-NT2RM1000770//DXS6673E PROTEIN././/1.40E-39//194aa//48%//Q14202  
 C-NT2RM1000772//VEGETABLE INCOMPATIBILITY PROTEIN HET-E-1././/7.30E-15//280aa//27%//Q00808  
 C-NT2RM1000800//Mus musculus partial mRNA for B-IND1 protein (B-indl gene).//1.10E-98//571bp//89%//Z97207  
 35 C-NT2RM1000811//Homo sapiens AC133 antigen mRNA, complete cds././/0//3524bp//99%//AF027208  
 C-NT2RM1000826//UNR PROTEIN././/0//678aa//98%//P18395  
 C-NT2RM1000833//Homo sapiens sec61 homolog mRNA, complete cds././/0//3541 bp//99%//AF08445 8  
 C-NT2RM1000850//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).//9.70E-42//333aa//36%//P16157  
 40 C-NT2RM1000852//Homo sapiens putative ATP-dependent RNA helicase ROK1 mRNA, complete cds././/0//2206bp//99%//AF077033  
 C-NT2RM1000874//Homo sapiens death effector domain-containing testicular molecule mRNA, complete cds././/1.40E-244//1113bp//99%//AF043733  
 C-NT2RM1000882//Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds././/4.30E-122//1394bp//69%//AF126799  
 45 C-NT2RM1000883//Homo sapiens I-1 receptor candidate protein mRNA, complete cds././/0//5107bp//99%//AF082516  
 C-NT2RM1000885//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME III././/1.80E-56//630aa//30%//P34537  
 50 C-NT2RM1000894//DNA-DIRECTED RNA POLYMERASE 1135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135).//0//1020aa//89%//P70700  
 C-NT2RM1000898//ACTIN, CYTOPLASMIC (ACTIN, MICRONUCLEAR).//8.90E-26//229aa//29%//P02583  
 C-NT2RM1000924//HYPOTHETICAL 39.7 KD PROTEIN C34E10.2 IN CHROMOSOME III././/1.00E-15//266aa//26%//P46577  
 55 C-NT2RM1001003//Homo sapiens alpha-catenin-like protein (CTNNAL1) mRNA, complete cds././/0//2230bp//99%//AF030233  
 C-NT2RM1001008//HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME I././/1.60E-13//119aa//36%//Q09701  
 C-NT2RM1001059//NUCLEAR POLYADENYLATED RNA-BINDING PROTEIN NAB4././/3.60E-11//180aa//28%//

Q99383  
 C-NT2RM1001072//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODEESTERASE GAMMA 1 (EC 3.1.4.11) (PLC-GAMMA-1) (PHOSPHOLIPASE C-GAMMA-1) (PLC-II) (PLC-148).//8.30E-47//259aa//35%//P08487  
 5 C-NT2RM1001092//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//3.60E-115//332aa//52%//Q05481  
 C-NT2RM1001102//Human HEM45 mRNA, complete cds.//2.30E-27//482bp//63%//U88964  
 C-NT2RM1001115//ENDOCHITINASE 2 PRECURSOR (EC 3.2.1.14).//5.60E-06//239aa//27%//P54197  
 10 C-NT2RM2000013//DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE III SUBUNIT 2).//2.20E-144//362aa//71%//P25167  
 C-NT2RM2000030//DYNEIN INTERMEDIATE CHAIN, CYTOSOLIC (DH IC) (CYTOPLASMIC DYNEIN INTERMEDIATE CHAIN).//0.00000043//136aa//31%//P54703  
 15 C-NT2RM2000092//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 8 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 8) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 8) (DEUBIQUITINATING ENZYME 8).//1.30E-36//160aa//40%//P50102  
 C-NT2RM2000191//Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds.//0//1574bp//99%//AF067223  
 C-NT2RM2000260//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).//3.60E-19//181aa//34%//P14918  
 20 C-NT2RM2000322//SPERMIDINE SYNTHASE (EC 2.5.1.16) (PUTRESCINE AMINOPROPYLTRANSFERASE) (AMINOPROPYLTRANSFERASE).//8.10E-06//167aa//29%//O48660  
 C-NT2RM2000363//BREAKPOINT CLUSTER REGION PROTEIN.//1.80E-14//245aa//29%//P11274  
 C-NT2RM2000368//Homo sapiens protein kinase C-binding protein RACK7 mRNA, partial cds.//0//1506bp//99%//U48251  
 25 C-NT2RM2000371//POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE (EC 2.7.7.8) (POLYNUCLEOTIDE).//1.70E-68//419aa//36%//P50849  
 C-NT2RM2000402//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHEROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPONENT).//1.60E-54//344aa//33%//P32802  
 30 C-NT2RM2000407//Mus musculus semaphorin Vla mRNA, complete cds.//9.70E-201//826bp//84%//AF030430  
 C-NT2RM2000422//SODIUM- AND CHLORIDE-DEPENDENT TRANSPORTER NTT73.//1.00E-222//237aa//89%//Q08469  
 C-NT2RM2000452//HYPOTHETICAL 63.6 KD PROTEIN IN YPT52-GCN3 INTERGENIC REGION.//1.00E-07//157aa//28%//P36113  
 35 C-NT2RM2000469//NITROGEN PERMEASE REACTIVATOR PROTEIN (EC 2.7.1.-).//8.90E-06//377aa//24%//P22211  
 C-NT2RM2000490//SYNAPTOTAGMIN (P65).//1.80E-13//166aa//34%//P41823  
 C-NT2RM2000502//Rattus norvegicus W307 mRNA, complete cds.//1.70E-58//381bp//86%//U78304  
 40 C-NT2RM2000504//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//0//1673bp//99%//AF061243  
 C-NT2RM2000522//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//1.30E-12//282aa//32%//P17437  
 C-NT2RM2000566//Homo sapiens integrin alpha-7 mRNA, complete cds.//0//2519bp//96%//AF032108  
 C-NT2RM2000577//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE-TRNA LIGASE) (ILERS).//1.70E-187//741aa//46%//P73505  
 45 C-NT2RM2000588//HISTONE DEACETYLASE HDA1.//2.80E-60//384aa//40%//P53973  
 C-NT2RM2000594//Homo sapiens DNA cytosine-5 methyltransferase 3 beta 3 (DNMT3B) mRNA, complete cds.//0//2712bp//99%//AF156487  
 C-NT2RM2000599//Homo sapiens F-box protein Lilina (LILINA) mRNA, complete cds.//4.90E-70//838bp//69%//AF179221  
 50 C-NT2RM2000609//Homo sapiens CTL1 gene.//0//1559bp//99%//AJ245620  
 C-NT2RM2000612//Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds.//2.60E-106//1069bp//74%//U35776  
 C-NT2RM2000624//SPLICING FACTOR, ARGinine/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//4.40E-32//319aa//35%//Q08170  
 55 C-NT2RM2000691//ACTIN-LIKE PROTEIN 3 (ACTIN-2).//3.70E-142//285aa//90%//P32391  
 C-NT2RM2000714//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1).//3.80E-23//184aa//36%//Q15404  
 C-NT2RM2000718//Homo sapiens endocrine regulator mRNA, complete cds.//0//1731bp//99%//AF121141

C-NT2RM2000735//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//2.90E-103//249aa//73%//P28160  
 C-NT2RM2000740//POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L//5.70E-53//266aa//43%//  
 P41877  
 5 C-NT2RM2000821//COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP).//9.50E-279//545aa//  
 98%//P23514  
 C-NT2RM2000951//Homo sapiens XYLB mRNA for xylulokinase, complete cds.//1.70E-200//927bp//99%//  
 AB015046  
 C-NT2RM2001035//CCR4-ASSOCIATED FACTOR 1 (CAF1).//8.20E-154//285aa//99%//Q60809  
 C-NT2RM2001065//Homo sapiens COP9 complex subunit 4 mRNA, complete cds.//0//1554bp//99%//AF100757  
 10 C-NT2RM2001100//HYPOTHETICAL 39.7 KD PROTEIN C34E10.2 IN CHROMOSOME III.//2.40E-15//266aa//  
 26%//P46577  
 C-NT2RM2001105//Drosophila melanogaster eyelid (eld) mRNA, complete cds.//1.20E-28//805bp//61%//  
 AF053091  
 C-NT2RM2001196//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//1.30E-20//267aa//35%//P05143  
 15 C-NT2RM2001201//EUkARYOTIC TRANSLATION INITIATION FACTOR 5 (EIF-5).//1.50E-07//95aa//35%//  
 P48724  
 C-NT2RM2001221//KALIRIN (PAM COOH-TERMINAL INTERACTOR PROTEIN 10) (P-CIP10).//3.60E-10//  
 177aa//32%//P97924  
 C-NT2RM2001238//GLUTAMINASE, KIDNEY ISOFORM PRECURSOR (EC 3.5.1.2) (GLS) (L-GLUTAMINE AMI-  
 20 DOHYDROLASE).//1.30E-180//328aa//99%//P13264  
 C-NT2RM2001256//PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR).//1.60E-166//312aa//98%//  
 P53995  
 C-NT2RM2001324//ZYXIN.//6.80E-55//200aa//41%//Q04584  
 C-NT2RM2001345//VEGETABLE INCOMPATIBILITY PROTEIN HET-E-1.//2.90E-08//334aa//22%//Q00808  
 25 C-NT2RM2001424//Homo sapiens mRNA for EIB-55kDa-associated protein.//0//1621bp//99%//AJ007509  
 C-NT2RM2001499//LOW-AFFINITY CATIONIC AMINO ACID TRANSPORTER-2 (CAT-2) (CAT2).//7.40E-121//  
 437aa//57%//P52569  
 C-NT2RM2001547//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//6.90E-27//  
 90aa//42%//P38660  
 30 C-NT2RM2001575//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)).//  
 4.30E-61//312aa//44%//P19474  
 C-NT2RM2001592//Rattus norvegicus rexo70 mRNA, complete cds.//3.10E-156//909bp//88%//AF032667  
 C-NT2RM2001605//Homo sapiens mRNA for PLU-1 protein.//0//3114bp//99%//AJ132440  
 C-NT2RM2001613//Homo sapiens sec61 homolog mRNA, complete cds.//0//2601 bp//99%//AF084458  
 35 C-NT2RM2001632//KES1 PROTEIN.//1.40E-31//342aa//34%//P35844  
 C-NT2RM2001635//NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 (PORE MEMBRANE PRO-  
 TEIN OF 121 KD) (P145).//1.20E-142//566aa//56%//P52591  
 C-NT2RM2001648//Homo sapiens sec61 homolog mRNA, complete cds.//0//2421 bp//99%//AF084458  
 C-NT2RM2001652//Homo sapiens guanine nucleotide exchange factor mRNA, complete cds.//0//2608bp//99%//  
 40 AF111162  
 C-NT2RM2001659//ZINC/CADMIUM RESISTANCE PROTEIN.//3.40E-39//161aa//34%//P20107  
 C-NT2RM2001664//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA complete cds.//0//  
 2471bp//99%//AF044195  
 C-NT2RM2001668//Homo sapiens putative WHSC1 protein (WHSC1) mRNA, alternative splice product ending in  
 45 intron 11, complete cds.//6.20E-16//464bp//62%//AFQ83391  
 C-NT2RM2001670//ZINC FINGER PROTEIN 29 (ZFP-29).//6.50E-104//407aa//43%//Q07230  
 C-NT2RM2001671//Oryctolagus cuniculus sarcolemmal associated protein (SLAP1) mRNA, complete cds.//0//  
 1843bp//94%//U21155  
 C-NT2RM2001688//HYPOTHETICAL 33.8 KD PROTEIN C5H10.01 IN CHROMOSOME I.//4.60E-20//253aa//  
 50 30%//Q09674  
 C-NT2RM2001698//Homo sapiens XGalT-1 mRNA for galactosyltransferase I, complete cds.//6.20E-253//  
 1170bp//99%//AB028600  
 C-NT2RM2001700//ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC (EC 1.3.99.-) (VLCAD)  
 (FRAGMENT).//5.70E-130//536aa//49%//P50544  
 55 C-NT2RM2001716//Homo sapiens BPTF mRNA for bromodomain PHD finger transcription factor, complete cds.//  
 0//1774bp//98%//AB032251  
 C-NT2RM2001730//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE K02C4.3 (EC 3.1.2.15)  
 (UBIQUITIN THIOESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING EN-

ZYME).//7.20E-16//381aa//27%//Q09931  
 C-NT2RM2001743//Homo sapiens cell cycle progression 2 protein (CPR2) mRNA, complete cds.//0//1498bp//99%//AF011792  
 5 C-NT2RM2001753//HYPOTHETICAL PROTEIN KIAA0210.//8.80E-11//119aa//36%//Q92609  
 C-NT2RM2001760//Homo sapiens sec61 homolog mRNA, complete cds.//0//2379bp//99%//AF084458  
 C-NT2RM2001771//ZINC FINGER PROTEIN 135.//6.40E-154//394aa//64%//P52742  
 C-NT2RM2001782//Homo sapiens GDP-mannose pyrophosphorylase A (GMPPA) mRNA, complete cds.//0//1470bp//99%//AF135422  
 10 C-NT2RM2001785//Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds.//0//2150bp//99%//AF126799  
 C-NT2RM2001803//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds.//0//2249bp//99%//AF044195  
 C-NT2RM2001823//CHD1 PROTEIN.//1.80E-106//631aa7/39%//P32657  
 15 C-NT2RM2001839//Homo sapiens calumein (Calu) mRNA, complete cds.//0//2415bp//97%//AF013759  
 C-NT2RM2001886//PAB-DEPENDENT POLY(A)-SPECIFIC RIBONUCLEASE SUBUNIT PAN2 (EC 3.1.13.4)  
 (PAB1P-DEPENDENT POLY(A)-NUCLEASE).//3.00E-54//337aa//39%//P53010  
 C-NT2RM2001896//CELL DIVISION PROTEIN FTSJ.//5.10E-26//204aa//34%//P28692  
 C-NT2RM2001930//M.musculus mRNA for semaphorin G.//5.20E-135//894bp//83%//X97818  
 20 C-NT2RM2001935//Homo sapiens single-strand selective monofunctional uracil DNA glycosylase mRNA, complete cds.//0//1454bp//99%//AF125182  
 C-NT2RM2001936//32.3 KD PROTEIN IN CWP1-MBR1 INTERGENIC REGION.//2.70E-27//216aa//34%//P28320  
 C-NT2RM2001950//HYPOTHETICAL 105.9 KD PROTEIN IN AAC3-RFC5 INTERGENIC REGION.//0.0000001//212aa//23%//P38250  
 25 C-NT2RM2001983//Homo sapiens RGS-GAIP interacting protein GIPC mRNA, complete cds.//0//1658bp//98%//AF089816  
 C-NT2RM2001989//NUCLEOLAR PROTEIN NOP4 (NUCLEOLAR PROTEIN NOP77).//1.90E-39//253aa//35%//P37838  
 C-NT2RM2001997//PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (EC 5.3.4.1).//1.30E-10//232aa//28%//Q12730  
 30 C-NT2RM2001998//HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOME L//3.10E-12//206aa//30%//Q09782  
 C-NT2RM2002004//LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG).//2.90E-08//83aa//44%//P40796  
 35 C-NT2RM2002014//HYPOTHETICAL 81.4 KD PROTEIN IN GREB-FEOA INTERGENIC REGION.//1.10E-89//425aa//41%//P46837  
 C-NT2RM2002030//Homo sapiens mRNA for Glutamine:fructose-6-phosphate amidotransferase, complete cds.//0//1959bp//99%//AB016789  
 C-NT2RM2002055//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS13.//0.00000099//338aa//24%//Q07878  
 40 C-NT2RM2002088//PUTATIVE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN X (HNRNP X) (CBP).//5.00E-62//104aa//57%//Q61990  
 C-NT2RM2002091//Drosophila melanogaster eyelid (eld) mRNA, complete cds.//7.10E-29//805bp//61 %//AF053091  
 45 C-NT2RM2002100//Homo sapiens mRNA for ATP-dependent RNA helicase, partial.//0//1807bp//99%//AJ010840  
 C-NT2RM2002109//Homo sapiens glioma amplified on chromosome 1 protein (GAC1) mRNA, complete cds.//0//1868bp//99%//AF030435  
 C-NT2RM2002128//PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).//4.90E-13//487aa//26%//P49695  
 50 C-NT2RM2002142//GASTRULATION SPECIFIC PROTEIN G12.//8.00E-31//105aa//47%//P47805  
 C-NT2RM2002145//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//8.50E-191//1524bp//81%//AF084928  
 C-NT2RM4000024//DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE III SUBUNIT 2).//7.10E-155//381aa//72%//P25167  
 55 C-NT2RM4000030//LAS1 PROTEIN.//5.60E-12//184aa//32%//P36146  
 C-NT2RM4000046//GOLIATH PROTEIN (G1 PROTEIN).//0.000008//112aa//31%//Q06003  
 C-NT2RM4000104//ZINC FINGER PROTEIN 135.//1.50E-81//251aa//53%//P52742  
 C-NT2RM4000139//R.norvegicus trg mRNA.//2.30E-114//1161bp//72%//X68101

C-NT2RM4000155//THREONYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.3) (THREONINE--TRNA LIGASE) (THRRS).//1.20E-157//321aa//61%//P26639  
 C-NT2RM4000156//H.sapiens HPBRII-7 gene.//3.60E-21//785bp//60%//X67336  
 C-NT2RM4000167//Homo sapiens mRNA for Chromokinesin (KIF 4 gene).//0/1946bp//99%//AJ271784  
 5 C-NT2RM4000169//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//4.80E-13//686aa//23%//P25386  
 C-NT2RM4000191//PUTATIVE ATP-DEPENDENT RNA HELICASE PL10.//9.20E-75//439aa//41%//P16381  
 C-NT2RM4000202//ZINC FINGER PROTEIN MOK-2 (HOK-2).//4.90E-32//170aa//41%//Q16600  
 C-NT2RM4000215//MAK16 PROTEIN.//1.30E-68//295aa//49%//P10962  
 10 C-NT2RM4000229//Gallus gallus actin filament-associated protein (AFAP-110) mRNA, complete cds.//1.10E-27//633bp//64%//L20303  
 C-NT2RM4000233//Mus musculus semaphorin Via mRNA, complete cds.//3.40E-231//1395bp//86%//AF030430  
 C-NT2RM4000290//Human transducin-like enhancer protein (TLE3) mRNA, complete cds.//2.20E-276//1124bp//97%//M99438  
 15 C-NT2RM4000344//Homo sapiens mRNA for ATP-dependent metalloprotease YME1L.//0//2030bp//99%//AJ132637  
 C-NT2RM4000354//LETHAL(2)DENTICLELESS PROTEIN (DTL83 PROTEIN).//1.50E-21//208aa//35%//Q24371  
 C-NT2RM4000356//RAS-RELATED PROTEIN RAB-17.//5.90E-80//213aa//75%//P35292  
 C-NT2RM4000386//Mus musculus ODZ3 (Odz3) mRNA, partial cds.//0//2156bp//87%//AF195418  
 20 C-NT2RM4000421//Homo sapiens mRNA for nuclear transport receptor.//0//1730bp//99%//AJ133769  
 C-NT2RM4000433//Mus musculus retinoic acid-responsive protein (Stra6) mRNA, complete cds.//4.10E-271//2085bp//77%//AF062476  
 C-NT2RM4000457//HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMOSOME I.//8.00E-20//393aa//24%//Q10297  
 25 C-NT2RM4000471//Homo sapiens cysteine desulfurase (nifS) mRNA, complete cds.//0//2092bp//99%//AF097025  
 C-NT2RM4000486//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CONTAINS: BASIC PEPTIDE IB-6; PEPTIDE P-H].//4.80E-11//242aa//31%//P04280  
 C-NT2RM4000496//SAP1 PROTEIN.//8.30E-53//434aa//29%//P39955  
 C-NT2RM4000515//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H)  
 30 (FRAGMENT).//1.10E-11//394aa//24%//P16884  
 C-NT2RM4000531//ZINC FINGER PROTEIN 29 (ZFP-29).//2.40E-89//389aa//43%//Q07230  
 C-NT2RM4000590//RING CANAL PROTEIN (KELCH PROTEIN).//1.00E-59//595aa//28%//Q04652  
 C-NT2RM4000595//PUTATIVE ADENYLATE CYCLASE REGULATORY PROTEIN.//8.70E-15//403aa//30%//P26337  
 35 C-NT2RM4000611//VEGETABLE INCOMPATIBILITY PROTEIN HET-E-1.//2.90E-09//108aa//31%//Q00808  
 C-NT2RM4000616//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME).//2.70E-146//420aa//60%//P27550  
 C-NT2RM4000657//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC  
 40 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III).//3.00E-68//297aa//40%//P51178  
 C-NT2RM4000674//HYPOTHETICAL SYMPORTER SLL13747//1.20E-28//180aa//30%//P74168  
 C-NT2RM4000712//Homo sapiens ubiquitin hydrolyzing enzyme 1 (UBH1) mRNA, partial cds.//1.00E-136//  
 45 1104bp//77%//AF022789  
 C-NT2RM4000733//TRANSCRIPTION TERMINATION FACTOR RHO.//0.00000041//207aa//29%//P52154  
 C-NT2RM4000734//Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds.//0//2071bp//  
 99%//AF221712  
 C-NT2RM4000741//Homo sapiens hSGT1 mRNA for hSgt1p, complete cds.//0//2184bp//99%//D88208  
 C-NT2RM4000751//ZINC FINGER PROTEIN 184 (FRAGMENT).//3.90E-125//301aa//53%//Q99676  
 C-NT2RM4000798//Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 mRNA, complete  
 50 cds.//0//2603bp//99%//AF084521  
 C-NT2RM4000820//VACUOLAR ATP SYNTHASE SUBUNIT AC45 PRECURSOR (EC 3.6.1.34) (V-ATPASE  
 AC45 SUBUNIT).//1.10E-24//138aa//44%//P40682  
 C-NT2RM4000857//LEUCINE-RICH ALPHA-2-GLYCOPROTEIN (LRG).//6.70E-22//250aa//29%//P02750  
 C-NT2RM4000996//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//8.00E-211//738aa//  
 55 50%//Q05481  
 C-NT2RM4001047//MO25 PROTEIN.//8.00E-140//333aa//80%//Q06138  
 C-NT2RM4001054//Homo sapiens sec61 homolog mRNA, complete cds.//3.10E-190//1315bp//81%//AF077032  
 C-NT2RM4001084//HYPOTHETICAL 105.6 KD PROTEIN C16C9.06C IN CHROMOSOME I.//0.000000032//  
 165aa//33%//Q09820

C-NT2RM4001092//ZINC FINGER PROTEIN GLO37/3.10E-24//265aa//33%//P38682  
 C-NT2RM4001116//HYPOTHETICAL 216.3 KD PROTEIN R06F6.8 IN CHROMOSOME II././/5.90E-86//292aa//  
 48%//Q09417  
 5 C-NT2RM4001140//HOMEobox PROTEIN MSH-D././/1.00E-11//103aa//38%//Q01704  
 C-NT2RM4001155//ADRENAL MEDULLA 50 KD PROTEIN././/4.10E-19//445aa//78%//Q27969  
 C-NT2RM4001178//PROBABLE ATP-DEPENDENT RNA HELICASE HAS1././/1.10E-48//218aa//43%//Q03532  
 C-NT2RM4001200//ZINC FINGER PROTEIN 135././/9.50E-135//375aa//60%//P52742  
 C-NT2RM4001203//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds././/0//2310bp//99%//  
 AF004828  
 10 C-NT2RM4001217//Mus musculus actin-binding protein (ENC-1) mRNA, complete cds././/3.10E-148//1445bp//  
 72%//U65079  
 C-NT2RM4001256//Xenopus laevis putative Zic3 binding protein mRNA, complete cds././/4.30E-55//289bp//77%//  
 AF129131  
 15 C-NT2RM4001313//PHOSPHATIDYLINOSITOL 3-KINASE VPS34-UKE (EC 2.7.1.137) (PI3-KINASE) (PTDINS-  
 3-KINASE) (PI3K).//3.50E-35//124aa//65%//P54676  
 C-NT2RM4001316//ACYL-COA DEHYDROGENASE, MEDIUM-CHAIN SPECIFIC PRECURSOR (EC 1.3.99.3)  
 (MCAD).//2.30E-31//334aa//30%//P08503  
 C-NT2RM4001320//Homo sapiens mRNA for Neuroblastoma, complete cds././/1.80E-39//728bp//64%//D89016  
 C-NT2RM4001340//UTR4 PROTEIN (UNKNOWN TRANSCRIPT 4 PROTEIN).//1.00E-28//171aa//37%//P32626  
 20 C-NT2RM4001344//HYPOTHETICAL GTP-BINDING PROTEIN IN POP2-HO1 INTERGENIC REGION././/8.10E-  
 30//265aa//33%//P53742  
 C-NT2RM4001347//Homo sapiens NY-REN-25 antigen mRNA, partial cds././/0//2300bp//99%//AF155103  
 C-NT2RM4001371//Homo sapiens IDN3 mRNA, partial cds././/0//2524bp//99%//AB019494  
 25 C-NT2RM4001382//Homo sapiens RanBP7/importin 7 mRNA, complete cds././/2.20E-237//1079bp//99%//  
 AF098799  
 C-NT2RM4001411//Mus musculus Pro-rich, PH, SH2 domain-containing signaling mediator (PSM) mRNA, com-  
 plete cds././/0//1962bp//87%//AF020526  
 C-NT2RM4001412//Homo sapiens nGAP mRNA, complete cds././/0//1918bp//99%//AF047711  
 30 C-NT2RM4001444//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE-TRNA LIGASE) (ILERS).//  
 1.40E-118//444aa//46%//P73505  
 C-NT2RM4001483//ZINC FINGER PROTEIN 136././/5.10E-106//357aa//55%//P52737  
 C-NT2RM4001566//NECDIN././/9.80E-44//227aa//41%//P25233  
 C-NT2RM4001582//Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds././/1.50E-284//  
 1082bp//90%//AF071317  
 35 C-NT2RM4001592//HYPOTHETICAL 128.5 KD HELICASE IN ATS1-TPD3 INTERGENIC REGION././/7.60E-56//  
 213aa//49%//P31380  
 C-NT2RM4001597//M.musculus red-1 gene././/12.10E-171//1414bp//78%//X92750  
 C-NT2RM4001611//SIS2 PROTEIN (HALOTOLERANCE PROTEIN HAL3).//2.60E-32//203aa//39%//Q12600  
 C-NT2RM4001629//MAGUK P55 SUBFAMILY MEMBER 3 (MPP3 PROTEIN) (DISCS, LARGE HOMOLOG 3).//  
 40 1.50E-93//278aa//38%//Q13368  
 C-NT2RM4001666//HYPOTHETICAL 48.6 KD PROTEIN IN ALPA-GABP INTERGENIC REGION././/2.70E-84//  
 410aa//42%//P37339  
 C-NT2RM4001714//SEPTIN 2 HOMOLOG (FRAGMENT).//8.90E-141//354aa//72%//Q14141  
 C-NT2RM4001731//Homo sapiens F-box protein Lilina (LILINA) mRNA, complete cds././/0//1922bp//100%//  
 45 AF179221  
 C-NT2RM4001758//PUTATIVE SERINE/THREONINE-PROTEIN KINASE EMK (EC 2.7.).//4.10E-186//639aa//  
 56%//Q05512  
 C-NT2RM4001783//ZINC FINGER PROTEIN HRX (ALL-1).//7.90E-66//311aa//35%//Q03164  
 C-NT2RM4001810//AGGRECAN CORE PROTEIN PRECURSOR (CARTILAGE-SPECIFIC PROTEOGLYCAN  
 50 CORE PROTEIN) (CSPCP) (CHONDROITIN SULFATE PROTEOGLYCAN CORE PROTEIN 1).//5.10E-07//  
 263aa//30%//P16112  
 C-NT2RM4001813//LECTIN BRA-2././/0.00000048//114aa//30%//P17346  
 C-NT2RM4001819//Human p58/GTA (galactosyltransferase associated protein kinase) mRNA, complete cds././/  
 8.10E-300//1395bp//98%//M37712  
 55 C-NT2RM4001823//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6)7/2.90E-55//325aa//37%//P28160  
 C-NT2RM4001828//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//5.90E-161//481aa//56%//  
 P51523  
 C-NT2RM4001858//T-BOX CONTAINING PROTEIN TBX6L (FRAGMENT).//6.50E-22//126aa//46%//P79779

C-NT2RM4001865//Homo sapiens mRNA for atopy related autoantigen CALC./.4.30E-244//1248bp//94%//Y17711

C-NT2RM4001876//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1).//6.50E-23//184aa//36%//Q15404

5 C-NT2RM4001880//PUTATIVE DNA HELICASE II HOMOLOG (EC 3.6.1.-).//5.90E-09//268aa//26%//P47486

C-NT2RM4001930//Homo sapiens dolichyl-P-Glc:Man9GlcNAc2-PP-dolichyl glucosyltransferase (ALG6) mRNA, complete cds./.0//1930bp//99%//AF102851

C-NT2RM4001940//Homo sapiens timeless homolog mRNA, complete cds./.0//2087bp//99%//AF098162

10 C-NT2RM4001969//R.norvegicus mRNA for IP63 protein./.2.60E-261//1563bp//84%//X99330

C-NT2RM4001979//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.80E-112//457aa//47%//P51523

C-NT2RM4001987//NEURAL CELL ADHESION MOLECULE 1, LARGE ISOFORM PRECURSOR (N-CAM 180) [CONTAINS: N-CAM 140].//3.20E-17//281aa//30%//P16170

15 C-NT2RM4002013//HYPOTHETICAL 89.4 KD TRP-ASP REPEATS CONTAINING PROTEIN IN PMT6-PCT1 INTERGENIC REGION./.6.90E-94//589aa//35%//P42935

C-NT2RM4002034//Homo sapiens hiwi mRNA, partial cds./.1.90E-53//1585bp//60%//AF104260

C-NT2RM4002062//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA LIGASE) (ASPRS).//1.90E-31//80aa//52%//P36419

20 C-NT2RM4002063//Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, complete cds./.0//1865bp//99%//U82267

C-NT2RM4002066//Homo sapiens thyroid hormone receptor-associated protein complex component TRAP230 mRNA, complete cds./.1.50E-211//1123bp//71 %//AF117755

C-NT2RM4002073//Mus musculus fatty acid transport protein 3 mRNA, partial cds./.9.30E-293//1751bp//83%//AF072758

25 C-NT2RM4002075//RING CANAL PROTEIN (KELCH PROTEIN).//2.80E-105//556aa//41 %//Q04652

C-NT2RM4002093//Homo sapiens neural polypyrimidine tract binding protein (PTB) mRNA, complete cds./.0//2550bp//99%//AF176085

C-NT2RM4002109//Homo sapiens mRNA for Chromokinesin (KIF 4 gene).//0//2572bp//99%//AJ271784

30 C-NT2RM4002145//SLIT PROTEIN PRECURSOR.//1.40E-09//127aa//33%//P24014

C-NT2RM4002146//Homo sapiens MAGOH mRNA, complete cds./.6.90E-70//454bp//85%//AF035940

C-NT2RM4002161//Homo sapiens laforin (EPM2A) mRNA, complete cds./.0//2671bp//99%//AF084535

C-NT2RM4002174//MRPPROTEIN.//9.10E-68//264aa//51%//P21590

35 C-NT2RM4002189//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//6.20E-33//688aa//27%//P08640

C-NT2RM4002194//Mus musculus semaphorin Vla mRNA, complete cds./.5.20E-297//1753bp//87%//AF030430

C-NT2RM4002205//ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G).//3.00E-37//122aa//72%//Q07803

40 C-NT2RM4002213//Homo sapiens protein phosphatase methylesterase-1 (PME-1) mRNA, complete cds./.0//2452bp//100%//AF157028

C-NT2RM4002226//GTPASE ACTIVATING PROTEIN ROTUND.//3.70E-19//147aa//41%//P40809

C-NT2RM4002251//ALPHA-1,3-MANNOSYL-GLYCOPROTEIN BETA-1,2-N-ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.101) (N-GLYCOSYLOLIGOSACCHARIDE-GLYCOPROTEIN N-ACETYLGLUCOSAMINYL-TRANSFERASE I) (GNT- I) (GLCNAC-T I).//2.20E-36//320aa//38%//P27808

C-NT2RM4002323//ANTIGEN GOR (FRAGMENT).//0.000000001//154aa//33%//P48778

45 C-NT2RM4002409//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE-COA LIGASE) (ACYL- ACTIVATING ENZYME).//1.30E-29//275aa//30%//P27095

C-NT2RM4002438//Xenopus laevis putative Zic3 binding protein mRNA, complete cds./.1.10E-49//611 bp//70%//AF129131

C-NT2RM4002460//ENV POLYPROTEIN (COAT POLYPROTEIN) [CONTAINS: COAT PROTEINS GP70, GP20].//0.0000016//226aa//24%//P51515

50 C-NT2RM4002527//VEGETATILE INCOMPATIBILITY PROTEIN HET-E-1.//8.90E-15//366aa//27%//Q00808

C-NT2RM4002532//PROTEIN HOM1.//2.00E-16//276aa//28%//P55137

C-NT2RM4002558//Homo sapiens fatty acid transport protein (FATP) mRNA, complete cds./.0//1797bp//99%//AF055899

55 C-NT2RM4002565//Mus musculus Sec8 mRNA, complete cds./.0//1915bp//87%//AF022962

C-NT2RM4002571//H.sapiens mRNA for UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase (T2).//4.60E-78//921bp//69%//X85019

C-NT2RM4002594//MSP1 PROTEIN HOMOLOG.//2.70E-68//236aa//58%//P54815

C-NT2RM4002623//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA UGASE) (ASPRS).//  
2.30E-101//488aa//45%//O32038  
C-NT2RP1000018//Homo sapiens mRNA for NIK, partial cds.//0//1747bp//99%//AB013385  
C-NT2RP1000035//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//0//1652bp//99%//AJ012449  
5 C-NT2RP1000040//Mus musculus donson protein (Donson) mRNA, partial cds.//5.90E-150//1025bp//82%//  
AF193608  
C-NT2RP1000086//H.sapiens mRNA for zinc finger protein, Hsa12.//0//1162bp//99%//X98834  
C-NT2RP1000111//COP1 REGULATORY PROTEIN.//4.00E-116//296aa//51%//P93471  
C-NT2RP1000130//HEPATOMA-DERIVED GROWTH FACTOR (HDGF).//4.50E-50//181aa//60%//P51859  
10 C-NT2RP1000163//Homo sapiens cell cycle progression 2 protein (CPR2) mRNA, complete cds.//3.40E-270//  
951bp//98%//AF011792  
C-NT2RP1000202//ANKYRIN.//1.00E-25//302aa//34%//Q02357  
C-NT2RP1000272//Mus musculus mRNA for neural specific sr protein NSSR 2, complete cds.//1.40E-267//  
1155bp//87%//AB015895  
15 C-NT2RP1000326//Homo sapiens metaxin 2 (MTX2) mRNA, nuclear gene encoding mitochondrial protein, com-  
plete cds.//1.30E-275//1249bp//99%//AF053551  
C-NT2RP1000333//ANTI-SILENCING PROTEIN 1.//8.70E-47//155aa//58%//P32447  
C-NT2RP1000348//REDUCED VIABILITY UPON STARVATION PROTEIN 161.//1.70E-15//162aa//30%//P25343  
C-NT2RP1000363//R.norvegicus LL5 mRNA7//7.90E-262//1175bp//83%//X74226  
20 C-NT2RP1000376//Homo sapiens Ca<sup>2+</sup>-independent phospholipase A2 long isoform (iPLA2) mRNA, complete  
cds.//0//2252bp//96%//AF102989  
C-NT2RP1000413//MEMBRANE-ASSOCIATED PROTEIN HEM-2 (NAP1 PROTEIN).//1.90E-153//230aa//99%//  
P55161  
C-NT2RP1000439//Xenopus laevis chromosome condensation protein XCAP-G mRNA, complete cds.//1.80E-  
25 C-NT2RP1000443//QUINONE OXIDOREDUCTASE (EC 1.6.5.5) (NADPH:QUINONE REDUCTASE) (ZETA-  
CRYSTALLIN).//2.40E-10//227aa//25%//Q08257  
C-NT2RP1000460//NUCLEAR MOVEMENT PROTEIN NUDC.//3.80E-19//149aa//36%//P17624  
C-NT2RP1000470//PUTATIVE ATP-DEPENDENT RNA HELICASE T26G10.1 IN CHROMOSOME III.//2.60E-94//  
30 254aa//47%//P34580  
C-NT2RP1000478//TUBULIN BETA-5 CHAIN (CLASS-V).//4.50E-240//445aa//97%//P09653  
C-NT2RP1000481//Homo sapiens antigen NY-CO-3 (NY-CO-3) mRNA, partial cds.//7.5e-315//1445bp//99%//  
AF039688  
C-NT2RP1000493//POSSIBLE DNA-REPAIR PROTEIN XP-E (POSSIBLE XERODERMA PIGMENTOSUM  
35 GROUP E PROTEIN) (UV-DAMAGED DNA-BINDING PROTEIN) (UV-DDB).//3.60E-30//534aa//23%//P33194  
C-NT2RP1000513//Human NifU-like protein (hNifU) mRNA, partial cds.//6.50E-171//516bp//99%//U47101  
C-NT2RP1000522//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THI-  
OLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING EN-  
ZYME 1).//8.20E-83//345aa//47%//Q61068  
40 C-NT2RP1000547//COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (FRAGMENT).//1.10E-  
27//193aa//35%//P49020  
C-NT2RP1000574//HOMEobox PROTEIN MEIS2 (MEIS1-RELATED PROTEIN 1).//3.50E-75//151aa//94%//  
P97367  
C-NT2RP1000630//NECDIN.//2.40E-44//227aa//41%//P25233  
45 C-NT2RP1000677//SODIUM-INDEPENDENT ORGANIC ANION TRANSPORTER (ORGANIC ANION TRANS-  
PORTING POLYPEPTIDE).//1.20E-78//483aa//31%//P46721  
C-NT2RP1000701//Homo sapiens phospholipase A2 activating protein (PLA2P) mRNA, complete cds.//0//  
1687bp//99%//AF145020  
C-NT2RP1000733//Human mRNA for GSPT1-TK protein,complete cds.//0//2057bp//99%//E14379  
50 C-NT2RP1000738//Homo sapiens Wolf-Hirschhorn syndrome candidate 2 protein (WHSC2) mRNA, complete  
cds.//0//2186bp//99%//AF101434  
C-NT2RP1000746//Homo sapiens 60S acidic ribosomal protein PO mRNA, complete cds.//9.70E-196//901bp//  
99%//AF173378  
C-NT2RP1000782//PLATELET-ENDOTHELIAL TETRASPIN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYC-  
55 OPROTEIN SFA-1) (CD151 ANTIGEN).//1.20E-30//232aa//30%//O35566  
C-NT2RP1000825//GTPASE-ACTIVATING PROTEIN RHOGAP (RHO-RELATED SMALL GTPASE PROTEIN  
ACTIVATOR) (CDC42 GTPASE-ACTIVATING PROTEIN) (P50-RHOGAP).//8.20E-83//334aa//50%//Q07960  
C-NT2RP1000833//Homo sapiens cGMP phosphodiesterase AI (PDE9A) mRNA, complete cds.//0//1494bp//99%//

AF067223  
 C-NT2RP1000834//Homo sapiens alpha-methylacyl-CoA racemase mRNA, complete cds./.1.80E-176//829bp//  
 98%//AF047020

5 C-NT2RP1000856//PLATELET-ENDOTHELIAL TETRASPAAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYC-  
 OPROTEIN SFA-1) (CD151 ANTIGEN).//1.20E-30//232aa//30%//O35566

C-NT2RP1000860//Homo sapiens KL04P mRNA, complete cds./.0//1555bp//99%//AF064094

C-NT2RP1000902//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOME III.//5.20E-20//306aa//  
 33%//Q09531

10 C-NT2RP1000915//AUTOANTIGEN NGP-1.//1.70E-19//343aa//25%//Q13823

C-NT2RP1000947//Human E2 ubiquitin conjugating enzyme UbcH5B (UBCH5B) mRNA, complete cds./.4.60E-  
 105//504bp//99%//U39317

C-NT2RP1000954//RING CANAL PROTEIN (KELCH PROTEIN).//1.40E-23//370aa//28%//Q04652

C-NT2RP1000958//AUTOANTIGEN NGP-1.//1.40E-19//343aa//25%//Q13823

C-NT2RP1000959//Human acidic ribosomal phosphoprotein P0 mRNA, complete cds./.2.50E-236//966bp//99%//  
 15 M17885

C-NT2RP1000966//NUCLEOLIN (PROTEIN C23).//8.90E-299//554aa//99%//P19338

C-NT2RP1001011//Drosophila melanogaster putative 43 kDa protein (TH1) mRNA, complete cds./.2.20E-78//  
 1529bp//61%//L01790

20 C-NT2RP1001013//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//7.70E-253//425aa//98%//  
 P51522

C-NT2RP1001033//Homo sapiens delta-tubulin mRNA, complete cds./.2.10E-285//1290bp//100%//AF201333

C-NT2RP1001073//Homo sapiens U6 snRNA-associated Sm-like protein LSm5 mRNA, complete cds./.8.10E-  
 107//504bp//99%//AF182291

25 C-NT2RP1001079//Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, complete cds./.0//2085bp//99%//  
 U82267

C-NT2RP1001080//PROBABLE ATP-DEPENDENT RNA HELICASE DBP9.//2.30E-116//319aa//46%//Q06218

C-NT2RP1001113//Homo sapiens CTL2 gene./.0//2790bp//98%//AJ245621

C-NT2RP1001177//Rattus norvegicus histone macroH2A1.2 mRNA, complete cds./.5.20E-108//1278bp//69%//  
 U79139

30 C-NT2RP1001185//Human isovaleryl-coA dehydrogenase (IVD) mRNA, complete cds./.1.90E-158//729bp//99%//  
 M34192

C-NT2RP1001247//Homo sapiens TGF-beta type secreted signaling protein LEFTYA mRNA, complete cds./.0//  
 2006bp//100%//AF081513

C-NT2RP1001253//Homo sapiens oscillin (hLn) mRNA, complete cds./.0//2020bp//99%//AF029914

35 C-NT2RP1001294//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//1.80E-38//258aa//32%//Q12024

C-NT2RP1001302//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//1.80E-38//258aa//32%//Q12024

C-NT2RP1001310//Homo sapiens mitochondrial carrier homolog 1 isoform a mRNA, partial cds; nuclear gene for  
 mitochondrial product./.0//1732bp//99%//AF176006

40 C-NT2RP1001313//Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds./.7.50E-121//1394bp//69%//  
 AF126799

C-NT2RP1001361//Homo sapiens NADH-ubiquinone oxidoreductase subunit B14.5B homolog mRNA, complete  
 cds./.6.50E-116//541bp//100%//AF070652

C-NT2RP1001385//HYPOTHETICAL 48.8 KD PROTEIN IN SSU81-SCS2 INTERGENIC REGION.//2.70E-22//  
 284aa//25%//P40074

45 C-NT2RP1001395//Homo sapiens COP9 complex subunit 7a mRNA, complete cds./.0//1782bp//99%//AF210052

C-NT2RP1001410//PUTATIVE GTP-BINDING PROTEIN W08E3.3./.8.90E-141//396aa//67%//P91917

C-NT2RP1001449//Mus musculus Gng31g mRNA, complete cds./.7.20E-165//800bp//87%//AF069954

C-NT2RP1001457//Homo sapiens partial mRNA for beta-transducin family protein (putative).//1.20E-137//629bp//  
 100%//AJ005257

50 C-NT2RP1001482//Mouse oncogene (ect2) mRNA, complete cds./.2.10E-158//755bp//86%//L11316

C-NT2RP1001494//MALE STERILITY PROTEIN 2.//7.20E-40//261aa//27%//Q08891

C-NT2RP1001543//MYO-INOSITOL-1-PHOSPHATE SYNTHASE (EC 5.5.1.4) (IPS).//1.60E-166//506aa//60%//  
 P42803

55 C-NT2RP1001546//PLATELET-ENDOTHELIAL TETRASPAAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYC-  
 OPROTEIN SFA-1) (CD151 ANTIGEN).//1.60E-30//232aa//30%//O35566

C-NT2RP1001569//SIGNAL RECOGNITION PARTICLE RECEPTOR BETA SUBUNIT (SR-BETA).//5.80E-121//  
 271aa//89%//P47758

C-NT2RP1001665//CALMODUUN.//0.00000051//83aa//30%//P02594

C-NT2RP2000006//DNAJ PROTEIN (40 KD HEAT SHOCK CHAPERONE PROTEIN) (HSP40).//9.80E-17//79aa//55%//O34136  
 C-NT2RP2000008//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//2.40E-177//726aa//47%//P51523  
 5 C-NT2RP2000032//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1)7/1.80E-22//184aa//34%//Q01730  
 C-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds.//0//1390bp//98%//AF061749  
 10 C-NT2RP2000054//Homo sapiens putative ring zinc finger protein NY-REN-43 antigen mRNA, complete cds.//0//2245bp//99%//AF155109  
 C-NT2RP2000056//PROTEIN-TYROSINE PHOSPHATASE EPSILON PRECURSOR (EC 3.1.3.48) (R-PTP- EP-SILON).//9.40E-16//45aa//100%//P49446  
 C-NT2RP2000067//Mus musculus ODZ3 (Odz3) mRNA, partial cds.//0//3546bp//99%//AF195418  
 15 C-NT2RP2000070//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//3.40E-51//383aa//32%//P33450  
 C-NT2RP2000076//Homo sapiens partial mRNA for polyhomeotic 2 protein (PH2 gene).//7.90E-20//265bp//73%//AJ242730  
 C-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds.//0//2244bp//99%//AB018356  
 20 C-NT2RP2000126//POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L.//2.50E-117//541aa//42%//P41877  
 C-NT2RP2000133//Homo sapiens Leman coiled-coil protein (LCCP) mRNA, complete cds.//0//1490bp//99%//AF175966  
 C-NT2RP2000147//CLATHRIN COAT ASSEMBLY PROTEIN AP47 (CLATHRIN COAT ASSOCIATED PROTEIN AP47) (GOLGI ADAPTOR AP-1 47 KD PROTEIN) (HA1 47 KD SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN  
 25 ASSEMBLY PROTEIN COMPLEX 1 MEDIUM CHAIN).//4.40E-226//423aa//99%//P35585  
 C-NT2RP2000153//GAR2 PROTEIN.//9.80E-23//311aa//28%//P41891  
 C-NT2RP2000157//MLO2 PROTEIN.//2.60E-11//62aa//40%//Q09329  
 C-NT2RP2000161//DIS3 PROTEIN HOMOLOG.//4.10E-35//184aa//44%//Q17632  
 30 C-NT2RP2000183//DIHYDROPYRIMIDINASE RELATED PROTEIN-2 (DRP-2) (NEURAL SPECIFIC PROTEIN NSP60).//3.30E-16//114aa//44%//O02675  
 C-NT2RP2000195//Homo sapiens androgen induced protein (AIG-1) mRNA, complete cds.//7.80E-152//704bp//99%//AF153605  
 C-NT2RP2000224//INSULIN RECEPTOR SUBSTRATE-1 (IRS-1).//0.000043//103aa//28%//P35568  
 35 C-NT2RP2000248//UDP-N-ACETYLGLUCOSAMINE--PEPTIDE N-ACETYLGLUCOSAMINYLTRANSFERASE 110 KD SUBUNIT (EC 2.4.1.-) (O-GLCNAC TRANSFERASE P110 SUBUNIT).//3.40E-21//210aa//33%//P56558  
 C-NT2RP2000257//PUTATIVE MITOCHONDRIAL CARRIER YIL006W.//9.70E-41//278aa//36%//P40556  
 C-NT2RP2000258//ACTIVATOR 1 140 KD SUBUNIT (REPLICATION FACTOR C LARGE SUBUNIT) (AI 140 KD SUBUNIT) (RF-C 140 KD SUBUNIT) (ACTIVATOR 1 LARGE SUBUNIT) (DNA-BINDING PROTEIN PO-GA).//  
 40 7.10E-12//213aa//23%//P35251  
 C-NT2RP2000270//Human putative G-protein coupled receptor (SH120) mRNA, complete cds.//1.30E-242//1043bp//99%//U78723  
 C-NT2RP2000288//HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMOSOME I.//1.60E-27//576aa//25%//Q10297  
 45 C-NT2RP2000297//ZINC FINGER PROTEIN 184 (FRAGMENT).//3.30E-186//256aa//60%//Q99676  
 C-NT2RP2000310//Human proline dehydrogenase/proline oxidase (PRODH) mRNA, complete cds.//4.30E-279//1193bp//99%//U82381  
 C-NT2RP2000329//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//2.00E-111//  
 50 226aa//92%//P08760  
 C-NT2RP2000346//Homo sapiens apoptosis associated protein (GADD34) mRNA, complete cds.//0//2331bp//99%//U83981  
 C-NT2RP2000414//Homo sapiens HnRNP F protein mRNA, complete cds.//0//1886bp//99%//L28010  
 C-NT2RP2000420//ZINC FINGER PROTEIN 165.//8.50E-33//155aa//52%//P49910  
 C-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//0//1757bp//99%//AF102265  
 55 C-NT2RP2000448//KES1 PROTEIN.//8.70E-54//392aa//38%//P35844  
 C-NT2RP2000523//APOLIPOPROTEIN B MRNA EDITING PROTEIN (HEPR) (APOBEC-1).//6.00E-16//124aa//34%//P41238  
 C-NT2RP2000660//SAP1 PROTEIN.//5.20E-68//474aa//32%//P39955

C-NT2RP2000668//SERINE/THREONINE PROTEIN KINASE PKPA (EC 2.7.1.-)//1.30E-27//349aa//32%//Q01577  
C-NT2RP2000710//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA LIGASE)//2.70E-100//488aa//44%//O32038  
5 C-NT2RP2000764//NIFS PROTEIN//6.60E-36//252aa//42%//P12623  
C-NT2RP2000809//Homo sapiens BAG-family molecular chaperone regulator-5 mRNA, complete cds//0//3347bp//99%//AF095195  
C-NT2RP2000812//DILUTE MYOSIN HEAVY CHAIN, NON-MUSCLE (MYOSIN 5A).//5.-60E-08//179aa//29%//Q99104  
10 C-NT2RP2000814//GELATION FACTOR (ACTIN BINDING PROTEIN 120) (ABP-120).//1.10E-07//96aa//29%//P13466  
C-NT2RP2000816//MAGNESIUM-CHELATASE 30 KD SUBUNIT//7.90E-08//172aa//28%//P26174  
C-NT2RP2000842//Human lysophosphatidic acid receptor homolog mRNA, complete cds//0//1562bp//99%//U80811  
15 C-NT2RP2000880//PROBABLE TRANSLATION INITIATION FACTOR IF-2//0//694aa//99%//O60841  
C-NT2RP2000892//Rattus norvegicus db83 mRNA, complete cds//2.90E-191//1094bp//85%//AB006135  
C-NT2RP2000931//MATRIN 3//2.40E-289//467aa//95%//P43244  
C-NT2RP2000943//Homo sapiens sec24D protein mRNA, complete cds//0//2767bp//99%//AF130464  
C-NT2RP2000965//Homo sapiens mRNA for fls353, complete cds//0//1989bp//96%//AB024704  
20 C-NT2RP2001070//PUTATIVE PYRIDOXAMINE 5'-PHOSPHATE OXIDASE (EC 1.4.3.5) (PNP/PMP OXIDASE).//5.80E-46//222aa//45%//Q20939  
C-NT2RP2001081//SYNAPTOTAGMIN IV.//4.20E-118//430aa//54%//P50232  
C-NT2RP2001127//Homo sapiens mRNA for PLU-1 protein.//0//2514bp//99%//AJ132440  
C-NT2RP2001168//VERPROLIN.//1.50E-09//143aa//33%//P37370  
25 C-NT2RP2001174//GASTRULA ZINC FINGER PROTEIN XLCGF46.1 (FRAGMENT).//6.00E-10//88aa//38%//P18722  
C-NT2RP2001233//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.00E-128//409aa//45%//Q05481  
C-NT2RP2001245//MYOSIN HEAVY CHAIN, NONMUSCLE (CELLULAR MYOSIN HEAVY CHAIN) (NMMHC).//2.20E-10//366aa//28%//P14105  
30 C-NT2RP2001290//BETA-SOLUBLE NSF ATTACHMENT PROTEIN (SNAP-BETA) (SNAP-ALPHA HOMOLOG) (BRAIN PROTEIN 147) (FRAGMENT).//4.40E-91//179aa//99%//P28663  
C-NT2RP2001295//ZINC/CADMIUM RESISTANCE PROTEIN.//8.30E-39//161aa//34%//P20107  
C-NT2RP2001327//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PRO-  
35 TEIN).//5.50E-116//311aa//71%//Q13829  
C-NT2RP2001378//MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).//2.00E-11//403aa//25%//Q02817  
C-NT2RP2001392//MTTOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR (EC 3.4.21.-).//8.40E-192//581aa//54%//P93647  
C-NT2RP2001394//Homo sapiens mRNA for SCML2 protein.//0//2068bp//99%//Y18004  
40 C-NT2RP2001397//Homo sapiens mRNA for cyclin B2, complete cds//1.9e-316//1428bp//100%//AB020981  
C-NT2RP2001420//Mus musculus nuclear protein NIP45 mRNA, complete cds//9.00E-112//742bp//82%//U76759  
C-NT2RP2001440//Homo sapiens mRNA for 14-3-3gamma, complete cds//0//3712bp//99%//AB024334  
C-NT2RP2001460//TRICHOHYAUN.//1.00E-14//521aa//24%//P37709  
C-NT2RP2001511//Homo sapiens putative RNA-binding protein Q99 mRNA, complete cds//3.20E-297//2206bp//  
45 75%//AF093097  
C-NT2RP2001520//Homo sapiens mRNA for mitochondrial carrier protein ARALAR1.//0//2502bp//99%//Y14494  
C-NT2RP2001536//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds//0//2326bp//99%//AF035586  
C-NT2RP2001560//VAV2 PROTEIN.//0.00000015//219aa//27%//Q60992  
50 C-NT2RP2001576//HYPOTHETICAL 62.2 KD PROTEIN C4G8.12C IN CHROMOSOME 1.//8.20E-29//294aa//31%//Q09837  
C-NT2RP2001597//RYANODINE RECEPTOR, CARDIAC MUSCLE.//0.000000036//127aa//36%//P30957  
C-NT2RP2001601//Homo sapiens SUMO-1-specific protease (SSP1) mRNA, complete cds//0//1748bp//99%//AF196304  
55 C-NT2RP2001613//MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT TOM40 (MOM38 PROTEIN) (TRANSLO-  
CASE OF OUTER MEMBRANE 40 KD SUBUNIT).//6.10E-12//184aa//31%//P24391  
C-NT2RP2001634//Homo sapiens alpha-catenin-like protein mRNA, complete cds//0//2445bp//99%//U97067  
C-NT2RP2001660//Homo sapiens putative 13 S Golgi transport complex 90kD subunit brain-specific isoform mR-

NA, complete cds./0//1287bp//99%//AF058718  
 C-NT2RP2001663//ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE), (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (FRAGMENT).//1.10E-47//126aa//53%//P42897  
 5 C-NT2RP2001740//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING ENZYME 1).//7.90E-52//220aa//44%//Q61068  
 10 C-NT2RP2001748//FARNESYL PYROPHOSPHATE SYNTHETASE (FPP SYNTHETASE) (FPS) (FARNESYL DIPHOSPHATE SYNTHETASE) (DIMETHYLALLYLTRANSFERASE (EC 2.5.1.1) / GERANYLTRANSTRANSFERASE (EC 2.5.1.10)) (KIAA0032).//5.40E-47//96aa/797%//P14324  
 15 C-NT2RP2001756//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.70E-49//411aa//32%//P51523  
 C-NT2RP2001839//SCY1 PROTEIN.//5.40E-32//621aa//24%//P53009  
 C-NT2RP2001869//ZINC FINGER PROTEIN 191.//7.10E-26//126aa//52%//O14754  
 20 C-NT2RP2001876//ALLOGRAFT INFLAMMATORY FACTOR-1 (AIF-1) (IONIZED CALCIUM BINDING ADAPTER MOLECULE 1).//1.20E-45//141aa//65%//P55008  
 C-NT2RP2001883//Homo sapiens CGI-01- protein mRNA, complete cds./0//2306bp//99%//AF132936  
 C-NT2RP2001898//Human inositol polyphosphate 5-phosphatase (5ptase) mRNA, 3' end./0//2518bp//98%//M74161  
 25 C-NT2RP2001900//ACTIN-LIKE PROTEIN ARP5.//2.30E-38//395aa//30%//P53946  
 C-NT2RP2001976//Mus musculus calmodulin-binding protein SHA1 (Sha1) mRNA, complete cds./4.70E-177//1538bp//74%//AF062378  
 C-NT2RP2001985//Homo sapiens high-risk human papilloma viruses E6 oncoproteins targeted protein E6TP1 alpha mRNA, complete cds./2.00E-38//435bp//67%//AF090989  
 30 C-NT2RP2001991//SODIUM- AND CHLORIDE-DEPENDENT TRANSPORTER NTT73.//6.50E-129//279aa//85%//Q08469  
 C-NT2RP2002025//NG-CAM RELATED CELL ADHESION MOLECULE PRECURSOR (NR-CAM) (BRAVO).//1.70E-47//247aa//52%//P35331  
 C-NT2RP2002046//Homo sapiens mRNA for transcription factor./0//1664bp//99%//AJ130894  
 35 C-NT2RP2002058//Homo sapiens WD repeat protein WDR3 (WDR3) mRNA, complete cds./0//2510bp//99%//AF083217  
 C-NT2RP2002066//Rattus norvegicus transmembrane receptor Unc5H2 mRNA, complete cds./1.60E-226//1301bp//88%//U87306  
 C-NT2RP2002078//PECANEX PROTEIN.//1.80E-09//195aa//32%//P18490  
 C-NT2RP2002079//HISTONE HI, GONADAL.//4.40E-11//214aa//34%//P02256  
 40 C-NT2RP2002099//Homo sapiens mRNA for E1B-55kDa-associated protein./0//33 89bp//99%//AJ007509  
 C-NT2RP2002105//H.sapiens MSH-R gene for melanocyte stimulating hormone receptor./0//1644bp//98%//X65634  
 C-NT2RP2002124//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME 4) (UBIQUITOUS NUCLEAR PROTEIN HOMOLOG).//4.30E-44//155aa//37%//Q13107  
 C-NT2RP2002185//Homo sapiens ubiquilin mRNA, complete cds./0//1789bp//99%//AF176069  
 C-NT2RP2002193//Homo sapiens PIAS3 mRNA for protein inhibitor of activated STAT3, complete cds./0//2809bp//99%//AB021868  
 45 C-NT2RP2002252//Mus musculus (clone pVZmSin3A9) mSin3A9 mRNA, complete cds./0//3118bp//91%//L38621  
 C-NT2RP2002256//Homo sapiens retinoic acid hydroxylase mRNA, complete cds./0//1528bp//98%//AF005418  
 C-NT2RP2002270//AF-9 PROTEIN.//1.20E-07//74aa//36%//P42568  
 C-NT2RP2002312//Homo sapiens mRNA for CDS2 protein./0//2333bp//99%//Y16521  
 C-NT2RP2002325//Homo sapiens mRNA for Pex11p, complete cds./8.40E-254//1158bp//99%//AB015594  
 50 C-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant mRNA, complete cds./4.30E-240//1105bp//99%//AF038958  
 C-NT2RP2002408//Homo sapiens mRNA for TOLLIP protein./3.20E-210//1136bp//93%//AJ242972  
 C-NT2RP2002442//HESA PROTEIN.//2.80E-14//163aa//30%//P46037  
 C-NT2RP2002464//DNA CROSS-LINK REPAIR PROTEIN PSO2/SNM1.//6.50E-07//171aa//27%//P30620  
 C-NT2RP2002479//Homo sapiens mRNA for ABC transporter 7 protein, complete cds./0//2180bp//99%//AB005289  
 55 C-NT2RP2002503//ZINC FINGER PROTEIN 45 (BRC1744).//4.60E-144//537aa//49%//Q02386  
 C-NT2RP2002520//Homo sapiens transcription factor RFX-B (RFXB) mRNA, complete cds./3.70E-34//668bp//61%//AF105427

C-NT2RP2002537//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X//6.20E-19//288aa//26%//Q11073  
 C-NT2RP2002591//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.20E-155//562aa//50%//P51523  
 5 C-NT2RP2002595//PROBABLE CALCIUM-BINDING PROTEIN ALG-2 (PMP41) (ALG-257).//7.50E-35//181aa//42%//P12815  
 C-NT2RP2002606//Rattus norvegicus Rabin3 mRNA, complete cds.//9.20E-147//874bp//87%//U19181  
 C-NT2RP2002609//2-HYDROXYMUCONIC SEMIALDEHYDE HYDROLASE (EC 3.1.1.-) (HMSH).//2.80E-08//109aa//37%//P19076  
 10 C-NT2RP2002618//PROTEIN ARGININE N-METHYLTRANSFERASE 2 (EC 2.1.1.).//1.70E-51//326aa//38%//P55345  
 C-NT2RP2002701//HYPOTHETICAL 38.1 KD PROTEIN C2F12.15C IN CHROMOSOME II//1.90E-14//210aa//30%//O14345  
 15 C-NT2RP2002710//SH3-BINDING PROTEIN 3BP-1.//4.90E-85//489aa//43%//P55194  
 C-NT2RP2002727//Rattus norvegicus tulip 2 mRNA, complete cds.//3.50E-74//727bp//72%//AF041107  
 C-NT2RP2002741//Homo sapiens mRNA for Neuroblastoma, complete cds.//9.90E-54//964bp//64%//D89016  
 C-NT2RP2002862//60S ACIDIC RIBOSOMAL PROTEIN P0 (LIGHT-INDUCED 34 KD PROTEIN).//8.80E-10//203aa//27%//P29764  
 20 C-NT2RP2002880//GLUCOSE REPRESSION MEDIATOR PROTEIN.//0.000039//206aa//23%//P14922  
 C-NT2RP2002928//Homo sapiens pre-mRNA splicing factor (PRP17) mRNA, complete cds.//1.90E-136//623bp//100%//AF038392  
 C-NT2RP2002929//HYPOTHETICAL 46.2 KD TRP-ASP REPEATS CONTAINING PROTEIN D2013.2 IN CHROMOSOME II.//4.10E-87//395aa//40%//Q18964  
 25 C-NT2RP2002939//ZINC FINGER PROTEIN 136.//5.40E-70//282aa//42%//P52737  
 C-NT2RP2002959//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2).//4.60E-80//147aa//100%//P51669  
 C-NT2RP2002980//30S RIBOSOMAL PROTEIN S10.//1.00E-08//98aa//36%//P10129  
 C-NT2RP2002986//Homo sapiens mRNA for Kelch motif containing protein, complete cds.//0//2209bp//99%//AB026190  
 30 C-NT2RP2002993//DNA-DIRECTED RNA POLYMERASE 1135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135).//0//716aa//91%//P70700  
 C-NT2RP2003000//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN).//L90E-11//132aa//38%//Q13829  
 35 C-NT2RP2003121//Mus musculus enhancer of polycmb (Epc1) mRNA, complete cds.//2.30E-82//642bp//68%//AF079765  
 C-NT2RP2003125//RING CANAL PROTEIN (KELCH PROTEIN).//2.40E-38//539aa//25%//Q04652  
 C-NT2RP2003137//UBIQUITIN.//0.000026//70aa//30%//P13117  
 C-NT2RP2003157//SPLICING FACTOR, ARGinine/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//1.30E-13//185aa//38%//Q08170  
 40 C-NT2RP2003158//Homo sapiens mRNA for proteasome subunit p58, complete cds.//0//2091bp//99%//D67025  
 C-NT2RP2003164//Homo sapiens mRNA for protein kinase.//0//2313bp//99%//AJ132545  
 C-NT2RP2003177//Homo sapiens recombination and sister chromatid cohesion protein homolog (hrec8) mRNA, partial cds.//0//1641bp//99%//AF006264  
 C-NT2RP2003228//H.sapiens PI-Cdc21 mRNA.//0//2870bp//98%//X74794  
 45 C-NT2RP2003230//Rattus norvegicus endo-alpha-D-mannosidase (Enman) mRNA, complete cds.//2.60E-186//1551bp//77%//AF023657  
 C-NT2RP2003243//Homo sapiens partial mRNA for putative p621 protein which interacts with transcription factor Sp1.//0//1544bp//99%//AJ242978  
 C-NT2RP2003265//Homo sapiens CGI-53 protein mRNA, complete cds.//0//1580bp//99%//AF151811  
 50 C-NT2RP2003272//Homo sapiens ubiquilin mRNA, complete cds.//0//1789bp//99%//AF176069  
 C-NT2RP2003277//NAM7 PROTEIN (NONSENSE-MEDIATED mRNA DECAY PROTEIN 1) (UP-FRAMESHIFT SUPPRESSOR 1).//1.90E-16//145aa//43%//P30771  
 C-NT2RP2003286//PROBABLE RNA 3'-TERMINAL PHOSPHATE CYCLASE (EC 6.5.1.4) (RNA-3'- PHOSPHATE CYCLASE) (RNA CYCLASE).//4.20E-88//374aa//47%//Q23400  
 55 C-NT2RP2003295//Homo sapiens RMP mRNA for RPB5 meidating protein, complete cds.//0//1526bp//99%//AB006572  
 C-NT2RP2003307//KINESIN LIGHT CHAIN (KLC).//2.20E-199//550aa//70%//Q07866  
 C-NT2RP2003308//CROOKED NECK PROTEIN.//5.40E-244//622aa//67%//P17886

C-NT2RP2003329//PUTATIVE ADENYLYL CYCLASE REGULATORY PROTEIN./.3.60E-14//332aa//32%//P26337

C-NT2RP2003347//BREAST CANCER TYPE 1 SUSCEPTIBILITY PROTEIN HOMOLOG./.0.000022//261aa//24%//P48754

5 C-NT2RP2003391//Homo sapiens mRNA for nuclear transport receptor./.0//1509bp//99%//AJ133769

C-NT2RP2003394//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1./.5.50E-13//302aa//26%//P25386

10 C-NT2RP2003401//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THIOESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING ENZYME 1).//9.60E-78//346aa//43%//Q61068

C-NT2RP2003433//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT./.5.00E-131//269aa//91%//P38378

C-NT2RP2003466//Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds./.0//2194bp//99%//AF126799

15 C-NT2RP2003480//Homo sapiens zinc finger DNA binding protein 99 (ZNF281) mRNA, complete cds./.0//3012bp//99%//AF125158

C-NT2RP2003506//NADPH-CYTQCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR).//5.40E-14//106aa//46%//P04175

C-NT2RP2003513//Homo sapiens mRNA for paralemmin./.0//2137bp//97%//Y14770

20 C-NT2RP2003517//Human c-sis/platelet-derived growth factor 2 (SIS/PDGF2) mRNA, complete cds./.0//1746bp//95%//M12783

C-NT2RP2003522//Homo sapiens zinc finger DNA binding protein 99 (ZNF281) mRNA, complete cds./.0//1764bp//99%//AF125158

C-NT2RP2003543//HYPOTHETICAL TRNA/RRNA METHYLTRANSFERASE SLR1673 (EC 2.1.1.-).//1.70E-17//148aa//34%//P74261

25 C-NT2RP2003564//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A))(RO(SS-A)).//2.10E-59//270aa//46%//P19474

C-NT2RP2003596//Mus musculus Fas-apoptosis inhibitory molecule (Faim) mRNA, complete cds./.4.80E-82//530bp//85%//AF130367

30 C-NT2RP2003604//Homo sapiens alpha-catenin-like protein (CTNNAL1) mRNA, complete cds./.0//2442bp//99%//AF030233

C-NT2RP2003643//Mus musculus mRNA for CMP-N-acetylneuraminc acid synthetase./.9.40E-243//1624bp//82%//AJ006215

C-NT2RP2003702//Homo sapiens 17 beta-hydroxysteroid dehydrogenase type VII (HSD17B7) mRNA, complete cds./.2.1e-313//978bp//99%//AF098786

35 C-NT2RP2003704//Homo sapiens mRNA for ATP-dependent metalloprotease YME1L./.1.80E-72//350bp//100%//AJ132637

C-NT2RP2003713//Homo sapiens ubiquitin-specific protease 3 (USP3) mRNA, complete cds./.0//2018bp//99%//AF073344

40 C-NT2RP2003714//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//5.40E-29//85aa//72%//Q05481

C-NT2RP2003737//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2).//1.70E-75//147aa//93%//P51669

45 C-NT2RP2003760//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP).//0//869aa//80%//P53620

C-NT2RP2003781//HYPOTHETICAL 36.7 KD PROTEIN AH6.2 IN CHROMOSOME II./.5.50E-63//253aa//50%//Q09201

C-NT2RP2003840//HYPOTHETICAL 48.1 KD PROTEIN B0403.2 IN CHROMOSOME X./.3.70E-21//137aa//43%//Q11076

50 C-NT2RP2003857//MYOTROPHIN (V-1 PROTEIN) (GRANULE CELL DIFFERENTIATION PROTEIN).//0.00000016//117aa//29%//Q91955

C-NT2RP2003871//Homo sapiens transposon-derived Buster1 transposase-like protein gene, complete cds./.0//2807bp//99%//AF205601

C-NT2RP2003912//SERINE/THREONINE-PROTEIN KINASE NEK1 (EC 2.7.1.-) (NIMA-RELATED PROTEIN KINASE 1).//6.10E-183//387aa//87%//P51954

55 C-NT2RP2003952//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE) (ARGININE AMINOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV) (AP-B).//1.50E-23//200aa//30%//O09175

C-NT2RP2003981//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS8./.1.40E-16//664aa//20%//

P39702  
C-NT2RP2004013//TRANSCRIPTION FACTOR BTF3 (RNA POLYMERASE B TRANSCRIPTION FACTOR 3).//  
2.30E-53//141aa//78%//P20290  
C-NT2RP2004041//SYNAPSINS IA AND B.//0.00000074//159aa//32%//P17599  
5 C-NT2RP2004066//Mus musculus Msx2 interacting nuclear target protein mRNA, complete cds.//2.70E-288//  
1994bp//81%//AF156529  
C-NT2RP2004098//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE).//5.40E-30//319aa//31%//Q01513  
C-NT2RP2004170//Homo sapiens mRNA for transducin (beta) like 1 protein.//1.10E-138//1236bp//74%//Y12781  
10 C-NT2RP2004187//ZINC FINGER PROTEIN 38 (ZFP-38) (CTF1N51) (TRANSCRIPTION FACTOR RU49).//  
5.60E-31//424aa//28%//Q07231  
C-NT2RP2004194//Rattus norvegicus Golgi SNARE GS15 mRNA, complete cds.//3.80E-52//397bp//82%//  
AF003998  
C-NT2RP2004232//Homo sapiens EPK2 mRNA for serine/threonine kinase, complete cds.//0//2272bp//99%//  
15 AB015982  
C-NT2RP2004239//Homo sapiens lok mRNA for protein kinase, complete cds.//0//3044bp//99%//AB015718  
C-NT2RP2004242//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H).//  
9.90E-12//427aa//26%//P19246  
C-NT2RP2004245//Mus musculus pantothenate kinase 1 beta (panK1beta) mRNA, complete cds.//6.40E-117//  
20 1122bp//72%//AF200357  
C-NT2RP2004270//PROTEIN PTM1 PRECURSOR.//1.40E-16//334aa//24%//P32857  
C-NT2RP2004366//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS 13.//1.30E-51//505aa//  
29%//Q07878  
C-NT2RP2004389//PROBABLE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN S9 PRECURSOR.//9.30E-15//  
25 126aa//39%//P38120  
C-NT2RP2004392//MNN4 PROTEIN7/1.40E-11//143aa//27%//P36044  
C-NT2RP2004396//Homo sapiens mRNA for activator of S phase Kinase, complete cds.//5.40E-243//1108bp//  
99%//AB028069  
C-NT2RP2004425//Mus musculus axotrophin mRNA, complete cds.//0//2321bp//86%//AF155739  
30 C-NT2RP2004476//Homo sapiens cyclin L ania-6a mRNA, complete cds.//0//2075bp//99%//AF180920  
C-NT2RP2004538//Mus musculus kinesin-like protein KIF1B (Kif1b) mRNA, complete cds.//0//1387bp//86%//  
AF090190  
C-NT2RP2004568//PUTATIVE ATP-DEPENDENT RNA HELICASE C30D11.03.//3.00E-117//625aa//40%//  
Q09903  
35 C-NT2RP2004587//NEUROFILAMENT TRIPLET M PROTEIN (160 KD NEUROFILAMENT PROTEIN) (NF-M).//  
7.30E-07//352aa//23%//P07197  
C-NT2RP2004655//Homo sapiens mRNA for leucine rich protein.//8.50E-233//1061bp//99%//AJ006291  
C-NT2RP2004681//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H).//  
2.60E-07//426aa//23%//P19246  
40 C-NT2RP2004689//HYPOTHETICAL 192.5 KD PROTEIN C6G9.10C IN CHROMOSOME 1.//5.60E-64//616aa//  
33%//Q92355  
C-NT2RP2004710//Mus musculus formin binding protein 30 mRNA, complete cds.//1.50E-280//1464bp//85%//  
U40750  
C-NT2RP2004732//NEUROFILAMENT TRIPLET M PROTEIN (160 KD NEUROFILAMENT PROTEIN) (NF-M).//  
45 7.30E-07//352aa//23%//P07197  
C-NT2RP2004768//SERINE/THREONINE-PROTEIN KINASE NRK1 (EC 2.7.1.-) (N-RICH KINASE 1).//1.30E-  
26//190aa//41%//P38692  
C-NT2RP2004791//PUTATIVE LEUCYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.4) (LEUCINE- TRNA  
LIGASE) (LEURS).//9.50E-73//153aa//59%//Q10490  
50 C-NT2RP2004799//PROBABLE SUCCINYL-COA LIGASE [GDP-FORMING], BETA-CHAIN PRECURSOR (EC  
6.2.1.4) (SUCCINYL-COA SYNTHETASE, BETA CHAIN) (SCS-BETA).//3.70E-135//414aa//62%//P53588  
C-NT2RP2004816//H58 PROTEIN.//9.00E-173//327aa//98%//P40336  
C-NT2RP2004920//TRANSCRIPTIONAL REGULATOR ATRX (X-LINKED NUCLEAR PROTEIN) (HETERO-  
CHROMATIN PROTEIN 2) (HP1 ALPHA-INTERACTING PROTEIN) (HP1-BP38 PROTEIN).//4.20E-09//804aa//  
22%//Q61687  
C-NT2RP2004933//Homo sapiens mRNA for ZIP-kinase, complete cds.//0//2103bp//99%//AB007144  
C-NT2RP2004959//P54 PROTEIN PRECURSOR.//0.00000095//297aa//20%//P13692  
55 C-NT2RP2004961//Rattus norvegicus KRAB/zinc finger suppressor protein 1 (KS1) mRNA, complete cds.//1.00E-

228//1666bp//75%//U56732  
 C-NT2RP2004978//ACTIN-LIKE PROTEIN ARP8//3.30E-47//353aa//30%//Q12386  
 C-NT2RP2005003//52 KD RO PROTEIN (SJOGEN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))//  
 1.80E-99//376aa//43%//P19474  
 5 C-NT2RP2005012//Homo sapiens mRNA for SEC63 protein//0//1693bp//99%//AJ011779  
 C-NT2RP2005037//ANTI-SILENCING PROTEIN 1//3.30E-47//155aa//59%//P32447  
 C-NT2RP2005038//DNA NUCLEOTIDYLEXOTRANSFERASE (EC 2.7.7.31) (TERMINAL ADDITION ENZYME)  
 (TERMINAL DEOXYNUCLEOTIDYLTRANSFERASE) (TERMINAL TRANSFERASE)//4.00E-91//218aa//44%//  
 Q92089  
 10 C-NT2RP2005116//PUTATIVE EUKARYOTIC TRANSLATION INITIATION FACTOR 3 ALPHA SUBUNIT (EIF-3  
 ALPHA)//2.00E-173//273aa//57%//P34466  
 C-NT2RP2005126//H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein)//0//2388bp//98%//  
 X98743  
 15 C-NT2RP2005139//2-5A-DEPENDENT RIBONUCLEASE (EC 3.1.26.-) (2-5A-DEPENDENT RNAASE) (RNASE  
 L) (RIBONUCLEASE 4) (FRAGMENT)//0.00000022//139aa//35%//Q05921  
 C-NT2RP2005144//Homo sapiens tubby like protein 3 (TULP3) mRNA, complete cds//0.00E-01//1437bp//98%//  
 AF045583  
 C-NT2RP2005162//Homo sapiens aspartyl aminopeptidase mRNA, complete cds//0//1615bp//99%//AF005050  
 C-NT2RP2005168//Homo sapiens mRNA for E1B-55kDa-associated protein//0//2769bp//98%//AJ007509  
 20 C-NT2RP2005204//Homo sapiens SUMO-1-activating enzyme E1N subunit (SUA1) mRNA, complete cds//0//  
 1262bp//99%//AF090385  
 C-NT2RP2005239//Homo sapiens cysteine desulfurase (nifS) mRNA, complete cds//0//2087bp//99%//AF097025  
 C-NT2RP2005276//Homo sapiens mRNA for Acyl-CoA synthetase 3, complete cds//0//2122bp//99%//D89053  
 25 C-NT2RP2005288//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds//0//2992bp//99%//  
 AF060219  
 C-NT2RP2005315//Homo sapiens meningioma-expressed antigen 5 (MEA5) mRNA, partial cds//1.90E-170//  
 780bp//100%//AF036144  
 C-NT2RP2005325//Homo sapiens LIM-homeodomain protein HLHX2 (LHX2) mRNA, complete cds//0//1643bp//  
 99%//AF124735  
 30 C-NT2RP2005336//TRICHOHYALIN//5.40E-10//545aa//22%//P37709  
 C-NT2RP2005344//PROBABLE CALCIUM-TRANSPORTING ATPASE 5 (EC 3.6.1.38)//2.10E-124//636aa//  
 38%//P32660  
 C-NT2RP2005358//Homo sapiens methyl-CpG binding domain-containing protein MBD3 (MBD3) mRNA, com-  
 plete cds//0//2199bp//99%//AF072247  
 35 C-NT2RP2005360//Homo sapiens sentrin/SUMO-specific protease (SENP1) mRNA, complete cds//1.30E-52//  
 753bp//67%//AF149770  
 C-NT2RP2005393//AUTOANTIGEN NGP-1//7.20E-39//224aa//35%//Q13823  
 C-NT2RP2005407//OXYSTEROL-BINDING PROTEIN//5.30E-63//410aa//40%//P22059  
 40 C-NT2RP2005436//SPLICING FACTOR, ARGinine/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR  
 SRP75)//1.20E-13//185aa//38%//Q08170  
 C-NT2RP2005441//Homo sapiens hypothalamus protein HT002 mRNA, complete cds//4.10E-202//962bp//98%//  
 AF113540  
 C-NT2RP2005457//Homo sapiens NADH-ubiquinone oxidoreductase subunit B14.5B homolog mRNA, complete  
 cds//1.20E-13 0//608bp//99%//AF070652  
 45 C-NT2RP2005465//MITOCHONDRIAL CARRIER PROTEIN RIM2//3.00E-44//252aa//41%//P38127  
 C-NT2RP2005476//Human pl90-B (pl90-B) mRNA, complete cds//3.40E-108//668bp//88%//U17032  
 C-NT2RP2005490//Mus musculus D3Mm3e (D3Mm3e) mRNA, complete cds//1.80E-175//1102bp//83%//  
 AF053628  
 C-NT2RP2005491//PARAMYOSIN (PMY) (ANTIGEN B)//0.00000015//279aa//26%//P35418  
 50 C-NT2RP2005496//ZINC FINGER PROTEIN 135//2.90E-146//398aa//59%//P52742  
 C-NT2RP2005498//PROTEIN PHOSPHATASE PP2A, 55 KD REGULATORY SUBUNIT, ALPHA ISOFORM (PRO-  
 TEIN PHOSPHATASE PP2A B SUBUNIT ALPHA ISOFORM) (ALPHA-PR55)//5.20E-81//166aa//88%//P36876  
 C-NT2RP2005509//Homo sapiens CGI-45 protein mRNA, complete cds//0//1825bp//99%//AF151803  
 C-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds//0//  
 3994bp//99%//AF092563  
 55 C-NT2RP2005525//Mus musculus kanadaptin mRNA, complete cds//2.40E-304//1687bp//85%//AF035526  
 C-NT2RP2005531//PROTEIN 4.1 (BAND 4.1) (P4.1)//5.50E-70//393aa//39%//P11171  
 C-NT2RP2005539//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//0//1560bp//98%//AJ012449

C-NT2RP2005549//PUTATIVE LACTOYLGLUTATHIONE LYASE (EC 4.4.1.5) (METHYLGlyOXALASE) (AL-DOKETOMUTASE) (GLYOXALASE I) (GLX I) (KETONE-ALDEHYDE MUTASE) (S-D-LACTOYLGLUTATHIONE METHYLGlyOXAL LYASE).//2.00E-20//181aa//36%//Q39366  
 5 C-NT2RP2005557//Homo sapiens clone 486790 diphosphoinositol polyphosphate phosphohydrolase mRNA, complete cds.//1.00E-46//576bp//70%//AF062529  
 C-NT2RP2005605//QUEUINE TRNA-RIBOSYLTRANSFERASE (EC 2.4.2.29) (TRNA-GUANINE TRANSGLYC-OSYLASE) (GUANINE INSERTION ENZYME).//8.20E-23//164aa//28%//O32053  
 C-NT2RP2005620//Homo sapiens epsin 2a mRNA, complete cds.//8.9e-313//1455bp//98%//AF062085  
 10 C-NT2RP2005635//PROBABLE NH(3)-DEPENDENT NAD(+) SYNTHETASE (EC 6.3.5.1).//1.00E-11//128aa//36%//P47623  
 C-NT2RP2005654//CYSTEINE STRING PROTEIN (CCCS1).//1.20E-13//74aa//45%//P56101  
 C-NT2RP2005669//Homo sapiens death effector domain-containing testicular molecule mRNA, complete cds.//1.60E-248//1129bp//99%//AF043733  
 15 C-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds.//4.40E-200//908bp//99%//AF089814  
 C-NT2RP2005694//X-LINKED RETINITIS PIGMENTOSA GTPASE REGULATOR.//2.60E-10//175aa//27%//Q92834  
 C-NT2RP2005701//ZINC-FINGER PROTEIN RFP (RET FINGER PROTEIN).//3.00E-63//323aa//39%//Q62158  
 20 C-NT2RP2005712//Homo sapiens myosin X (MYO10) mRNA, partial cds.//0//2681 bp//99%//AF132022  
 C-NT2RP2005719//GPI-ANCHORED PROTEIN P137.//4.00E-14//99aa//43%//Q14444  
 C-NT2RP2005722//Homo sapiens ZK1 mRNA for Kruppel-type zinc finger protein, complete cds.//0//2545bp//99%//AB011414  
 C-NT2RP2005723//HNRNP ARGININE N-METHYLTRANSFERASE (EC 2.1.1.-) (ODP1 PROTEIN).//3.00E-09//169aa//28%//P38074  
 25 C-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds.//0//1968bp//99%//AF068868  
 C-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//0//1966bp//99%//AF082516  
 C-NT2RP2005763//EUKARYOTIC INITIATION FACTOR 4A (EIF-4A).//1.70E-61//374aa//38%//P47943  
 30 C-NT2RP2005767//G.gallus PB1 gene.//5.00E-163//1158bp//81%//X90849  
 C-NT2RP2005773//Homo sapiens pyrroline 5-carboxylate reductase isoform (P5CR2) mRNA, complete cds.//2.70E-180//656bp//99%//AF151351  
 C-NT2RP2005775//NEUROLYSIN PRECURSOR (EC 3.4.24.16) (NEUROTENSIN ENDOPEPTIDASE) (MITO-CHONDRIAL OLIGOPEPTIDASE M) (MICROSOMAL ENDOPEPTIDASE) (MEP) (SOLUBLE ANGIOTENSIN-BINDING PROTEIN) (SABP).//2.10E-213//249aa//85%//Q02038  
 35 C-NT2RP2005776//POLY(A) POLYMERASE TYPE 2 (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYL-TRANSFERASE).//4.40E-55//358aa//42%//P51005  
 C-NT2RP2005784//Homo sapiens ubiquitin-conjugating enzyme variant Kua (UBE2V) mRNA, complete cds.//0//2191bp//92%//AF155120  
 40 C-NT2RP2005812//HYPOTHETICAL 39.3 KD PROTEIN IN GCN4-WBP1 INTERGENIC REGION.//2.30E-39//318aa//31%//P40004  
 C-NT2RP2005835//SHP1 PROTEIN.//1.80E-28//208aa//32%//P34223  
 C-NT2RP2005841//Homo sapiens mRNA for ALEX3, complete cds.//3.50E-52//1091bp//59%//AB039669  
 45 C-NT2RP2005933//NUCLEOPORIN NUP57 (NUCLEAR PORE PROTEIN NUP57).//5.00E-11//155aa//34%//P48837  
 C-NT2RP2005942//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANSFERASE).//1.50E-67//388aa//44%//P25500  
 C-NT2RP2006043//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//1.50E-13//185aa//38%//Q08170  
 50 C-NT2RP2006071//Homo sapiens adaptor protein APPL mRNA, complete cds.//5.80E-120//1257bp//64%//AF169797  
 C-NT2RP2006219//H.sapiens mRNA for DGCR6 protein.//1.10E-214//1026bp//97%//X96484  
 C-NT2RP2006238//Rattus norvegicus CTD-binding SR-like protein rA8 mRNA, complete cds.//0//1669bp//88%//U49055  
 55 C-NT2RP2006275//MICROTUBULE-ASSOCIATED PROTEIN 1B [CONTAINS: LIGHT CHAIN LC1].//2.00E-59//388aa//32%//P46821  
 C-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds.//2.80E-274//1236bp//99%//AF035262  
 C-NT2RP2006436//ANTERIOR-RESTRICTED HOMEOBOX PROTEIN (RATHKE POUCH HOMEO BOX).//

3.40E-07//50aa//50%//Q61658  
 C-NT2RP2006456//Homo sapiens leucine-rich glioma-inactivated protein precursor (LGI1) mRNA, complete cds.//  
 1.30E-37//484bp//65%//AF055636  
 C-NT2RP2006464//Homo sapiens mRNA for AND-1 protein.//0//2181bp//99%//AJ006266  
 5 C-NT2RP2006534//5'-AMP-ACTIVATED PROTEIN KINASE, CATALYTIC ALPHA-1 CHAIN (EC 2.7.1.-) (AMPK  
 ALPHA-1 CHAIN) (FRAGMENT).//3.20E-11//32aa//96%//Q13131  
 C-NT2RP2006565//Homo sapiens secretory carrier-associated membrane protein (SCAMP) mRNA, complete  
 cds.//3.10E-272//1220bp//95%//AF038966  
 C-NT2RP2006571//CYTOCHROME P450 2G1 (EC 1.14.14.1) (CYP1I1G1) (P450-NMB) (OLFACTIVE).//4.20E-  
 10 134//486aa//50%//P24461  
 C-NT2RP2006573//2',3'-CYCLIC NUCLEOTIDE 3'-PHOSPHODIESTERASE (EC 3.1.4.37) (CNP).//0.0000055//  
 169aa//25%//P09543  
 C-NT2RP2006598//Homo sapiens retinoid x receptor interacting protein mRNA, complete cds.//3.10E-295//  
 1193bp//99%//AF113538  
 15 C-NT2RP3000031//HISTONE DEACETYLASE HDA1.//1.10E-71//350aa//42%//P53973  
 C-NT2RP3000046//MITOCHONDRIAL GTPASE MSS1 PRECURSOR.//4.60E-78//421aa//37%//P32559  
 C-NT2RP3000047//NPL4 PROTEIN.//1.10E-85//526aa//36%//P33755  
 C-NT2RP3000050//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.20E-150//490aa//  
 53%//Q05481  
 20 C-NT2RP3000068//SON OF SEVENLESS PROTEIN HOMOLOG 1 (SOS-1) (MSOS-1 ).//2.20E-06//165aa//27%//  
 Q62245  
 C-NT2RP3000085//ACETYL-PROPYONYL-COENZYME A CARBOXYLASE ALPHA CHAIN [CONTAINS: BIOTIN  
 CARBOXYLASE (EC 6.3.4.14); BIOTIN CARBOXYL CARRIER PROTEIN (BCCP)].//1.90E-123//436aa//50%//  
 P46401  
 25 C-NT2RP3000109//P54 PROTEIN PRECURSOR.//0.0000065//358aa//22%//P13692  
 C-NT2RP3000207//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSI-  
 DASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//2.90E-11//721aa//23%//P08640  
 C-NT2RP3000233//RING CANAL PROTEIN (KELCH PROTEIN).//9.30E-84//453aa//42%//Q04652  
 30 C-NT2RP3000252//Homo sapiens GTP-binding protein NGB mRNA, complete cds.//0//2388bp//99%//AF120334  
 C-NT2RP3000299//Rattus norvegicus mRNA for Crk-associated substrate, pi 30, complete cds.//0//2730bp//82%//  
 D29766  
 C-NT2RP3000320//Homo sapiens partial mRNA for putative p621 protein which interacts with transcription factor  
 Sp1.//0//1544bp//100%//AJ242978  
 35 C-NT2RP3000333//Rattus norvegicus db83 mRNA, complete cds.//2.90E-191//1094bp//85%//AB006135  
 C-NT2RP3000341//Homo sapiens mitochondrial inner membrane preprotein translocase Tim17a mRNA, nuclear  
 gene encoding mitochondrial protein, complete cds.//1.50E-246//1124bp//99%//AF106622  
 C-NT2RP3000350//Homo sapiens GTP-binding protein NGB mRNA, complete cds.//0//2392bp//99%//AF120334  
 C-NT2RP3000359//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//2.00E-111//  
 226aa//92%//P08760  
 40 C-NT2RP3000361//Homo sapiens mRNA, complete cds, similar to yeast pre-mRNA splicing factors, Prp1/Zer1  
 and Prp6.//0//2072bp//98%//AB019219  
 C-NT2RP3000366//RAS-RELATED PROTEIN RAB-18.//2.10E-107//206aa//99%//P35293  
 C-NT2RP3000393//Rattus norvegicus DNA-binding protein PREB (Preb) mRNA, complete cds.//5.80E-266//  
 1373bp//86%//AF061817  
 45 C-NT2RP3000397//PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE (DEAH BOX PROTEIN 13).//  
 1.70E-139//679aa//41%//O43143  
 C-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cds.//0//2364bp//99%//AF071185  
 C-NT2RP3000439//HYPOTHETICAL 46.4 KD PROTEIN IN FFH-GRPE INTERGENIC REGION.//2.90E-15//  
 319aa//26%//P37908  
 50 C-NT2RP3000441//Homo sapiens squamous cell carcinoma antigen recognized by T cell (SART-2) mRNA, com-  
 plete cds.//3.40E-42//645bp//67%//AF098066  
 C-NT2RP3000512//Human HOX2G mRNA from the Hox2 locus.//0//1934bp//99%//X16667  
 C-NT2RP3000527//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//4.80E-28//536aa//27%//P28160  
 55 C-NT2RP3000531//POLIOVIRUS RECEPTOR PRECURSOR (CD155 ANTIGEN).//1.90E-12//192aa//30%//  
 P15151  
 C-NT2RP3000562//Homo sapiens putative RNA-binding protein Q99 mRNA, complete cds.//0//2165bp//99%//  
 AF093097  
 C-NT2RP3000578//HES1 PROTEIN.//1.30E-22//229aa//27%//P35843

C-NT2RP3000590//UVS-2 PROTEIN//1.30E-22//458aa//24%//P33288  
 C-NT2RP3000596//TRICHOHYALIN//2.50E-17//304aa//28%//Q07283  
 C-NT2RP3000603//NEUROGENIC DIFFERENTIATION FACTOR 1//3.70E-11//90aa//42%//Q13562  
 C-NT2RP3000605//Mus musculus mRNA for wizL, complete cds//0//2232bp//82%//AB012265  
 5 C-NT2RP3000624//Rattus norvegicus mRNA for SECIS binding protein 2 (sbp2 gene)//5.80E-234//1562bp//81%//  
 AJ251245  
 C-NT2RP3000632//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2)//3.00E-140//499aa//46%//  
 P51523  
 10 C-NT2RP3000739//ATROPHIN-1 (DENTATORUBRAL-PALLIDOLUYSIAN ATROPHY PROTEIN)//1.40E-24//  
 155aa//37%//Q10149  
 C-NT2RP3000742//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC  
 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III) (FRAGMENT)//4.10E-165//371aa//49%//  
 P10895  
 C-NT2RP3000753//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H)//  
 15 2.00E-10//565aa//24%//P12036  
 C-NT2RP3000759//ADP-RIBOSYLATION FACTOR//7.00E-28//176aa//34%//Q94650  
 C-NT2RP3000825//NEUROGENIC LOCUS NOTCH 3 PROTEIN//2.50E-36//417aa//31%//Q61982  
 C-NT2RP3000826//Homo sapiens mRNA for seven transmembrane protein TM7SF3, complete cds//0//2522bp//  
 99%//AB032470  
 20 C-NT2RP3000845//PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78 (EC 2.7.1.-)//8.30E-108//331aa//  
 50%//P27448  
 C-NT2RP3000868//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete  
 cds//6.90E-69//1611bp//61%//U53445  
 C-NT2RP3000869//Drosophila melanogaster AAA family protein Bor (bor) mRNA, complete cds//2.60E-138//  
 25 1673bp//67%//AF227209  
 C-NT2RP3000875//MEVALONATE KINASE (EC 2.7.1.36) (MK)//7.70E-87//175aa//98%//Q03426  
 C-NT2RP3000917//DHP1 PROTEIN//1.00E-193//428aa//55%//P40848  
 C-NT2RP3000919//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds//  
 30 2.70E-185//585bp//88%//AF015264  
 C-NT2RP3000968//40S RIBOSOMAL PROTEIN S15A//1.90E-46//73aa//98%//P39027  
 C-NT2RP3000994//MATERNAL EFFECT PROTEIN STAUFEN//0.00000006//78aa//48%//P25159  
 C-NT2RP3001055//Drosophila melanogaster separation anxiety protein (san) mRNA, complete cds//3.80E-38//  
 462bp//70%//AF225902  
 C-NT2RP3001057//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7)//9.00E-201//584aa//  
 35 54%//Q05481  
 C-NT2RP3001081//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds//7.10E-47//537bp//  
 74%//AF060219  
 C-NT2RP3001096//Rattus norvegicus leprecan (lepre1) mRNA, complete cds//1.70E-94//787bp//66%//  
 AF087433  
 40 C-NT2RP3001107//PEREGRIN (BR140 PROTEIN)//3.00E-44//260aa//40%//P55201  
 C-NT2RP3001111//Homo sapiens TRF-proximal protein mRNA, complete cds//1.50E-149//731bp//97%//  
 AF097725  
 C-NT2RP3001113//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1//2.90E-11//631aa//23%//  
 P25386  
 45 C-NT2RP3001120//ZINC FINGER, PROTEIN 136//7.80E-170//512aa//58%//P52737  
 C-NT2RP3001140//F-SPONDIN PRECURSOR//9.90E-238//419aa//96%//P35446  
 C-NT2RP3001150//TRANSCRIPTION TERMINATION FACTOR RHO//0.00000031//207aa//29%//P52154  
 C-NT2RP3001155//Homo sapiens mRNA for AND-1 protein//0//2732bp//99%//AJ006266  
 C-NT2RP3001176//HYPOTHETICAL 65.3 KD PROTEIN IN MAD1-SCY1 INTERGENIC REGION//1.70E-10//  
 50 196aa//27%//P53154  
 C-NT2RP3001216//CYLICIN I (MULTIPLE-BAND POLYPEPTIDE I) (FRAGMENT)//0.0000023//137aa//33%//  
 P35663  
 C-NT2RP3001221//GAMMA-BUTYROBETAINE,2-OXOGLUTARATE DIOXYGENASE (EC 1.14.11.1) (GAMMA-  
 BUTYROBETAINE HYDROXYLASE)//1.90E-31//353aa//30%//P80193  
 55 C-NT2RP3001239//MICROTUBULE-ASSOCIATED PROTEIN 1B (MAP1.2) (MAP1(X)) [CONTAINS: LIGHT  
 CHAIN LC1]//1.20E-166//395aa//51%//P14873  
 C-NT2RP3001253//NUF1 PROTEIN (SPINDLE POLY BODY SPACER PROTEIN SPC110)//1.70E-10//540aa//  
 23%//P32380

C-NT2RP3001268//Homo sapiens zinc finger protein ZNF228 (ZNF228) mRNA, complete cds./0//3606bp//99%//AF198358  
 C-NT2RP3001272//Mus musculus mRNA for macrophage actin-associated-tyrosine-phosphorylated protein./1.30E-99//669bp//83%//Y18101  
 5 C-NT2RP3001307//Gallus gallus RPE65 mRNA, complete cds./4.20E-29//530bp//63%//AB017594  
 C-NT2RP3001338//ZINC FINGER PROTEIN 81 (FRAGMENT).//2.40E-16//175aa//28%//P51508  
 C-NT2RP3001355//TRICARBOXYLATE TRANSPORT PROTEIN PRECURSOR (CITRATE TRANSPORT PROTEIN) (CTP) (TRICARBOXYLATE CARRIER PROTEIN).//3.60E-25//129aa//34%//P32089  
 C-NT2RP3001383//Mus musculus ARL-6 interacting protein-6 (Aip-6) mRNA, partial cds./3.40E-40//355bp//79%//  
 10 AF133913  
 C-NT2RP3001384//Homo sapiens mRNA for LA95 protein./0//1214bp//99%//AJ243467  
 C-NT2RP3001398//TRANSCRIPTIONAL REPRESSOR CTCF./1.30E-61//374aa//36%//P49711  
 C-NT2RP3001399//SSU72 PROTEIN./1.30E-16//84aa//52%//P53538  
 C-NT2RP3001407//SCY1 PROTEIN./0.00000033//143aa//25%//P53009  
 15 C-NT2RP3001426//DNAJ PROTEIN (FRAGMENT).//1.00E-16//77aa//46%//O33529  
 C-NT2RP3001427//WERNER SYNDROME HEUCASE HOMOLOG./2.70E-10//159aa//33%//O09053  
 C-NT2RP3001428//NUCLEOPROTEIN TPR./1.40E-128//152aa//99%//P 12270  
 C-NT2RP3001453//ANTIGEN PEPTIDE TRANSPORTER 2 (APT2) (HISTOCOMPATIBILITY ANTIGEN MODIFIER 2).//3.20E-90//157aa//59%//P36371  
 20 C-NT2RP3001457//Drosophila melanogaster Melted (melt) mRNA, partial cds./4.60E-20//792bp//59%//AF205831  
 C-NT2RP3001472//NONHISTONE CHROMOSOMAL PROTEIN 6A./9.10E-13//87aa//43%//P11632  
 C-NT2RP3001495//Human oxidoreductase (HHCMA56) mRNA, complete cds./0//1475bp//99%//U13395  
 25 C-NT2RP3001497//Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA, complete cds./0//2295bp//99%//AF064801  
 C-NT2RP3001527//Human Sp140 protein (Sp140) mRNA, complete cds./4.30E-290//793bp//93%//U63420  
 C-NT2RP3001529//SPOOB-ASSOCIATED GTP-BINDING PROTEIN./1.00E-61//345aa//42%//P20964  
 C-NT2RP3001538//HYPOTHETICAL 39.0 KD PROTEIN T28D9.3 IN CHROMOSOME II./9.10E-10//158aa//  
 30 31%//Q10022  
 C-NT2RP3001554//MICROTUBULE-ASSOCIATED PROTEIN 1B [CONTAINS: LIGHT CHAIN LC1].//1.40E-76//  
 388aa//32%//P46821  
 C-NT2RP3001580//Mus musculus strain C57BL/J germ cell-less protein (Gcl) mRNA, complete cds./0//1730bp//  
 85%//AF163665  
 C-NT2RP3001587//Human anthracycline-associated resistance ARX mRNA, complete cds./0//2617bp//99%//  
 35 U35832  
 C-NT2RP3001642//HYPOTHETICAL PROTEIN KIAA0210./6.80E-18//91aa//38%//Q92609  
 C-NT2RP3001646//WD-40 REPEAT PROTEIN MSI2./8.80E-09//132aa//31%//O22468  
 C-NT2RP3001671//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//0//1557bp//98%//AJ012449  
 C-NT2RP3001672//Homo sapiens Sex comb on midleg homolog 1 isoform 2 (SCMH1) mRNA, complete cds./0//  
 40 2836bp//99%//AF149046  
 C-NT2RP3001679//Homo sapiens rec mRNA, complete cds./0//2495bp//99%//AB023584  
 C-NT2RP3001688//Homo sapiens DNA binding protein p96PIF mRNA, complete cds./0//1869bp//99%//  
 AF173868  
 C-NT2RP3001690//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1./0.00000024//481aa//21%//  
 45 P25386  
 C-NT2RP3001708//TWISTED GASTRULATION PROTEIN PRECURSOR./3.40E-33//161aa//32%//P54356  
 C-NT2RP3001712//Homo sapiens HP1-BP74 protein mRNA, complete cds./0//1788bp//99%//AF113534  
 C-NT2RP3001723//Homo sapiens cell recognition molecule Caspr2 (CASPR2) mRNA, complete cds./1.40E-58//  
 1138bp//63%//AF193613  
 50 C-NT2RP3001724//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds./1.10E-  
 240//902bp//99%//AF054177  
 C-NT2RP3001727//Rattus norvegicus implantation-associated protein (IAG2) mRNA, partial cds./6.90E-132//  
 774bp//88%//AF008554  
 C-NT2RP3001730//SEPTIN 2 HOMOLOG (FRAGMENT).//7.10E-132//294aa//84%//Q14141  
 55 C-NT2RP3001739//HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME I./1.40E-15//190aa//32%//  
 Q09701  
 C-NT2RP3001792//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN M (HNRNP M).//1.80E-117//  
 462aa//55%//P52272

C-NT2RP3001799//MYOSIN HEAVY CHAIN, STRIATED MUSCLE./.1.60E-11//348aa//27%//P24733  
 C-NT2RP3001819//RING CANAL PROTEIN (KELCH PROTEIN).//7.40E-18//249aa//30%//Q04652  
 C-NT2RP3001854//Homo sapiens novel retinal pigment epithelial cell protein (NORPEG) mRNA, complete cds./.0//2742bp//99%//AF155135  
 5 C-NT2RP3001855//HOMEOBOX PROTEIN PKNOX1 (HOMEOBOX PROTEIN PREP-1).//8.10E-125//302aa//60%//P55347  
 C-NT2RP3001857//VEGETABLE INCOMPATIBILITY PROTEIN HET-E-1./.1.20E-14//242aa//24%//Q00808  
 C-NT2RP3001898//Homo sapiens mRNA for UDP-N-acetylglucosamine: alpha-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV, complete cds./.0//1587bp//100%//AB000624  
 10 C-NT2RP3001931//Rattus norvegicus clone C48 CDK5 activator-binding protein mRNA, complete cds./.4.30E-91//656bp//81%//AF177478  
 C-NT2RP3001938//SPORULATION-SPECIFIC PROTEIN 1 (EC 2.7.1.-).//1.30E-22//227aa//33%//P08458  
 C-NT2RP3001944//HYPOTHETICAL 47.6 KD PROTEIN C16C10.5 IN CHROMOSOME III./.3.10E-92//314aa//51%//Q09251  
 15 C-NT2RP3001969//TRICHOHYALIN./.2.70E-11//442aa//23%//P37709  
 C-NT2RP3002004//H.sapiens mRNA for FAST kinase./.1.50E-192//475bp//94%//X86779  
 C-NT2RP3002007//SAP1 PROTEIN./.1.1 OE-68//474aa//32%//P39955  
 C-NT2RP3002014//HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III./.5.30E-25//139aa//48%//Q09232  
 20 C-NT2RP3002045//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT).//1.00E-299//397aa//94%//P18484  
 C-NT2RP3002056//RETINOBLASTOMA BINDING PROTEIN 1 (RBBP-1).//2.00E-48//475aa//35%//P29374  
 C-NT2RP3002062//Homo sapiens BAG-family molecular chaperone regulator-5 mRNA, complete cds./.0//3764bp//99%//AF095195  
 25 C-NT2RP3002081//Xenopus laevis chromosome condensation protein XCAP-G mRNA, complete cds./.4.10E-233//1896bp//69%//AF111423  
 C-NT2RP3002108//DEC1 PROTEIN (MDM20 PROTEIN).//7.90E-09//181aa//22%//Q12387  
 C-NT2RP3002151//G1 TO S PHASE TRANSITION PROTEIN 1 HOMOLOG (GTP-BINDING PROTEIN GST1-HS).//2.80E-253//474aa//93%//P15170  
 30 C-NT2RP3002165//TRANSCRIPTIONAL REGULATOR PROTEIN HCNGP./.1.90E-151//223aa//91%//Q02614  
 C-NT2RP3002273//SCD6 PROTEIN./.1.30E-09//295aa//28%//P45978  
 C-NT2RP3002303//PROBABLE UNDECAPRENYL PYROPHOSPHATE SYNTHETASE (EC 2.5.1.31) (UPP SYNTHETASE) (DI-TRANS-POLY-CIS-DECAPRENYLCISTERNFERASE).//8.60E-49//243aa//43%//Q58767  
 35 C-NT2RP3002330//Homo sapiens eRFS mRNA, complete cds./.0//2443bp//99%//U87791  
 C-NT2RP3002351//Human mRNA for NAD-dependent methylene tetrahydrofolate dehydrogenase cyclohydrolase (EC 1.5.1.15).//4.20E-70//590bp//76%//X16396  
 C-NT2RP3002399//DNA REPLICATION LICENSING FACTOR MCM4 (CDC21 HOMOLOG) (P1-CDC21).//8.60E-79//416aa//34%//P33991  
 40 C-NT2RP3002501//THREONINE DEHYDRATASE CATABOLIC (EC 4.2.1.16) (THREONINE DEAMINASE).//3.70E-43//318aa//37%//P05792  
 C-NT2RP3002529//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS45./.8.90E-95//542aa//38%//P38932  
 C-NT2RP3002549//HYPOTHETICAL 26.6 KD PROTEIN T19C3.4 IN CHROMOSOME III./.5.80E-40//161aa//52%//Q10010  
 45 C-NT2RP3002602//PROBABLE PROTEIN DISULFIDE ISOMERASE ER-60 PRECURSOR (EC 5.3.4.1) (ERP60) (58 KD MICROSOMAL PROTEIN) (P58) (HIP-70) (Q-2).//2.90E-19//173aa//28%//P11598  
 C-NT2RP3002628//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//2.50E-26//90aa//42%//P38660  
 50 C-NT2RP3002631//Homo sapiens Ran binding protein 11 mRNA, complete cds./.0//1703bp//99%//AF111109  
 C-NT2RP3002650//Mus musculus growth suppressor 1L (Gros1) mRNA, complete cds./.0//2109bp//87%//AF165163  
 C-NT2RP3002663//Homo sapiens putative glycolipid transfer protein mRNA, complete cds./.8.10E-263//1243bp//97%//AF103731  
 55 C-NT2RP3002671//ELONGATION FACTOR 2 (EF-2).//2.50E-73//179aa//36%//P13060  
 C-NT2RP3002682//Homo sapiens CGI-145 protein mRNA, complete cds./.0//1596bp//98%//AF151903  
 C-NT2RP3002688//Mouse mRNA for kinesin-like protein (Kif1b), complete cds./.1.10E-93//1205bp//69%//D17577  
 C-NT2RP3002770//MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD116./.1.00E-07//70aa//

41%//P17564  
 C-NT2RP3002785//LETHAL(2)DENTICLELESS PROTEIN (DTL83 PROTEIN).//2.50E-55//187aa//39%//Q24371  
 C-NT2RP3002810//HISTIDINE-RICH PROTEIN KE4.//2.20E-10//260aa//26%//Q31125  
 C-NT2RP3002818//INSERTION ELEMENT IS2A HYPOTHETICAL 48.2 KD PROTEIN.//5.70E-226//303aa//97%//  
 5 P51026  
 C-NT2RP3002869//Mus musculus semaphorin VIa mRNA, complete cds.//2.50E-232//1282bp//85%//AF030430  
 C-NT2RP3002876//Drosophila melanogaster eyelid (eld) mRNA, complete cds.//1.30E-29//805bp//61%//  
 AF053091  
 C-NT2RP3002909//P53-BINDING PROTEIN 2 (53BP2) (BCL2-BINDING PROTEIN) (BBP).//1.50E-125//512aa//  
 10 47%//Q13625  
 C-NT2RP3002948//RING CANAL PROTEIN (KELCH PROTEIN).//2.00E-111//551aa//42%//Q04652  
 C-NT2RP3002953//Homo sapiens protocadherin beta 5 (PCDH-beta5) mRNA, complete cds.//0//2388bp//99%//  
 AF152498  
 C-NT2RP3002969//Homo sapiens mRNA for Acyl-CoA synthetase 3, complete cds.//0//2722bp//99%//D89053  
 15 C-NT2RP3002972//Halocynthia roretzi mRNA for HrPET-1, complete cds.//3.90E-52//899bp//64%//AB029333  
 C-NT2RP3002988//Homo sapiens IκB kinase-β (IKK-β) mRNA, complete cds.//1.80E-292//1325bp//99%//  
 AF080158  
 C-NT2RP3003032//Homo sapiens okadaic acid-inducible and cAMP-regulated phosphoprotein 19 (ARPP-19) mR-  
 NA, complete cds.//0//2656bp//99%//AF084555  
 20 C-NT2RP3003059//Rattus norvegicus potassium channel regulator 1 mRNA, complete cds.//3.80E-152//1007bp//  
 82%//U78090  
 C-NT2RP3003061//ANKYRIN.//1.40E-20//200aa//37%//Q02357  
 C-NT2RP3003071//NEUROGENIC PROTEIN BIG BRAIN.//1.10E-05//258aa//24%//P23645  
 C-NT2RP3003078//Rattus norvegicus mRNA for ischemia related factor NYW-1, complete cds.//2.60E-112//  
 25 633bp//88%//AB027149  
 C-NT2RP3003101//Mouse mRNA for tetracycline transporter-like protein, complete cds.//3.60E-83//807bp//72%//  
 D88315  
 C-NT2RP3003133//Homo sapiens ZK1 mRNA for Kruppel-type zinc finger protein, complete cds.//0//1998bp//  
 91%//AB011414  
 30 C-NT2RP3003138//Homo sapiens kinesin superfamily motor KIF4 mRNA, complete cds.//0//2159bp//98%//  
 AF071592  
 C-NT2RP3003145//Mus musculus metallocarboxypeptidase CPX-1 mRNA, complete cds.//0//2251bp//81%//  
 AF077738  
 C-NT2RP3003185//TROPOMYOSIN1, FUSION PROTEIN 33.//2.80E-06//402aa//23%//P49455  
 35 C-NT2RP3003193//ZINC FINGER PROTEIN 135.//7.30E-98//269aa//62%//P52742  
 C-NT2RP3003197//HYPOTHETICAL 33.8 KD PROTEIN C5H10.01 IN CHROMOSOME 1.//5.70E-09//169aa//  
 31%//Q09674  
 C-NT2RP3003203//Rattus norvegicus golgi stacking protein homolog GRASP55 mRNA, complete cds.//2.00E-  
 210//1851 bp//76%//AF110267  
 40 C-NT2RP3003212//Rattus norvegicus lamina associated polypeptide 1C (LAP1C) mRNA, complete cds.//4.30E-  
 187//1750bp//75%//U20286  
 C-NT2RP3003230//Homo sapiens mRNA for hCRNN4, complete cds.//0//2350bp//99%//AB030656  
 C-NT2RP3003242//Homo sapiens stanniocalcin-related protein mRNA, complete cds.//0//2366bp//99%//  
 AF098462  
 45 C-NT2RP3003251//52 KD RO PROTEIN (SJOGEN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)).//  
 4.20E-86//366aa//48%//P19474  
 C-NT2RP3003282//Homo sapiens dynamin (DNM) mRNA, complete cds.//0//2596bp//98%//L36983  
 C-NT2RP3003290//Mus musculus mRNA for Ndr1 related protein Ndr3, complete cds.//1.5e-310//1468bp//82%//  
 AB033922  
 50 C-NT2RP3003301//MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR (EC 3.4.21.-).//1.10E-170//  
 585aa//54%//O64948  
 C-NT2RP3003313//Homo sapiens thyroid hormone receptor-associated protein complex component TRAP80 mR-  
 NA, complete cds.//0//2476bp//99%//AF117657  
 C-NT2RP3003327//52 KD RO PROTEIN (SJOGEN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))  
 55 (RO52).//1.30E-35//178aa//44%//Q62191  
 C-NT2RP3003353//HYPOTHETICAL 26.2 KD PROTEIN IN GDI1-COX15 INTERGENIC REGION.//2.80E-07//  
 161aa//28%//P40084  
 C-NT2RP3003385//Mus musculus SKD3 mRNA, complete cds.//0//2133bp//85%//U09874

C-NT2RP3003409//Human DHHC-domain-containing cysteine-rich protein mRNA, complete cds./.9.20E-45//  
782bp//65%//U90653

C-NT2RP3003411//Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds./.6.30E-270//  
743bp//90%//AF071317

5 C-NT2RP3003490//Homo sapiens mRNA for putative phospholipase, complete cds./.4.50E-81//649bp//67%//  
AB019435

C-NT2RP3003491//Drosophila melanogaster Pelle associated protein Pellino (Pli) mRNA, complete cds./.5.60E-  
36//842bp//62%//AF091624

10 C-NT2RP3003500//SCY1 PROTEIN./.9.20E-27//601aa//23%//P53009

C-NT2RP3003555//HYPOTHETICAL 32.6 KD PROTEIN IN MET30-PIG2 INTERGENIC REGION./.4.50E-30//  
191aa//40%//P40529

C-NT2RP3003589//Homo sapiens ras-related GTP-binding protein mRNA, complete cds./.0//3131bp//94%//  
AF106681

15 C-NT2RP3003659//HES1 PROTEIN./.5.90E-22//229aa//27%//P35843

C-NT2RP3003665//Homo sapiens mRNA for beta-ureidopropionase, complete cds./.0//1690bp//99%//AB013885

C-NT2RP3003672//T-CELL SURFACE GLYCOPROTEIN E2 PRECURSOR (E2 ANTIGEN) (CD99) (MIC2 PRO-  
TEIN) (.12E7).//2.20E-13//146aa//42%//P14209

C-NT2RP3003701//F-SPONDIN PRECURSOR./.1.80E-17//324aa//26%//P35446

C-NT2RP3003716//SLIT PROTEIN PRECURSOR./.6.60E-10//150aa//34%//P24014

20 C-NT2RP3003726//Homo sapiens spermatogenesis associated PD1 mRNA, complete cds./.0//2568bp//99%//  
U28164

C-NT2RP3003799//Rattus norvegicus Srg1 (Sytr1) mRNA, complete cds./.9.00E-238//1529bp//84%//U71294

C-NT2RP3003800//Rattus norvegicus tyrosine protein kinase pp60-c-src mRNA, complete cds./.1.90E-163//  
924bp//89%//AF130457

25 C-NT2RP3003809//SAV PROTEIN./.1.10E-131//576aa//41%//Q07590

C-NT2RP3003825//PHOSPHATIDYLCHOLINE TRANSFER PROTEIN (PC-TP).//9.60E-19//174aa//31%//  
P02720

C-NT2RP3003831//Homo sapiens ENDOGL-1 (alias ENGL-a) mRNA for endonuclease G-like protein-1, complete  
cds./.2.2e-316//1436bp//99%//AB020523

30 C-NT2RP3003846//Homo sapiens mRNA for putative phospholipase, complete cds./.4.80E-277//1255bp//99%//  
AB019435

C-NT2RP3003876//Rattus norvegicus Rabin3 mRNA, complete cds./.4.50E-147//874bp//87%//U19181

C-NT2RP3003914//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-)  
(DUGT).//2.20E-20//76aa//64%//Q09332

35 C-NT2RP3003918//Homo sapiens VAMP-associated protein B (VAP-B) mRNA, complete cds./.0//2191bp//99%//  
AF086628

C-NT2RP3004013//M.musculus Spnr mRNA for RNA binding protein./.6.50E-240//1215bp//94%//X84692

C-NT2RP3004016//TRANSCRIPTION INTERMEDIARY FACTOR 1-BETA (NUCLEAR COREPRESSOR KAP-1)  
(KRAB-ASSOCIATED PROTEIN 1).//1.50E-17//226aa//26%//Q13263

40 C-NT2RP3004078//H.sapiens HRFX2 mRNA./.0//1806bp//99%//X76091

C-NT2RP3004125//Mus musculus zinc finger protein splice variant FIZ1-B (Fiz1) mRNA, complete cds./.4.60E-  
229//1560bp//78%//AF126747

C-NT2RP3004148//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSI-  
DASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//7.90E-05//271aa//22%//P08640

45 C-NT2RP3004155//Homo sapiens COQ7 protein mRNA, complete cds./.1.10E-179//823bp//100%//AF098948

C-NT2RP3004189//VEGETABLE INCOMPATIBILITY PROTEIN HET-E-1./.1.30E-14//242aa//24%//Q00808

C-NT2RP3004206//CROOKED NECK PROTEIN./.1.40E-220//567aa//67%//P17886

C-NT2RP3004207//Homo sapiens mRNA for type I transmembrane receptor (psk-1 gene).//.0//2445bp//100%//  
AJ245820

50 C-NT2RP3004209//Homo sapiens ubiquitin processing protease (Ubp-M) mRNA, complete cds./.0//2320bp//  
99%//AF126736

C-NT2RP3004242//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FA-  
CIOGENITAL DYSPLASIA PROTEIN HOMOLOG).//4.70E-13//118aa//33%//P52734

C-NT2RP3004258//Homo sapiens ZIS1 mRNA, complete cds./.0//1861bp//99%//AF065391

55 C-NT2RP3004262//Homo sapiens heat shock protein hsp40-3 mRNA, complete cds./.2.40E-248//1126bp//100%//  
AF088982

C-NT2RP3004282//Homo sapiens torsinA (DYT1) mRNA, complete cds./.5.10E-24//597bp//61%//AF007871

C-NT2RP3004348//R.norvegicus mRNA for cytosolic resiniferatoxin-binding protein./.1.10E-185//1130bp//82%//

X67877  
 C-NT2RP3004378//Drosophila melanogaster separation anxiety protein (san) mRNA, complete cds./.3.90E-38//  
 462bp//70%//AF225902  
 5 C-NT2RP3004424//Homo sapiens mRNA for stromal antigen 3 (STAG3 gene).//1.00E-66//364bp//93%//AJ007798  
 C-NT2RP3004428//CHROMODOMAIN HELICASE-DNA-BINDING PROTEIN 4 (CHD-4) (MI-2 AUTOANTIGEN  
 218 KD PROTEIN) (MI2-BETA).//5.20E-09//212aa//25%//Q14839  
 C-NT2RP3004472//GERM CELL-LESS PROTEIN.//1.60E-61//170aa//40%//Q01820  
 C-NT2RP3004480//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS35.//3.30E-113//466aa//  
 10 42%//P34110  
 C-NT2RP3004490//Homo sapiens mRNA for Musashi, complete cds./.4.00E-303//1385bp//99%//AB012851  
 C-NT2RP3004498//Mus musculus ROSA 26 transcription AS ROSA26AS mRNA, complete cds./.2.00E-249//  
 1777bp//80%//U83176  
 C-NT2RP3004504//M.musculus mRNA for CPEB protein.//1.90E-295//893bp//92%//Y08260  
 C-NT2RP3004507//MOB1 PROTEIN (MPS1 BINDER 1).//3.70E-37//190aa//39%//P40484  
 15 C-NT2RP3004534//Mouse oncogene (ect2) mRNA, complete cds./.0//2075bp//87%//L11316  
 C-NT2RP3004544//THYROID RECEPTOR INTERACTING PROTEIN 10 (TRIP10) (FRAGMENT).//1.00E-22//  
 1.3aa//53%//Q15642  
 C-NT2RP3004566//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.20E-95//434aa//43%//  
 P51523  
 20 C-NT2RP3004569//ANKYRIN, BRAIN VARIANT 1 (ANKYRIN B) (ANKYRIN, NONERYTHROID).//3.80E-08//  
 150aa//28%//Q01484  
 C-NT2RP3004572//Homo sapiens TATA binding protein associated factor (TAFII150) mRNA, complete cds./.0//  
 1853bp//99%//AF040701  
 C-NT2RP3004578//MYOSIN HEAVY CHAIN, CLONE 203 (FRAGMENT).//5.50E-12//396aa//23%//P39922  
 25 C-NT2RP3004594//Homo sapiens mRNA for AND-1 protein./.0//1807bp//99%//AJ006266  
 C-NT2RP3004617//ZINC-BINDING PROTEIN A33.//7.20E-75//464aa//35%//Q02084  
 C-NT2RP3004618//Homo sapiens putative RNA-binding protein Q99 mRNA, complete cds./.0//3972bp//98%//  
 AF093097  
 C-NT2RP3004669//ETHANOLAMINE KINASE (EC 2.7.1.82) (EASILY SHOCKED PROTEIN).//1.70E-72//254aa//  
 30 45%//P54352  
 C-NT2RP3004670//Homo sapiens GN6ST mRNA for N-acetylglucosamine-6-O-sulfotransferase (GlcNAc6ST),  
 complete cds./.0//2393bp//99%//AB014679  
 C-NT2RP400008//CHLORINE CHANNEL PROTEIN P64.//2.60E-98//239aa//64%//P35526  
 C-NT2RP400051//SYNAPTONEMAL COMPLEX PROTEIN SC65.//4.90E-51//335aa//37%//Q64375  
 35 C-NT2RP400078//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//0//2160bp//99%//AJ012449  
 C-NT2RP4000109//Homo sapiens mRNA for MEGF5, partial cds./.0//2161bp//99%//AB011538  
 C-NT2RP4000111//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100  
 KD SUBUNIT).//0//728aa//99%//Q10568  
 C-NT2RP4000129//Xenopus laevis F-box protein 28 (Fbx28) mRNA, partial cds./.1.40E-28//296bp//75%//  
 40 AF176667  
 C-NT2RP4000147//Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, com-  
 plete cds./.4.30E-188//1543bp//78%//U35776  
 C-NT2RP4000210//PAIRED AMPHIPATHIC HELIX PROTEIN.//1.00E-71//396aa//36%//P22579  
 C-NT2RP4000212//ATRIAL GLAND-SPECIFIC ANTIGEN PRECURSOR (AGSA).//5.90E-15//104aa//40%//  
 45 P15287  
 C-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP).//0//1932bp//99%//AJ006470  
 C-NT2RP4000246//NPC DERIVED PROLINE RICH PROTEIN 1 (NDPP-1).//2.70E-84//208aa//76%//Q03173  
 C-NT2RP4000259//GLUTATHIONE PEROXIDASE.2 (EC 1.11.1.9).//5.50E-29//153aa//43%//O23968  
 C-NT2RP4000290//HYPOTHETICAL 116.5 KD PROTEIN C20G8.09C IN CHROMOSOME I.//3.50E-297//  
 50 1024aa//55%//P87115  
 C-NT2RP4000312//ADENYLATECYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE).//1.50E-26//237aa//28%//Q01631  
 C-NT2RP4000323//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN).//3.00E-07//101aa//  
 32%//P26372  
 55 C-NT2RP4000367//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds./.0//  
 4782bp//99%//AF044195  
 C-NT2RP4000370//MITOCHONDRIAL PEPTIDE CHAIN RELEASE FACTOR 1 PRECURSOR (MRF-1).//2.60E-  
 77//262aa//54%//O75570

C-NT2RP4000376//Homo sapiens mRNA for phospholipase A2 activating protein./.0//2412bp//99%//AJ238243  
 C-NT2RP4000398//ZINC FINGER PROTEIN 140./.2.90E-110//435aa//50%//P52738  
 C-NT2RP4000415//Drosophila melanogaster fumble (fumble) mRNA, complete cds./.6.20E-19//902bp//57%//  
 AF221546

5 C-NT2RP4000417//MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE (EC 3.2.1.113)(MAN(9)-AL-  
 PHA-MANNOSIDASE)(FRAGMENT).//2.60E-51//438aa//33%//P45701  
 C-NT2RP4000449//Homo sapiens sirtuin type 1 (SIRT1) mRNA, complete cds./.0//3143bp//99%//AF083106  
 C-NT2RP4000455//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0./.3.00E-07//175aa//27%//P09309  
 C-NT2RP4000457//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 15 (EC 3.1.2.15) (UBIQUITIN THI-  
 10 OLESTERASE 15) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 15)(DEUBIQUITINATING ENZYME 15).//  
 2.50E-37//291aa//38%//P50101  
 C-NT2RP4000481//ATP-DEPENDENT RNA HELICASE DOB1 (MRNA TRANSPORT REGULATOR MTR4).//  
 1.90E-67//721aa//29%//Q09475  
 C-NT2RP4000498//MOB1 PROTEIN (MPS1 BINDER 1).//8.80E-50//214aa//50%//P40484  
 15 C-NT2RP4000518//ATP-DEPENDENT RNA HELICASE ROK1./.1.50E-106//495aa//45%//P45818  
 C-NT2RP4000524//Mus musculus Sec8 mRNA, complete cds./.0//3131bp//87%//AF022962  
 C-NT2RP4000528//NPL4 PROTEIN./.9.80E-86//515aa//37%//P33755  
 C-NT2RP4000556//SUR4 PROTEIN (SRE1 PROTEIN).//7.40E-14//233aa//31%//P40319  
 C-NT2RP4000614//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds./.2.90E-188//863bp//  
 20 99%//AF067730  
 C-NT2RP4000648//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0./.3.70E-07//175aa//27%//P09309  
 C-NT2RP4000657//SPORE COAT POLYSACCHARIDE BIOSYNTHESIS PROTEIN SPSE./.1.10E-32//350aa//  
 30 30%//P39625  
 C-NT2RP4000713//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X./.1.10E-13//295aa//  
 27%//Q11073  
 C-NT2RP4000724//RETROVIRUS-RELATED ENV POLYPROTEIN./.3.20E-191//199aa//78%//P10267  
 C-NT2RP4000737//Mus musculus F-box protein FBL10 mRNA, partial cds./.4.60E-250//1462bp//84%//AF176524  
 C-NT2RP4000781//HYPOTHETICAL 27.7 KD PROTEIN IN CPT1-SPC98 INTERGENIC REGION./.0.00000032//67aa//31%//P53915  
 35 C-NT2RP4000817//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN1,4-ALPHA- GLUCOSI-  
 DASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//9.80E-11//503aa//23%//P08640  
 C-NT2RP4000837//Homo sapiens mRNA for zinc finger protein SALL1./.4.30E-94//810bp//65%//Y18265  
 C-NT2RP4000839//VEGETABLE INCOMPATIBILITY PROTEIN HET-E-1./.8.50E-21//271aa//28%//Q00808  
 C-NT2RP4000855//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE)(ARGININE AMI-  
 40 NOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV) (AP-B).//5.70E-82//324aa//48%//O09175  
 C-NT2RP4000865//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//4.10E-85//174aa//55%//P16415  
 C-NT2RP4000878//MYELOID UPREGULATED PROTEIN./.6.20E-91//173aa//87%//O35682  
 C-NT2RP4000879//UBIQUITIN-ACTIVATING ENZYME EI (A1S9 PROTEIN).//9.60E-96//513aa//42%//P22314  
 C-NT2RP4000907//Mouse NLRR-1 mRNA for leucine-rich-repeat protein, complete cds./.0//2127bp//86%//  
 45 D45913  
 C-NT2RP4000925//FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN).//2.60E-26//  
 227aa//36%//Q06828  
 C-NT2RP4000927//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THI-  
 50 OLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING EN-  
 ZYME 1).//1.50E-76//346aa//43%//Q61068  
 C-NT2RP4000928//Homo sapiens mRNA for CDS2 protein./.0//2487bp//99%//Y16521  
 C-NT2RP4000929//PUTATIVE ATP-DEPENDENT RNA HEUCASE MJ1505./.1.40E-07//185aa//25%//Q58900  
 C-NT2RP4000973//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//1.40E-26//  
 55 90aa//42%//P38660  
 C-NT2RP4000979//Homo sapiens putative HIV-1 infection related protein mRNA, partial cds./.2.30E-81//389bp//  
 100%//AF094583  
 C-NT2RP4000989//UNC-47 PROTEIN./.8.20E-06//173aa//25%//P34579  
 C-NT2RP4000997//DNA-DIRECTED RNA POLYMERASE 1135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA  
 POLYMERASE I SUBUNIT 2) (RPA135).//0//838aa//87%//P70700  
 C-NT2RP4001004//VACUOLAR PROTEIN 8./.3.70E-16//401aa//26%//P39968  
 C-NT2RP4001010//Rattus norvegicus PSD-95/SAP90-associated protein-4 mRNA, complete cds./.3.50E-257//  
 1377bp//91%//U67140  
 C-NT2RP4001029//Homo sapiens transcription factor LBP-1b (LBP-1) mRNA, complete cds./.0//2002bp//98%//

AF198487  
 C-NT2RP4001041//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE-TRNA LIGASE)//1.50E-92//443aa//44%//Q09996  
 5 C-NT2RP4001064//SYNAPTONEMAL COMPLEX PROTEIN SC65.//6.70E-51//335aa//37%//Q64375  
 C-NT2RP4001079//CALCIUM-TRANSPORTING ATPASE 1 (EC 3.6.1.38) (GOLGI CA<sup>2+</sup>-ATPASE).//1.30E-123//563aa//46%//P13586  
 C-NT2RP4001080//Homo sapiens mRNA for Rod1, complete cds.//0//1439bp//99%//AB023967  
 C-NT2RP4001086//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H).//2.30E-07//474aa//22%//P12036  
 10 C-NT2RP4001095//DOUBLE-STRANDED RNA-SPECIFIC EDITASE 1 (EC 3.5.--) (DSRNA ADENOSINE DEAMINASE) (RNA EDITING ENZYME 1).//2.60E-17//121aa//36%//P51400  
 C-NT2RP4001117//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//1.90E-115//224aa//100%//P38378  
 C-NT2RP4001122/mPD PROTEIN.//1.40E-65//253aa7/41%//O15736  
 15 C-NT2RP4001126/TRICHOHYALIN.//2.90E-18//380aa//26%//Q07283  
 C-NT2RP4001143//SUCCINYL-DIAMINOPIMELATE DESUCCINYLASE (EC 3.5.1.18) (SDAP).//2.10E-07//93aa//33%//P44514  
 C-NT2RP4001148//SOF1 PROTEIN.//1.30E-104//236aa//52%//P33750  
 C-NT2RP4001149//Homo sapiens cleft lip and palate transmembrane protein 1 (CLPTM1) mRNA, complete cds.//20  
 20 4.40E-187//731bp//100%//AF037339  
 C-NT2RP4001150//NG-CAM RELATED CELL ADHESION MOLECULE PRECURSOR (NR-CAM) (BRAVO).//3.40E-29//385aa//29%//P35331  
 C-NT2RP4001174//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT).//4.70E-29//227aa//35%//P52178  
 25 C-NT2RP4001206//Drosophila melanogaster strawberry notch (sno) mRNA, complete cds.//4.40E-104//1460bp//65%//U95760  
 C-NT2RP4001207//Homo sapiens Ran binding protein 11 mRNA, complete cds.//0//2940bp//99%//AF111109  
 C-NT2RP4001213//ZINC FINGER PROTEIN 184 (FRAGMENT).//5.70E-141//511aa//43%//Q99676  
 30 C-NT2RP4001219//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//6.20E-27//90aa//42%//P38660  
 C-NT2RP4001228//RING CANAL PROTEIN (KELCH PROTEIN).//1.80E-103//508aa//43%//Q04652  
 C-NT2RP4001256//Homo sapiens mRNA for gamma tubulin ring complex protein (76p gene).//0//2006bp//100%//AJ249677  
 35 C-NT2RP4001260//Homo sapiens F-box protein Fbx21 (FBX21) mRNA, complete cds.//0//1866bp//100%//AF174601  
 C-NT2RP4001274//Human transporter protein (g17) mRNA, complete cds.//4.40E-58//1196bp//61%//U49082  
 C-NT2RP4001276/TRICHOHYALIN.//7.90E-09//126aa//32%//Q07283  
 C-NT2RP4001313//MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT TOM40 (MOM38 PROTEIN) (TRANSLOCASE OF OUTER MEMBRANE 40 KD SUBUNIT).//5.90E-17//296aa//29%//P24391  
 40 C-NT2RP4001315//Bos taurus mRNA for Rab5 GDP/GTP exchange factor, Rabex5.//8.50E-213//1129bp//92%//AJ001119  
 C-NT2RP4001336//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN.//0.000016//186aa//29%//O24076  
 C-NT2RP4001339//Homo sapiens mRNA for AMMERC1 protein.//9.20E-160//736bp//99%//AJ007014  
 45 C-NT2RP4001345//Homo sapiens mRNA for LCAT-like lysophospholipase (LLPL), complete cds.//2.7e-310//1400bp//100%//AB017494  
 C-NT2RP4001351//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds.//1.40E-58//2425bp//59%//U53445  
 C-NT2RP4001372//IRREGULAR CHIASM C-ROUGHEST PROTEIN PRECURSOR (IRREC PROTEIN).//1.60E-19//222aa//30%//Q08180  
 C-NT2RP4001375//NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE 1).//9.20E-17//146aa//35%//P18160  
 C-NT2RP4001379//HYPOTHETICAL 49.1 KD PROTEIN C11D3.06 IN CHROMOSOME 1.//2.00E-53//436aa//30%//Q10085  
 55 C-NT2RP4001389//KESIPROTEIN.//1.70E-31//342aa//34%//P35844  
 C-NT2RP4001407//TRICHOHYALIN.//1.90E-05//298aa//21%//P22793  
 C-NT2RP4001414//SEPTIN 2 HOMOLOG (FRAGMENT).//7.70E-190//422aa//82%//Q14141  
 C-NT2RP4001433//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.20E-138//419aa//54%//Q99676

C-NT2RP4001474//Xenopus laevis putative Zic3 binding protein mRNA, complete cds/J/2.70E-66//738bp//71%//AF129131

C-NT2RP4001483//2-OXOGLUTARATE DEHYDROGENASE EI COMPONENT PRECURSOR (EC 1.2.4.2) (AL-PHA-KETOGLUTARATE DEHYDROGENASE).//0//962aa/78%//Q02218

5 C-NT2RP4001498//ANKYRIN REPEAT-CONTAINING PROTEIN AKR1././/1.00E-27//374aa//29%//P39010

C-NT2RP4001529//Homo sapiens transcription factor LBP-1b (LBP-1) mRNA, complete cds././/0//2002bp//98%//AF198487

C-NT2RP4001547//HYPOTHETICAL 45.0 KD PROTEIN IN NOT1/CDC39-HMR INTERGENIC REGION././/5.70E-54//242aa/38%//P25656

10 C-NT2RP4001551//Homo sapiens chromatin-specific transcription elongation factor FACT 140 kDa subunit mRNA, complete cds././/0//3202bp//99%//AF152961

C-NT2RP4001555//PUTATIVE ENDONUCLEASE VIII (EC 3.2.-.-).//4.70E-09//216aa//24%//P96902

C-NT2RP4001567//ARMADILLO SEGMENT POLARITY PROTEIN././/5.40E-07//213aa//26%//Q02453

C-NT2RP4001568//ZINC FINGER PROTEIN GCS1././/1.80E-10//109aa/36%//P35197

15 C-NT2RP4001574//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP).//0//874aa//96%//P53620

C-NT2RP4001575//Rattus norvegicus mRNA for ARE1 protein././/0//1087bp//87%//AJ223830

C-NT2RP4001592//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE-TRNA LIGASE) (ILERS).//1.70E-141//373aa/747%//P73505

20 C-NT2RP4001634//CENTROMERIC PROTEIN E (CENP-E PROTEIN).//2.80E-14//652aa//22%//Q02224

C-NT2RP4001638//DNA REPAIR/TRANSCRIPTION PROTEIN MET18/MMS19././/5.10E-46//234aa/32%//P40469

C-NT2RP4001644//MYOSIN UGHT CHAIN KINASE (EC 2.7.1.117) (MLCK).//6.40E-19//111aa/45%//P25323

25 C-NT2RP4001656//VACUOLAR BIOGENESIS PROTEIN END1 (PEP5 PROTEIN).//1.10E-45//310aa//27%//P12868

C-NT2RP4001696//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT).//4.00E-10//243aa//25%//Q10568

C-NT2RP4001725//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT././/3.00E-10//128aa/32%//Q10282

30 C-NT2RP4001730//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT).//6.40E-170//1168aa/33%//Q09332

C-NT2RP4001753//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3.90E-236//665aa//58%//P51523

C-NT2RP4001760//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FA-CIOGENITAL DYSPLASIA PROTEIN).//4.10E-16//263aa//27%//P98174

35 C-NT2RP4001790//Homo sapiens zinc finger protein ZFP-95 (ZFP95) mRNA, alternatively spliced, complete cds././/0//3053bp//99%//AF170025

C-NT2RP4001822//PLATELET-ENDOTHELIAL TETRASPAAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN).//1.20E-30//241aa/30%//O35566

40 C-NT2RP4001823//MICROFIBRIL-ASSOCIATED GLYCOPROTEIN 4././/1.10E-19//77aa//54%//P55083

C-NT2RP4001838//Homo sapiens CoREST protein (COREST) mRNA, complete cds././/6.30E-99//555bp//73%//AF155595

C-NT2RP4001849//SH3-BINDING PROTEIN 3BP-1././/1.40E-85//489aa//43%//P55194

C-NT2RP4001861//HTUCHOHYALIN././/1.00E-35//307aa//34%//P37709

45 C-NT2RP4001896//VEGETATILE INCOMPATIBILITY PROTEIN HET-E-1././/1.40E-08//345aa/725%//Q00808

C-NT2RP4001927//MICROTUBULE-ASSOCIATED PROTEIN YTM1././/1.30E-38//258aa//32%//Q12024

C-NT2RP4001938//TRANSCRIPTIONAL REPRESSOR CTCF././/9.80E-60//303aa/38%//P49711

C-NT2RP4001946//PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (EC 2.1.1.77) (PROTEIN- BETA-ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L-ISO-50 ASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE).//1.50E-13//211aa//28%//Q43209

C-NT2RP4001950//GLUTAMIC ACID-RICH PROTEIN PRECURSOR././/1.20E-13//356aa//27%//P13816

C-NT2RP4001966//Mus musculus ODZ3 (Odz3) mRNA, partial cds././/0//3203bp//87%//AF195418

C-NT2RP4001975//Homo sapiens golgi membrane protein GP73 mRNA, complete cds././/0//3024bp//99%//AF236056

55 C-NT2RP4002018//RING CANAL PROTEIN (KELCH PROTEIN).//6.90E-24//370aa//27%//Q04652

C-NT2RP4002047//GTP-BINDING PROTEIN LEPA././/1.50E-168//601aa//52%//O67618

C-NT2RP4002058//PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE (DEAH BOX PROTEIN 13).//1.00E-137//679aa//40%//O43143

C-NT2RP4002078//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//3.00E-150//722aa//39%//Q05481  
 5 C-NT2RP4002081//TRANSCRIPTION INITIATION FACTOR IIA ALPHA AND BETA CHAINS (TFIILA P35 AND PI 9 SUBUNITS) (TFIILA-42) (TFIILAL).//6.70E-06//250aa//31%//P52655  
 C-NT2RP4002408//PROTEIN KINASE CEK1 (EC 2.7.1.-).//1.50E-63//159aa//53%//P38938  
 C-NT2RP4002791//NUCLEOPROTEIN TPR.//6.50E-05//659aa//23%//P12270  
 C-NT2RP5003461//RLR1 PROTEIN.//9.70E-22//177aa//27%//P53552  
 C-NT2RP5003477//VEGETATILE INCOMPATIBILITY PROTEIN HET-E-1.//5.50E-15//280aa//27%//Q00808  
 10 C-NT2RP5003500//Mus musculus mRNA for heparan sulfate 6-sulfotransferase 2, complete cds.//1.30E-237//820bp//87%//AB024565  
 C-NT2RP5003506//Homo sapiens putative G protein-coupled receptor (RAIG1) mRNA, complete cds.//0//2289bp//99%//AF095448  
 C-NT2RP5003522//NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR).//3.30E-23//219aa//40%//P37116  
 15 C-OVARC1000001//Homo sapiens mRNA for actin binding protein ABP620, complete cds.//7.00E-217//683bp//99%//AB029290  
 C-OVARC1000006//HISTONE H2A.1.//1.10E-55//117aa//99%//P02262  
 C-OVARC1000013//APOPTOTIC PROTEASE ACTIVATING FACTOR 1 (APAF-1).//4.20E-06//102aa//32%//O14727  
 20 C-OVARC1000014//Homo sapiens GLE1 (GLE1) mRNA, complete cds.//J/2.60E-295//1393bp//97%//AF058922  
 C-OVARC1000060//EXTRACELLULAR RIBONUCLEASE LE PRECURSOR (EC 3.1.27.1) (RNASE LE).//3.20E-07//60aa//45%//P80022  
 C-OVARC1000071//Homo sapiens NTF2-related export protein NXT1 (NXT1) mRNA, complete cds.//1.50E-47//727bp//67%//AF156957  
 25 C-OVARC1000085//Human mRNA for proteasome subunit HC5.//1.00E-151//699bp//100%//D00761  
 C-OVARC1000087//HISTONE MACRO-H2A.1.//1.60E-12//174aa//26%//Q02874  
 C-OVARC1000091//HOST CELL FACTOR C1 (HCF) (VP16 ACCESSORY PROTEIN) (HFC1) (VCAF) (CFF).//8.40E-14//259aa//30%//P51610  
 C-OVARC1000106//TROPOMYOSIN 1, FUSION PROTEIN 33.//0.000032//165aa//27%//P49455  
 30 C-OVARC1000139//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THIOESTERASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME 4) (UBIQUITOUS NUCLEAR PROTEIN HOMOLOG).//2.70E-12//120aa//32%//Q13107  
 C-OVARC1000151//Homo sapiens partial mRNA for putative protein p38 interacting with transcription factor Spl.//2.50E-95//461bp//98%//AJ242975  
 35 C-OVARC1000209//Oryza sativa submergence induced protein 2A mRNA, complete cds.//1.80E-32//511bp//65%//AF068332  
 C-OVARC1000241//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN) (MEMBER OF PAS PROTEIN 1) (MOP1) (HIF1 ALPHA).//8.20E-120//351aa//54%//Q16665  
 C-OVARC1000288//VACUOLAR AMINOPEPTIDASE I PRECURSOR (EC 3.4.11.22) (POLYPEPTIDASE)(LEUCINE AMINOPEPTIDASE IV) (LAIV) (AMINOPEPTIDASE III)(AMINOPEPTIDASE YSCI).//5.40E-53//384aa//30%//P14904  
 C-OVARC1000304//PROTEIN MOV-10.//1.10E-249//519aa//87%//P23249  
 C-OVARC1000309//THREONINE SYNTHASE (EC 4.2.99.2).//2.70E-40//154aa//38%//P29363  
 40 C-OVARC1000326//Rattus norvegicus lamina-associated polypeptide 1C (LAP1C) mRNA, complete cds.//9.20E-148//787bp//76%//U19614  
 C-OVARC1000335//HYPOTHETICAL 39.3 KD PROTEIN IN GCN4-WBP1 INTERGENIC REGION.//5.90E-14//200aa//27%//P40004  
 C-OVARC1000437//TENSIN.//7.90E-181//340aa//84%//Q04205  
 C-OVARC1000465//PROTEIN TRANSPORT PROTEIN SEC7.//1.20E-25//227aa//25%//P11075  
 45 C-OVARC1000473//DUAL SPECIFICITY PROTEIN PHOSPHATASE 3 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE VHR).//3.10E-10//125aa//35%//P51452  
 C-OVARC1000479//Rattus norvegicus mRNA for TIP120, complete cds.//0//1872bp//89%//D87671  
 C-OVARC1000520//Homo sapiens supervillin mRNA, complete cds.//2.20E-157//892bp//91%//AF051850  
 C-OVARC1000556//RIBOSOMAL PROTEIN S6 KINASE II ALPHA 2 (EC 2.7.1.-) (S6KII-ALPHA 2) (P90-RSK 2)  
 50 (RIBOSOMAL S6 KINASE 3) (RSK3) (PP90RSK3).//3.30E-67//132aa//95%//Q15349  
 C-OVARC1000564//Homo sapiens sorting nexin 5 (SNX5) mRNA, complete cds.//1.0e-310//1440bp//98%//AF121855  
 C-OVARC1000649//Human squamous cell carcinoma of esophagus mRNA for GRB-7 SH2 domain protein, com-

plete cds.//0//1812bp//98%//D43772  
 C-OVARC1000679//Homo sapiens myosin-IXa mRNA, complete cds.//0//808bp//99%//AF117888  
 C-OVARC1000682//PROCESSING ALPHA-1,2-MANNOSIDASE (EC 3.2.1.-) (ALPHA-1,2-MANNOSIDASE 1B).//  
 1.10E-209//293aa//95%//P39098  
 5 C-OVARC1000722//Homo sapiens chromosome 1q21-1q23 beta-1,4-galactosyltransferase mRNA, complete  
 cds.//0//759bp//98%//AF038661  
 C-OVARC1000746//MATERNAL EFFECT PROTEIN STAUFEN.//0.000000017//78aa//48%//P25159  
 C-OVARC1000751//PROBABLE PROTEIN PHOSPHATASE 2C T23F11.1 (EC 3.1.3.16) (PP2C).//5.60E-11//  
 74aa//37%//P49596  
 10 C-OVARC1000771//RAS-RELATED PROTEIN RAB-2.//1.10E-46//121aa//79%//P08886  
 C-OVARC1000800//MITOCHONDRIAL STRESS-70 PROTEIN PRECURSOR (75 KD GLUCOSE REGULATED  
 PROTEIN) (GRP 75).//3.90E-46//78aa//98%//O35501  
 C-OVARC1000834//Homo sapiens mRNA for atopy related autoantigen CALC.//2.80E-258//1183bp//99%//Y17711  
 C-OVARC1000846//NUCLEOLIN (PROTEIN C23).//0.0000097//109aa//30%//P08199  
 15 C-OVARC1000850//Homo sapiens PB39 mRNA, complete cds.//0//2095bp//99%//AF045584  
 C-OVARC1000862//M.musculus mRNA for FT1.//5.90E-226//1498bp//81%//Z67963  
 C-OVARC1000876//MOB1 PROTEIN (MPS1 BINDER 1).//2.20E-50//206aa//52%//P40484  
 C-OVARC1000885//OXIDOREDUCTASE UCPA (EC 1.---).//1.30E-32//170aa//34%//P37440  
 20 C-OVARC1000915//Homo sapiens histone deacetylase 5 mRNA, complete cds.//1.60E-121//591bp//97%//  
 AF132608  
 C-OVARC1000936//COAT PROTEIN GP37 (ENV PROTEIN GP37).//0.0000054//135aa//28%//P03398  
 C-OVARC1000937//S-PHASE ENTRY CYCLIN 6.//4.90E-10//61aabp//49%//P32943  
 C-OVARC1000945//Rattus norvegicus mRNA for atypical PKC specific binding protein, complete cds.//0//1961bp//  
 82%//AB005549  
 25 C-OVARC1000959//HYPOTHETICAL PROTEIN MJ0933.//1.20E-17//127aa//33%//Q58343  
 C-OVARC1000999//ANKYRIN HOMOLOG PRECURSOR.//4.10E-11//189aa//32%//Q06527  
 C-OVARC1001034//Mus musculus Fn54 mRNA, partial cds.//1.50E-178//1113bp//86%//AF001533  
 C-OVARC1001038//Homo sapiens mRNA for Ariadne-2 protein.//0//1172bp//97%//AJ130978  
 30 C-OVARC1001051//EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN  
 EPS15) (AF-1P PROTEIN).//1.10E-08//216aa//23%//P42566  
 C-OVARC1001055//PRE-B CELL ENHANCING FACTOR PRECURSORS.//1.90E-35//76aa//98%//P43490  
 C-OVARC1001065//Homo sapiens CGI-12 protein mRNA, complete cds.//1.00E-215//1027bp//98%//AF132946  
 C-OVARC1001068//Homo sapiens Era GTPase A protein (HERA-A) mRNA, partial cds.//0//1819bp//99%//  
 AF082657  
 35 C-OVARC1001092//Homo sapiens mRNA for JM5 protein, complete CDS (clone IMAGE 53337,  
 LLNLc110F1857Q7 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin)).//2.00E-214//769bp//97%//AJ005897  
 C-OVARC1001107//Homo sapiens protein methyltransferase (JBP1) mRNA, complete cds.//6.10E-276//594bp//  
 98%//AF167572  
 C-OVARC1001113//Homo sapiens diaphanous 1 (HDIA1) mRNA, complete cds.//5.1e-310//1588bp//93%//  
 40 AF051782  
 C-OVARC1001154//Homo sapiens clone 24720 epithelin 1 and 2 mRNA, complete cds.//2.30E-296//1561bp//  
 93%//AF055008  
 C-OVARC1001171//Homo sapiens translation initiation factor 3 47 kDa subunit mRNA, complete cds.//5.70E-151//  
 436bp//92%//U94855  
 45 C-OVARC1001180//UBIQUITIN-LIKE PROTEIN DSK2.//1.10E-11//221aa//25%//P48510  
 C-OVARC1001200//Mus musculus mRNA for HS1 binding protein 3.//5.80E-88//658bp//80%//AJ132192  
 C-OVARC1001232//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF  
 100 KD SUBUNIT).//5.10E-22//83aa//37%//Q10568  
 C-OVARC1001244//H.sapiens mRNA for Drosophila female sterile homeotic (FSH) homologue.//0//1467bp//99%//  
 50 X62083  
 C-OVARC1001271//NUCLEOLAR TRANSCRIPTION FACTOR 1 (UPSTREAM BINDING FACTOR 1) (UBF-1).//  
 0.0000014//224aa//26%//P25976  
 C-OVARC1001306//N-MYC PROTO-ONCOGENE PROTEIN.//0.00000073//247aa//27%//P18444  
 C-OVARC1001342//40S RIBOSOMAL PROTEIN S8.//1.40E-110//207aa//99%//P09058  
 55 C-OVARC1001372//Homo sapiens liprin-alpha4 mRNA, partial cds.//2.00E-252//1146bp//99%//AF034801  
 C-OVARC1001381//Homo sapiens mRNA for candidate tumor suppressor involved in B-CLL.//6.00E-148//683bp//  
 99%//AJ224819  
 C-OVARC1001417//Homo sapiens thyroid hormone receptor-associated protein complex component TRAP170

mRNA, complete cds.//0//1715bp//99%//AF135802  
 C-OVARC1001419//Homo sapiens GOK (STIM1) mRNA, complete cds.//4.90E-48//586bp//69%//U52426  
 C-OVARC1001436//ENL PROTEIN.//0.00000009/81aa//39%//Q03111  
 C-OVARC1001476//Mus musculus YGR163w mRNA homologue, complete cds.//1.80E-187//510bp//89%//  
 5 AB017616  
 C-OVARC1001496//Homo sapiens C-terminal binding protein 2 mRNA, complete cds.//0//1876bp//98%//  
 AF016507  
 C-OVARC1001506//POLYCYSTIN PRECURSOR (AUTOSOMAL DOMINANT POLYCYSTIC KIDNEY DISEASE  
 PROTEIN 1).//0//777aa//91%//P98161  
 10 C-OVARC1001555//NGG1-INTERACTING FACTOR 3.//4.40E-19//130aa//40%//P53081  
 C-OVARC1001577//Homo sapiens SRp46 splicing factor transcribed retropseudogene.//0//1167bp//100%//  
 AF031165  
 C-OVARC1001610//Homo sapiens choline/ethanolaminephosphotransferase (CEPT1) mRNA, complete cds.//0//  
 15 1870bp//99%//AF068302  
 C-OVARC1001703//Mus musculus ARL-6 interacting protein-2 (Aip-2) mRNA, complete cds.//3.50E-16//399bp//  
 61%//AF133670  
 C-OVARC1001711//CORNIFIN B (SMALL PROLINE-RICH PROTEIN 1B) (SPR1B) (SPR1 B).//2.80E-10//106aa//  
 38%//Q62267  
 20 C-OVARC1001713//ENDOZEPINE-RELATED PROTEIN PRECURSOR (MEMBRANE-ASSOCIATED DI-  
 AZEPAM BINDING INHIBITOR) (MA-DBI).//4.40E-40//195aa//41%//P07106  
 C-OVARC1001726//APICAL-LIKE PROTEIN (APXL PROTEIN).//4.30E-16//116aa//43%//Q13796  
 C-OVARC1001731//TROPOMYOSIN ALPHA CHAIN, FIBROBLAST ISOFORM F2.//4.00E-122//282aa//85%//  
 P08942  
 25 C-OVARC1001762//N-TERMINAL ACETYLTRANSFERASE 1 (EC 2.3.1.88) (AMINO-TERMINAL, ALPHA- AMI-  
 NO, ACETYLTRANSFERASE 1).//6.40E-85//514aa//34%//P12945  
 C-OVARC1001766//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds.//  
 0//963bp//99%//U97670  
 C-OVARC1001809//Mus musculus sphingosine kinase (SPHK1a) mRNA, partial cds.//2.70E-190//1624bp//76%//  
 AF068748  
 30 C-OVARC1001942//N-TERMINAL ACETYLTRANSFERASE 1 (EC 2.3.1.88) (AMINO-TERMINAL, ALPHA- AMI-  
 NO, ACETYLTRANSFERASE 1).//3.10E-81//497aa//35%//P12945  
 C-OVARC1001943//Mus musculus DEBT-91 mRNA, complete cds.//0//2035bp//87%//AF143859  
 C-OVARC1001987//Homo sapiens prolactin regulatory element-binding protein (PREB) mRNA, complete cds.//  
 0//1083bp//99%//AF203687  
 35 C-OVARC1002050//Homo sapiens mRNA for actin binding protein ABP620, complete cds.//0//1019bp//99%//  
 AB029290  
 C-OVARC1002112//HISTONE MACRO-H2A.1.//3.00E-174//371aa//90%//Q02874  
 C-OVARC1002127//SODIUM-INDEPENDENT ORGANIC ANION TRANSPORTER 2 (BRAIN DIGOXIN CARRI-  
 40 ER PROTEIN) (BRAIN-SPECIFIC ORGANIC ANION TRANSPORTER) (OATP-B1).//5.40E-52//306aa//35%//  
 O35913  
 C-OVARC100213 8/SAP1 PROTEIN.//7.60E-60//128aa//59%//P39955  
 C-OVARC1002156//Danio rerio uridine kinase mRNA, complete cds.//6.00E-16//262bp//64%//AF195851  
 C-OVARC1002165//3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 2 (EC 1.3.99.5) (STEROID 5-ALPHA-  
 REDUCTASE 2) (SR TYPE 2).//7.60E-08//114aa//37%//P31213  
 45 C-OVARC1002182//BETA-TRCP (BETA-TRANSDUCIN REPEAT-CONTAINING PROTEIN) (BTRCP).//1.70E-  
 09//207aa//30%//Q91854  
 C-PLACE100004//Homo sapiens IDN3-B mRNA, complete cds.//0//2365bp//99%//AB019602  
 C-PLACE100007//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE R10E11.3 (EC 3.1.2.15)  
 50 (UBIQUITIN THIOESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING EN-  
 ZYME).//1.60E-81//212aa//70%//P34547  
 C-PLACE1000040//TRANSFORMING PROTEIN P21/K-RAS 2B.//1.40E-17//185aa//32%//P08643  
 C-PLACE1000061//Human ribosomal protein L37a mRNA sequence.//7.90E-54//190bp//94%//L22154  
 C-PLACE1000066//SSU72 PROTEIN.//1.10E-39//206aa//43%//P53538  
 C-PLACE1000081//Human SEC7 homolog Tic (TIC) mRNA, complete cds.//0//2077bp//99%//U63127  
 55 C-PLACE1000133//TRANSCRIPTION FACTOR BTF3 (RNA POLYMERASE B TRANSCRIPTION FACTOR 3).//  
 1.80E-62//158aa//81%//P20290  
 C-PLACE1000142//3-HYDROXYBUTYRYL-COA DEHYDRATASE (EC 4.2.1.55) (CROTONASE).//2.80E-29//  
 134aa//43%//P52046

C-PLACE1000184//Homo sapiens estrogen-related receptor gamma mRNA, complete cds./.1.30E-305//1417bp//98%//AF058291  
 C-PLACE1000185//Homo sapiens mRNA for N-Acetylglucosamine kinase./.4.90E-258//1183bp//99%//AJ242910  
 C-PLACE1000213//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//4.50E-05//197aa//26%//P08640  
 C-PLACE1000383//Homo sapiens mRNA for MTMR1 protein./.0//753bp//99%//AJ224979  
 C-PLACE1000401//POLIOVIRUS RECEPTOR PRECURSOR (CD155 ANTIGEN).//2.70E-30//352aa//31%//P15151  
 C-PLACE1000406//PTB-ASSOCIATED SPLICING FACTOR (PSF).//1.20E-132//334aa//72%//P23246  
 10 C-PLACE1000420//7,8-DIHYDRO-8-OXOGUANINE TRIPHOSPHATASE (EC 3.1.6.-) (8-OXO-DGTPASE).//2.80E-06//134aa//29%//P53368  
 C-PLACE1000492//Rat vacuolar protein sorting homolog r-vps33b mRNA, complete cds./.0//2041bp//87%//U35245  
 15 C-PLACE1000547//Homo sapiens GDP-mannose pyrophosphorylase B (GMPPB) mRNA, complete cds./.3.70E-241//1124bp//98%//AF135421  
 C-PLACE1000583//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//1.60E-47//207aa//46%//P51522  
 C-PLACE1000588//INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1 (GUANINE NUCLEOTIDE-BINDING PROTEIN 1).//1.60E-270//437aa//86%//P32455  
 20 C-PLACE1000596//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//.0//1540bp//99%//AJ012449  
 C-PLACE1000610//MSN5 PROTEIN./.0.0000026//136aa//26%//P52918  
 C-PLACE1000611//Rattus norvegicus neural membrane protein 35 mRNA, complete cds./.2.00E-55//779bp//67%//AF044201  
 C-PLACE1000636//MALE STERILITY PROTEIN 2./.1.20E-39//261aa//27%//Q08891  
 25 C-PLACE1000653//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds./.0//1992bp//99%//AF180371  
 C-PLACE1000656//Homo sapiens mRNA for JM4 protein, complete CDS (clone IMAGE 546750 and LLNL C110F1857Q7 (RZPD Berlin)).//2.10E-277//1260bp//99%//AJ005896  
 C-PLACE1000706//Homo sapiens transcriptional intermediary factor 1 gamma mRNA, complete cds./.0//1366bp//99%//AF119043  
 30 C-PLACE1000755//Homo sapiens mRNA for Helicase-MOI, complete cds./.4.60E-250//1189bp//97%//AB028449  
 C-PLACE1000769//Homo sapiens CGI-18 protein mRNA, complete cds./.0//1985bp//98%//AF132952  
 C-PLACE1000786//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FA-CIOGENITAL DYSPLASIA PROTEIN HOMOLOG).//7.10E-09//59aa//47%//P52734  
 35 C-PLACE1000793//NEUROGENIC PROTEIN BIG BRAIN./.1.70E-07//251aa//24%//P23645  
 C-PLACE1000863//PUTATIVE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN YHR148W./.2.50E-49//181aa//54%//P32899  
 C-PLACE1000909//ANKYRIN REPEAT-CONTAINING PROTEIN AKR1./.2.60E-19//404aa//26%//P39010  
 C-PLACE1000977//BETA-CHIMAERIN (BETA-CHIMERIN).//4.40E-22//129aa//35%//Q03070  
 40 C-PLACE1000979//ZINC FINGER PROTEIN 135./.2.50E-153//326aa//64%//P52742  
 C-PLACE1000987//Rattus norvegicus late gestation lung 2 protein (Lgl2) mRNA, complete cds./.5.90E-278//1476bp//92%//AF110195  
 C-PLACE1001036//Homo sapiens mRNA for alpha integrin binding protein 63, partial./.0//1988bp//99%//AJ131721  
 C-PLACE1001054//Homo sapiens mRNA for RuvB-like DNA helicase TIP49b, complete cds./.4.00E-300//45  
 1355bp//100%//AB024301  
 C-PLACE1001062//Homo sapiens mRNA for lysine-ketoglutarate reductase/saccharopine dehydrogenase, partial CDS./.1.60E-207//742bp//99%//AJ007714  
 C-PLACE1001092//Homo sapiens sorting nexin 4 mRNA, complete cds./.0//1500bp//99%//AF065485  
 C-PLACE1001104//MYOSIN HEAVY CHAIN, NON-MUSCLE (ZIPPER PROTEIN) (MYOSIN II).//6.80E-18//529aa//23%//Q99323  
 C-PLACE1001118//ZINC FINGER PROTEIN 135./.5.40E-147//443aa//57%//P52742  
 C-PLACE1001171//MYOTUBULARIN./.7.10E-84//198aa//73%//Q13496  
 C-PLACE1001238//Mouse mRNA for RNA polymerase I associated factor (PAF53), complete cds./.2.00E-202//1333bp//80%//D14336  
 55 C-PLACE1001257//RING CANAL PROTEIN (KELCH PROTEIN).//4.30E-54//257aa//46%//Q04652  
 C-PLACE1001294//Mus musculus XY body protein (Xybp) mRNA, complete cds./.6.20E-223//1092bp//78%//AF120207  
 C-PLACE1001304//Homo sapiens C2H2 (Kruppel-type) zinc finger protein mRNA, complete cds./.0//2145bp//

99%//AF159567  
C-PLACE1001377//Homo sapiens ADAM10 (ADAM10) mRNA, complete cds.//5.90E-228//827bp//99%//  
AF009615  
C-PLACE1001383//ZINC-FINGER PROTEIN UBI-D4 (APOPTOSIS RESPONSE ZINC FINGER PROTEIN REQ-  
UIEM).//3.00E-33//138aa//42%//Q61103  
C-PLACE1001387//EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8.//2.30E-61//  
132aa//46%//Q12929  
C-PLACE1001517//Homo sapiens gene for glycosylphosphatidylinositol anchor attachment 1 (GPAA1), complete  
cds.//4.60E-112//392bp//87%//AB002137  
C-PLACE1001602//CCR4-ASSOCIATED FACTOR 1 (CAF1).//5.70E-130//244aa//99%//Q60809  
C-PLACE1001632//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.40E-118//429aa//48%//  
P51523  
C-PLACE1001672//PROBABLE AMINOTRANSFERASE T01B11.2 (EC 2.6.1.-).//4.30E-66//174aa//45%//P91408  
C-PLACE1001692//S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN (EC 3.1.2.14)  
(THIOESTERASE II).//4.00E-81//263aa//56%//P08635  
C-PLACE1001739//PUTATIVE ATP-DEPENDENT RNA HEUCASE PL10.//3.50E-75//439aa//41%//P16381  
C-PLACE1001748//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//0//2602bp//99%//AF061243  
C-PLACE1001771//Homo sapiens mRNA for transient receptor potential protein TRP6.//0//2900bp//99%//  
AJ006276  
C-PLACE1001781//PROBABLE PHOSPHOMANNOMUTASE (EC 5.4.2.8) (PMM).//5.40E-63//427aa//35%//  
Q57290  
C-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds.//  
0//1995bp//99%//AF058953  
C-PLACE1001845//Mus musculus cyclin ania-6a mRNA, complete cds.//3.30E-31//925bp//62%//AF159159  
C-PLACE1001869//L-RIBULOKINASE (EC 2.7.1.16).//2.00E-27//270aa//31%//P94524  
C-PLACE1001920//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds.//0//1729bp//99%//AF099935  
C-PLACE1001983//HYPOTHETICAL 46.4 KD PROTEIN IN FFH-GRPE INTERGENIC REGION.//7.50E-16//  
319aa//26%//P37908  
C-PLACE1001989//PUTATIVE AMIDASE (EC 3.5.1.4).//1.40E-78//496aa//37%//Q49091  
C-PLACE1002046//UGATIN (FRAGMENT).//1.70E-240//560aa//80%//Q61211  
C-PLACE1002073//ADENYLATE CYCLASE (EC 4.6.1.1)(ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE).//5.30E-07//188aa//29%//P49606  
C-PLACE1002090//SIGNAL RECOGNITION PARTICLE 72 KD PROTEIN (SRP72).//6.50E-58//112aa//100%//  
O76094  
C-PLACE1002140//Rattus norvegicus apelin mRNA, complete cds.//1.40E-43//425bp//74%//AF179679  
C-PLACE1002171//TRANSCRIPTION REGULATORY PROTEIN SWI3 (SWI/SNF COMPLEX COMPONENT  
SWI3) (TRANSCRIPTION FACTOR TYE2).//0.00005//179aa//23%//P32591  
C-PLACE1002395//Mus musculus mRNA for UBE-1c1, UBE-1c2, UBE-1c3, complete cds.//7.90E-100//966bp//  
75%//AB030505  
C-PLACE1002433//CHROMOSOME ASSEMBLY PROTEIN XCAP-E.//5.10E-05//278aa//24%//P50533  
C-PLACE1002437//ATP-BINDING CASSETTE TRANSPORTER 1.//4.50E-76//180aa//83%//P41233  
C-PLACE1002438//ZINC FINGER PROTEIN 151 (MIZ-1 PROTEIN).//4.20E-06//133aa//29%//Q13105  
C-PLACE1002450//Human zinc finger protein mRNA, complete cds.//0//2565bp//99%//U69274  
C-PLACE1002474//Mus musculus matrilin-2 precursor mRNA, complete cds.//0//2092bp//84%//U69262  
C-PLACE1002493//Homo sapiens signal transducing adaptor molecule 2A (STAM2) mRNA, complete cds.//1.70E-  
113//545bp//98%//AF042273  
C-PLACE1002500//Rattus norvegicus zinc transporter (ZnT-2) mRNA, complete cds.//2.90E-58//465bp//80%//  
U50927  
C-PLACE1002532//HOMEobox PROTEIN DLX-5.//1.20E-152//289aa//96%//P70396  
C-PLACE1002571//ACTIN-LIKE PROTEIN 13E.//5.00E-99//386aa//48%//P45890  
C-PLACE1002583//GLUTAMATE RECEPTOR, IONOTROPIC KAINATE 2 PRECURSOR (GLUTAMATE RECEP-  
TOR 6) (GLUR-6) (GLUTAMATE RECEPTOR BETA-2) (GLUR BETA-2) (FRAGMENT).//5.60E-34//76aa//98%//  
P39087  
C-PLACE1002591//CORONIN-UKE PROTEIN P57.//4.40E-70//208aa//66%//P31146  
C-PLACE1002598//OLIGORIBONUCLEASE (EC 3.1.--).//5.50E-17//76aa//56%//P45340  
C-PLACE1002655//ADSEVERIN (SCINDERIN) (SC).//2.50E-278//543aa//92%//Q28046  
C-PLACE1002665//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.//0//2462bp//89%//  
AF079765

C-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds.//0//1750bp//99%//AF068180  
 C-PLACE1002714//MYOSIN HEAVY CHAIN, NON-MUSCLE (ZIPPER PROTEIN) (MYOSIN II).//9.40E-13//500aa//21%//Q99323  
 5 C-PLACE1002722//PROBABLE G PROTEIN-COUPLED RECEPTOR KIAA0001.//9.00E-45//305aa//33%//Q15391  
 C-PLACE1002775//PEREGRIN (BR140 PROTEIN).//3.80E-13//272aa//28%//P55201  
 C-PLACE1002782//Rattus norvegicus zinc transporter (ZnT-2) mRNA, complete cds.//3.80E-43//385bp//77%//U50927  
 10 C-PLACE1002816//HISTONE DEACETYLASE HDA1.//2.20E-48//217aa//46%//P53973  
 C-PLACE1002834//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//5.50E-203//396aa//86%//P51522  
 C-PLACE1002908//Homo sapiens XGalT-1 mRNA for galactosyltransferase I, complete cds.//0//1654bp//99%//AB028600  
 15 C-PLACE1002991//PUTATIVE AMIDASE (EC 3.5.1.4).//1.40E-78//496aa//37%//Q49091  
 C-PLACE1003030//Homo sapiens snRNA activating protein complex 190kD subunit (SNAP190) mRNA, complete cds.//8.50E-44//225bp//100%//AF032387  
 C-PLACE1003045//POLYCYSTIN 2 (AUTOSOMAL DOMINANT POLYCYSTIC KIDNEY DISEASE TYPE II PRO-  
 20 TEIN) (POLYCYSTWIN) (R48321).//1.70E-05//150aa//24%//Q13563  
 C-PLACE1003100//HEP27 PROTEIN (PROTEIN D).//2.60E-79//253aa//60%//Q13268  
 C-PLACE1003174//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN  
 LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42).//3.80E-37//143aa//51%//P42743  
 C-PLACE1003176//Homo sapiens clone pHN1868 tyrosyl-DNA phosphodiesterase protein (TDP1) mRNA, partial  
 25 cds.//1.70E-148//687bp//99%//AF182003  
 C-PLACE1003190//SOF1 PROTEIN.//1.90E-110//325aa//48%//P33750  
 C-PLACE1003238//PROBABLE G PROTEIN-COUPLED RECEPTOR KIAA0001.//4.90E-76//309aa//47%//Q15391  
 C-PLACE1003258//EARLY EMBRYOGENESIS ZYG-11 PROTEIN.//7.90E-22//70aa//47%//P21541  
 C-PLACE1003302//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//6.90E-206//396aa//86%//  
 30 P51522  
 C-PLACE10033537//Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3) mRNA, complete  
 cds.//0//2435bp//99%//U92715  
 C-PLACE1003366//Homo sapiens otoferlin (OTOF) mRNA, complete cds.//1.40E-78//542bp//67%//AF107403  
 C-PLACE1003394//Homo sapiens RAB14 protein (RAB14) mRNA, complete cds.//2.60E-139//648bp//99%//  
 35 AF152463  
 C-PLACE1003420//PUTATIVE MITOCHONDRIAL CARRIER YIL006W.//1.30E-40//278aa//36%//P40556  
 C-PLACE1003493//ENDOTHELIAL CELL MULTIMERIN PRECURSOR.//1.70E-23//322aa//26%//Q13201  
 C-PLACE1003519//H.sapiens hnRNP-E2 mRNA.//5.10E-218//905bp//99%//X78136  
 C-PLACE1003521//HYPOTHETICAL HELICASE C28H8.3 IN CHROMOSOME III.//0.0000011//101aa//32%//  
 40 Q09475  
 C-PLACE1003537//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHE-  
 ROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPO-  
 NENT).//7.70E-68//404aa//33%//P32802  
 C-PLACE1003596//OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG.//2.60E-93//270aa//66%//  
 45 P46975  
 C-PLACE1003602//Homo sapiens mRNA expressed in placenta.//5.90E-278//1275bp//99%//D83200  
 C-PLACE1003605//HAP5 TRANSCRIPTIONAL ACTIVATOR.//0.0000023//82aa//35%//Q02516  
 C-PLACE1003611//Homo sapiens anaphase-promoting complex subunit 4 (APC4) mRNA, complete cds.//6.20E-  
 50 169//683bp//99%//AF191338  
 C-PLACE1003625//ARMADILLO SEGMENT POLARITY PROTEIN.//3.20E-10//380aa//25%//P18824  
 C-PLACE1003669//TRICHOHYALIN.//5.60E-09//219aa//30%//P22793  
 C-PLACE1003704//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR  
 SRP75).//8.00E-19//209aa//34%//Q08170  
 C-PLACE1003709//Homo sapiens mitotic checkpoint kinase Bub1 (BUB1) mRNA complete cds.//6.20E-282//  
 55 1316bp//98%//AF053305  
 C-PLACE1003738//ZINC FINGER PROTEIN 135.//9.60E-118//350aa//46%//P52742  
 C-PLACE1003760//Homo sapiens tetraspanin TM4-A mRNA, complete cds.//5.20E-289//1313bp//97%//  
 AF133423

C-PLACE1003885//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANSFERASE).//3.70E-222//651aa//66%//P25500  
 5 C-PLACE1003888//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III) (FRAGMENT).//6.70E-113//501aa//46%//P10895  
 C-PLACE1003903//CTP SYNTHASE (EC 6.3.4.2) (UTP--AMMONIA LIGASE) (CTP SYNTHETASE).//1.40E-243//584aa//74%//P17812  
 10 C-PLACE1003915//PROBABLE ARGINYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.19) (ARGININE-TRNA UGASE) (ARGRS).//2.40E-108//581aa//40%//Q05506  
 C-PLACE1003923//Homo sapiens p53 regulated PA26-T2 nuclear protein (PA26) mRNA, complete cds.//0//1670bp//99%//AF033120  
 15 C-PLACE1003968//5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK GAMMA-1 CHAIN).//2.40E-124//326aa//73%//P80385  
 C-PLACE1004104//Rattus norvegicus rsec5 mRNA, complete cds.//0//2384bp//86%//AF032666  
 C-PLACE1004128//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT 4 (TRANSDUCIN BETA CHAIN 4).//6.10E-181//340aa//96%//P29387  
 20 C-PLACE1004149//Rattus norvegicus GERp95 mRNA, complete cds.//3.30E-41//452bp//65%//AF195534  
 C-PLACE1004183//Homo sapiens for TOM1-like protein.//0//1279bp//97%//AJ010071  
 C-PLACE1004197//BUTYROPHILIN PRECURSOR (BT).//4.50E-10//208aa//27%//Q62556  
 25 C-PLACE1004203//Homo sapiens GPI-anchored membrane protein CDw108 precursor, mRNA, complete cds.//0//1882bp//99%//AF069493  
 C-PLACE1004256//Mus musculus short coiled coil protein SCOCO (Scoc) mRNA, complete cds.//2.00E-93//960bp//76%//AF115778  
 C-PLACE1004258//Homo sapiens vanilloid receptor-like protein 1 (VRL-1) mRNA//0//1144bp//98%//AF129112  
 30 25 C-PLACE1004270//TRANSMEMBRANE PROTEASE, SERINE 2 (EC 3.4.21.-).//9.70E-36//389aa//31%//O15393  
 C-PLACE1004277//Homo sapiens two pore domain K<sup>+</sup> channel (TASK-2) mRNA, complete cds.//0//1498bp//99%//AF084830  
 C-PLACE1004302//SOF1 PROTEIN.//1.90E-110//325aa//48%//P33750  
 C-PLACE1004316//H.sapiens mRNA for apoptosis specific protein.//0//1767bp//99%//Y11588  
 35 C-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1 mRNA, complete cds.//0//2512bp//99%//AF100153  
 C-PLACE1004428//PRISTANOYL-COA OXIDASE (EC 1.3.3.-).//1.20E-39//385aa//33%//Q63448  
 C-PLACE1004437//Human NAD<sup>+</sup>-specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene encoding mitochondrial protein, complete cds.//0//985bp//99%//U49283  
 40 C-PLACE1004460//MATERNAL TUDOR PROTEIN.//0.0000002//218aa//23%//P25823  
 C-PLACE1004471//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1)7/2.90E-56//276aa//41%//P51522  
 C-PLACE1004506//Homo sapiens carboxyl terminal LIM domain protein (CLIM1) mRNA, complete cds.//2.10E-16//402bp//62%//U90878  
 45 C-PLACE1004510//Homo sapiens TATA binding protein associated factor (TAFII150) mRNA, complete cds.//3.40E-227//1037bp//99%//AF040701  
 C-PLACE1004550//Homo sapiens CGI-20 protein mRNA, complete cds.//3.50E-274//1305bp//97%//AF132954  
 C-PLACE1004564//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT).//0//525aa//99%//Q10568  
 50 C-PLACE1004629//PROTEIN OS-9 PRECURSOR.//7.70E-18//264aa//32%//Q13438  
 C-PLACE1004646//B.taurus mRNA for retinal pigment epithelial membrane receptor p63.//4.40E-42//985bp//59%//X66277  
 C-PLACE1004674//Homo sapiens calcium binding protein (ALG-2) mRNA, complete cds.//1.30E-195//982bp//96%//AF035606  
 55 C-PLACE1004743//PROBABLE N-END-RECOGNIZING PROTEIN (UBIQUITIN-PROTEIN LIGASE E3 COMPLEX) (N- RECOGNIN).//4.40E-35//578aa//27%//O60152  
 C-PLACE1004751//Homo sapiens mRNA for alpha2,3-sialyltransferase ST3Gal VI, complete cds.//7.10E-224//790bp//98%//AB022918  
 C-PLACE1004777//N-CHIMAERIN (NC) (N-CHIMERIN) (ALPHA CHIMERIN) (A-CHIMAERIN).//1.90E-32//259aa//32%//P30337  
 C-PLACE1004793//RETROVIRUS-RELATED ENV POLYPROTEIN.//5.20E-47//577aa//25%//P10267  
 C-PLACE1004804//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE).//4.70E-65//695aa//29%//Q01631

C-PLACE1004814//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//5.90E-19//196aa//36%//Q08170  
 C-PLACE1004868//MALE STERILITY PROTEIN 27/3.90E-39//261aa//27%//Q08891  
 C-PLACE1004902//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C.//9.30E-11//94aa//47%//O42643  
 C-PLACE1004918//L-LACTATE DEHYDROGENASE M CHAIN (EC 1.1.1.27) (LDH-A).//4.90E-48//198aa//44%//P06151  
 C-PLACE1004930//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds//0//1853bp//98%//AF099936  
 C-PLACE1004937//SEL-10 PROTEIN.//6.30E-125//357aa//58%//Q93794  
 C-PLACE1004969//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//2.00E-14//205aa//26%//Q11073  
 C-PLACE1005052//Homo sapiens CGI-16 protein mRNA, complete cds.//6.6e-313//1413bp//99%//AF132950  
 C-PLACE1005102//RING CANAL PROTEIN (KELCH PROTEIN).//2.60E-56//565aa//30%//Q04652  
 C-PLACE1005176//Homo sapiens hypothalamus protein HT001 mRNA, complete cds.//3.90E-212//1040bp//96%//AF113539  
 C-PLACE1005187//APAG PROTEIN.//3.80E-13//122aa//36%//P05636  
 C-PLACE1005243//SERINE/THREONINE PROTEIN KINASE PKPA (EC 2.7.1.-).//1.30E-27//349aa//32%//Q01577  
 C-PLACE1005287//INNER CENTROMERE PROTEIN (INCENP).//2.30E-13//269aa//28%//P53352  
 C-PLACE1005305//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//2.00E-111//226aa//92%//P08760  
 C-PLACE1005331//Homo sapiens 7h3 protein mRNA, partial cds.//1.20E-226//748bp//95%//AF209931  
 C-PLACE1005373//tRNA PSEUDOURIDINE SYNTHASE B (EC 4.2.1.70) (tRNA PSEUDOURIDINE 55 SYNTHASE) (PSI55 SYNTHASE) (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE).//8.60E-09//194aa//27%//O33335  
 C-PLACE1005467//PENICILLIN-BINDING PROTEIN 4\* (PBP 4\*) (PBP 4A).//1.10E-09//93aa//31%//P32959  
 C-PLACE1005494//Homo sapiens mRNA for transient receptor potential protein TRP6.//0//1649bp//99%//AJ006276  
 C-PLACE1005530//HYPOTHETICAL 47.6 KD PROTEIN C16C10.5 IN CHROMOSOME III.//5.60E-52//173aa//57%//Q09251  
 C-PLACE1005549//Homo sapiens mRNA for Rho guanine nucleotide-exchange factor, splice variant NET1A.//7.60E-97//1287bp//67%//AJ010046  
 C-PLACE1005577//60S RIBOSOMAL PROTEIN L27.//1.90E-11//60aa//48%//P46288  
 C-PLACE1005584//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICPQ (P135 PROTEIN) (IER 2.9/ER2.6).//6.80E-09//267aa//30%//P29128  
 C-PLACE1005611//Mus musculus mRNA for mDj10, complete cds.//2.00E-33//379bp//66%//AB028860  
 C-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete cds.//0//2130bp//99%//AF083255  
 C-PLACE1005656//RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M2 CHAIN (EC 1.17.4.1) (RIBONUCLEOTIDE REDUCTASE).//2.10E-148//321aa//83%//P31350  
 C-PLACE10057277//Homo sapiens STRIN protein (STRIN) mRNA, complete cds.//2.00E-118//378bp//98%//AF162680  
 C-PLACE1005739//INTERFERON-GAMMA INDUCIBLE PROTEIN MG11//1.30E-237//585aa//72%//Q60710  
 C-PLACE1005763//S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN (EC 3.1.2.14) (THIOESTERASE II).//2.50E-79//209aa//53%//P08635  
 C-PLACE1005803//Homo sapiens mRNA for transcription factor (SMIF gene).//0//1985bp//99%//AJ275986  
 C-PLACE1005804//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds.//1.10E-217//994bp//99%//AF027156  
 C-PLACE1005813//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.//0//2040bp//99%//AF065482  
 C-PLACE1005876//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT).//0//730aa//99%//Q10568  
 C-PLACE1005890//BEM46 PROTEIN (FRAGMENT).//9.90E-42//224aa//43%//P54069  
 C-PLACE1005921//AIG1 PROTEIN.//3.00E-31//284aa//31%//P54120  
 C-PLACE1005951//Homo sapiens prolactin regulatory element-binding protein (PREB) mRNA, complete cds.//1.10E-264//661bp//99%//AF203687  
 C-PLACE1005953//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//6.70E-30//198aa//37%//P43636  
 C-PLACE1005955//VACUOLAR AMINOPEPTIDASE I PRECURSOR (EC 3.4.11.22) (POLYPEPTIDASE).//5.40E-54//455aa//32%//P14904

C-PLACE1005966//TRANSCRIPTION INITIATION FACTOR TFIID 90 KD SUBUNIT (TAFII-90)7/1.40E-07//  
254aa//25%//P38129

C-PLACE1006003//Homo sapiens CGI-94 protein mRNA, complete cds.//2.40E-177//829bp//99%//AF151852

C-PLACE1006011//Homo sapiens mRNA for poly(ADP-ribose) polymerase-2.//0//1564bp//99%//AJ236876

5 C-PLACE1006040//Homo sapiens mRNA for alpha endosulfine.//4.70E-161//744bp//99%//X99906

C-PLACE1006119//Homo sapiens Ran-GTP binding protein mRNA, partial cds.//1.50E-148//681bp//99%//  
AF039023

C-PLACE1006157//E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1)  
(ELAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E).//2.00E-28//  
236aa//30%//P98110

C-PLACE1006167//PAF1 PROTEIN.//7.30E-15//437aa//24%//P38351

C-PLACE1006170//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE  
CHAIN)(100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA  
C SUBUNIT).//1.70E-169//373aa//88%//P17427

10 C-PLACE1006196//PUTATIVE ATP-DEPENDENT RNA HELICASE C12C2.06.//2.70E-116//496aa//48%//Q09747

C-PLACE1006239//BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN).//2.00E-16//244aa//31%//  
P28675

C-PLACE1006288//VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN 1 (VDAC1) (PLASMA-  
LEMMAL PORIN) (OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN) (PORIN 31HL) (PORIN 31HM).//  
20 4.60E-117//147aa//80%//P21796

C-PLACE1006318//Mus musculus skm-BOP2 (Bop) mRNA, complete cds.//3.00E-07//376bp//59%//U76374

C-PLACE1006335//Homo sapiens NY-REN-50 antigen mRNA, partial cds.//0//1649bp//99%//AF155112

C-PLACE1006368//HYALURONAN-MEDIATED MOTILITY RECEPTOR (HYALURONIC ACID RECEPTOR).//  
1.30E-18//460aa//24%//Q00547

25 C-PLACE1006385//Homo sapiens epsin 2a mRNA, complete cds.//0//1168bp//99%//AF062085

C-PLACE1006438//ZINC FINGER PROTEIN 165.//2.50E-45//122aa//43%//P49910

C-PLACE1006469//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE-COA LIGASE) (ACYL- AC-  
TIVATING ENZYME).//1.20E-83//313aa//49%//P27550

C-PLACE1006482//TRANSCRIPTION FACTOR MAFF.//7.70E-55//142aa//85%//Q90595

30 C-PLACE1006488//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//1.10E-229//367aa//96%//  
Q00004

C-PLACE1006492//Homo sapiens transmembrane protein 2 (TMEM2) mRNA, complete cds.//0//2618bp//99%//  
AF137030

C-PLACE1006506//Homo sapiens anaphase-promoting complex subunit 4 (APC4) mRNA, complete cds.//0//  
35 2170bp//99%//AF191338

C-PLACE1006531//Homo sapiens putative RNA-binding protein Q99 mRNA, complete cds.//0//1967bp//99%//  
AF093097

C-PLACE1006534//POLYPEPTIDE N-ACETYLGLACTOSAMINYLTRANSFERASE (EC 2.4.1.41)(PROTEIN-  
40 UDP ACETYLGLACTOSAMINYLTRANSFERASE)(UDP-GALNAC:POLYPEPTIDE, N-ACETYLGLACTOSAM-  
INYLTTRANSFERASE) (GALNAC-T1).//8.30E-08//100aa//41%//Q10472

C-PLACE1006552//MYOSIN HEAVY CHAIN, CLONE 203 (FRAGMENT).//1.20E-09//426aa//21%//P39922

C-PLACE1006615//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds.//  
0//1464bp//99%//U97670

C-PLACE1006626//Homo sapiens mRNA for Helicase-MOI, complete cds.//0//1760bp//99%//AB028449

45 C-PLACE1006678//Homo sapiens mRNA for type II membrane protein, complete cds, clone:HP10328.//5.80E-  
24//734bp//62%//AB015630

C-PLACE1006731//RIBOFLAVIN KINASE (EC 2.7.1.26) (FLAVOKINASE) / FMN ADENYLYLTRANSFERASE (EC  
2.7.7.2) (FAD PYROPHOSPHORYLASE).(FAD SYNTHETASE).//6.90E-13//177aa//33%//Q59263

C-PLACE1006754//BILARY GLYCOPROTEIN 1 PRECURSOR (BGP-1) (ANTIGEN CD66) (CD66A ANTIGEN).//  
50 6.20E-63//191aa//43%//P13688

C-PLACE1006819//UNE-1 REVERSE TRANSCRIPTASE HOMOLOG.//9.80E-213//232aa//80%//P08547

C-PLACE1006829//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THIOLESTE-  
RASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME 4) (UBIQUI-  
TOUS NUCLEAR PROTEIN).//2.00E-15//188aa//29%//P35123

55 C-PLACE1006878//TRNA-SPlicing ENDONUCLEASE SUBUNIT SEN2 (EC 3.1.27.9) (TRNA-INTRON ENDO-  
NUCLEASE).//1.90E-08//122aa//36%//P16658

C-PLACE1006917//HSH49 PROTEIN.//5.50E-12//97aa//35%//Q99181

C-PLACE1006935//HYPOTHETICAL 95.2 KD PROTEIN R144.6 IN CHROMOSOME III.//6.70E-48//278aa//41%//

Q10000  
C-PLACE1006956//ATP-DEPENDENT PERMEASE MDL1./.1.30E-86//522aa/36%//P97998  
C-PLACE1006958//Homo sapiens mRNA for heat shock protein apg-1, complete cds./.0//1770bp//99%//  
AB023421

5 C-PLACE1007014//36 KD NUCLEOLAR PROTEIN HNP36 (DELAYED-EARLY RESPONSE PROTEIN 12)  
(DER12).//3.20E-35//180aa/33%//Q14542  
C-PLACE1007105//Homo sapiens muskelin (MKLN1) mRNA, complete cds./.0//2449bp//98%//AF047489  
C-PLACE1007140//TRICHOHYALIN./.1.30E-25//816aa/22%//P37709  
C-PLACE1007226//PROBABLE OXYGEN-INDEPENDENT COPROPORPHRINOGEN III OXIDASE (EC 1.---)  
10 (COPROPORPHRINOGENASE) (COPROGEN OXIDASE).//1.00E-42//370aa/31%//P54304  
C-PLACE1007239//Homo sapiens mRNA for transcription elongation factor S-II, hS-II-T1, complete cds./.6.50E-  
216//1068bp//96%//D50495  
C-PLACE1007243//UNC-47 PROTEIN./.1.70E-07//211aa/27%//P34579  
C-PLACE1007257//Homo sapiens mRNA for dia-12c protein./.0//2052bp//99%//Y15908  
15 C-PLACE1007317//Drosophila melanogaster Adrift (adrift) mRNA, complete cds./.4.10E-17//1037bp//56%//  
AF117649  
C-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EBBP) mRNA, complete cds./.0//2366bp//  
99%//AF096870  
C-PLACE1007375//PHORBOL ESTER/DIACYLGLYCEROL-BINDING PROTEIN UNC-13./.0.00000044//127aa/  
20 30%//P27715  
C-PLACE1007409//WHTTE PROTEIN./.1.10E-64//428aa/32%//Q17320  
C-PLACE1007416//DIPEPTIDYL PEPTIDASE IV (EC 3.4.14.5) (DPP IV) (T-CELL ACTIVATION ANTIGEN CD26)  
(TP103) (ADENOSINE DEAMINASE COMPLEXING PROTEIN-2) (ADABP).//8.80E-25//140aa/35%//P27487  
C-PLACE1007488//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FA-  
25 CIOGENITAL DYSPLASIA PROTEIN HOMOLOG).//5.40E-53//426aa/33%//P52734  
C-PLACE1007511//KERATIN, TYPE I CYTOSKELETAL 19 (CYTOKERATIN 19) (K19) (CK 19).//1.40E-85//  
385aa/45%//P08728  
C-PLACE1007537//Homo sapiens ankyrin repeat-containing protein ASB-2 mRNA, complete cds./.8.9e-316//  
1485bp//98%//AF159164  
30 C-PLACE1007547//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME III./.1.00E-49//361aa/  
36%//P34537  
C-PLACE1007598//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.60E-143//666aa/44%//Q99676  
C-PLACE1007632//POLIOVIRUS RECEPTOR PRECURSOR./.1.00E-07//228aa/31%//P32506  
C-PLACE1007649//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSI-  
35 DASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//4.50E-05//197aa/26%//P08640  
C-PLACE1007688//LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG).//  
8.70E-09//279aa/28%//Q26457  
C-PLACE1007697//GCN20 PROTEIN./.7.60E-119//717aa/38%//P43535  
C-PLACE1007705//Mus musculus mRNA for Ndr1 related protein Ndr3, complete cds./.1.10E-184//1096bp//82%//  
40 AB033922  
C-PLACE1007706//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds./.0//3431bp//99%//AF061243  
C-PLACE1007729//RETROVIRUS-RELATED PROTEASE (EC 3.4.23.-).//1.50E-44//231aa/42%//P10265  
C-PLACE1007791//Homo sapiens IDN3-B mRNA, complete cds./.0//1836bp//99%//AB019602  
C-PLACE1007897//Homo sapiens FLASH mRNA, complete cds./.0//2145bp//99%//AF154415  
45 C-PLACE1007946//MYOSIN HEAVY CHAIN, NON-MUSCLE (ZIPPER PROTEIN) (MYOSIN II).//2.60E-14//  
370aa/25%//Q99323  
C-PLACE1007954//HYPOTHETICAL 45.5 KD PROTEIN IN FIG1-GIP1 INTERGENIC REGION./.6.70E-13//  
168aa/31%//P38226  
C-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds./.0//2252bp//99%//  
50 AF084530  
C-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds./.0//2300bp//  
99%//AF079529  
C-PLACE1007969//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN M (HNRNP M).//1.10E-36//202aa/  
48%//P52272  
55 C-PLACE1008000//CHANNEL ASSOCIATED PROTEIN OF SYNAPSE-110 (CHAPSYN-110) (SYNAPTIC DEN-  
SITY PROTEIN PSD-93).//6.10E-14//128aa/39%//Q63622  
C-PLACE1008044//NUCLEAR PORE COMPLEX PROTEIN NUP107 (NUCLEOPORIN NUP107) (107 KD NU-  
CLEOPORIN) (P105).//4.6e-318//613aa/94%//P52590

C-PLACE1008080//Homo sapiens mRNA for HEXIM1 protein, complete cds.//0//2152bp//99%//AB021179  
 C-PLACE1008111//PROBABLE OXIDOREDUCTASE (EC 1.---).//3.00E-25//208aa//37%//Q03326  
 C-PLACE1008132//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOME III.//1.30E-24//395aa//  
 31%//Q09531  
 5 C-PLACE1008177//TRICHOHYALIN.//2.30E-29//487aa//26%//P37709  
 C-PLACE1008201//Rattus rattus zinc finger protein, complete cds.//0//2265bp//83%//L23077  
 C-PLACE1008244//VEGETABLE INCOMPATIBILITY PROTEIN HET-E-1.//9.50E-21//148aa//38%//Q00808  
 C-PLACE1008273//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP).//1.30E-283//  
 671aa//77%//P53620  
 10 C-PLACE1008275//DNA REPAIR PROTEIN REV1 (EC 2.7.7.-).//2.30E-18//162aa//37%//P12689  
 C-PLACE1008309//Rattus norvegicus putative four repeat ion channel mRNA, complete cds.//5.20E-137//672bp//  
 77%//AF078779  
 C-PLACE1008330//EOSINOPHIL LYSOPHOSPHOLIPASE (EC 3.1.1.5) (CHARCOT-LEYDEN CRYSTAL PRO-  
 15 TEIN) (LYSOLECITHIN ACYLHYDROLASE) (CLC) (GALACTIN-10).//2.20E-23//94aa//47%//Q05315  
 C-PLACE1008356//Homo sapiens meningioma-expressed antigen 5 (MEA5) mRNA, partial cds.//1.90E-170//  
 780bp//100%//AF036144  
 C-PLACE1008368//RING CANAL PROTEIN (KELCH PROTEIN).//5.30E-26//309aa//30%//Q04652  
 C-PLACE1008398//GENE 33 POLYPEPTIDE.//7.30E-114//243aa//87%//P05432  
 20 C-PLACE1008402//GENERAL VESICULAR TRANSPORT FACTOR P115 (TRAN-SCYTOSIS ASSOCIATED  
 PROTEIN) (TAP).//0//698aa//95%//P41541  
 C-PLACE1008426//RESTIN (CYTOPLASMIC LINKER PROTEIN-170) (CLIP-170).//1.80E-11//365aa//25%//  
 O42184  
 C-PLACE1008429//ANKYRIN HOMOLOG PRECURSOR.//3.10E-11//189aa//32%//Q06527  
 25 C-PLACE1008465//Homo sapiens mRNA for rapa-1 (rapa gene).//6.60E-243//1102bp//99%//AJ277275  
 C-PLACE1008533//101 KD MALARIA ANTIGEN (P101) (ACIDIC BASIC REPEAT ANTIGEN).//1.10E-09//62aa//  
 48%//P22620  
 C-PLACE1008603//NUCLEAR PORE COMPLEX PROTEIN NUP155 (NUCLEOPORIN NUP155) (155 KD NU-  
 CLEOPORIN) (P140).//7.80E-236//453aa//96%//P37199  
 C-PLACE1008627//Homo sapiens mRNA for cysteine-rich protein.//0//1850bp//99%//AJ006591  
 30 C-PLACE1008643//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (III HEAVY CHAIN  
 H2).//5.20E-90//483aa//38%//O02668  
 C-PLACE1008650//PRL1/PRL2-LIKE PROTEIN.//2.00E-127//354aa//62%//O13615  
 C-PLACE1008696//Homo sapiens NADH dehydrogenase-ubiquinone Fe-S protein 8 23 kDa subunit (NDUFS8)  
 35 gene, nuclear gene encoding mitochondrial protein, complete cds.//0//3002bp//99%//AF03 8406  
 C-PLACE1008790//Homo sapiens importin alpha 7 subunit mRNA, complete cds.//0//1670bp//99%//AF060543  
 C-PLACE1008808//Homo sapiens mRNA for cell cycle checkpoint protein rad1A.//2.30E-269//1225bp//99%//  
 AJ004974  
 C-PLACE1008813//Rattus norvegicus rsec15 mRNA, complete cds.//8.80E-268//1171bp//90%//AF032668  
 C-PLACE1009020//NIFS PROTEIN.//3.90E-55//279aa//41%//P12623  
 40 C-PLACE1009027//Homo sapiens mRNA for doublecortin.//0//1919bp//99%//AJ003112  
 C-PLACE1009060//BRO1 PROTEIN.//6.70E-19//567aa//24%//P48582  
 C-PLACE1009094//FURIN-LIKE PROTEASE 2 PRECURSOR (EC 3.4.21.75) (FURIN 2).//1.90E-44//480aa//  
 30%//P30432  
 C-PLACE1009099//ZINC FINGER PROTEIN 41 (FRAGMENT).//1.10E-179//452aa//67%//P51814  
 45 C-PLACE1009113//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds.//  
 0//2529bp//99%//AF035586  
 C-PLACE1009130//UBIQUITIN-PROTEIN LIGASE E3A (EC 6.3.2.-) (ONCOGENIC PROTEIN-ASSOCIATED  
 PROTEIN E6-AP).//2.00E-68//181aa//43%//Q05086  
 C-PLACE1009158//Mus musculus mRNA for death inducer-obliterator-1 (Dio-1).//5.40E-200//1790bp//75%//  
 50 AJ238332  
 C-PLACE1009186//Homo sapiens small zinc finger-like protein (TIM9b) mRNA, complete cds.//9.60E-255//  
 1179bp//98%//AF150105  
 C-PLACE1009246//POLLEN SPECIFIC PROTEIN SF3.//4.40E-16//82aa//43%//P29675  
 C-PLACE1009298//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS35.//2.00E-78//262aa//43%//  
 55 P34110  
 C-PLACE1009308//GLUCOSE REPRESSION MEDIATOR PROTEIN.//4.00E-06//439aa//23%//P14922  
 C-PLACE1009319//Rattus norvegicus outer membrane protein (OMP25) mRNA, complete cds; nuclear gene for  
 mitochondrial product.//2.10E-132//1229bp//75%//AF107295

C-PLACE1009368//METAL HOMEOSTASIS FACTOR ATX27/2.50E-10//151aa//29%//Q12067  
C-PLACE1009398//ZINC FINGER PROTEIN 135./.6.20E-97/361aa//51%//P52742  
C-PLACE1009404//HYPOTHETICAL 105.6 KD PROTEIN C16C9.06C IN CHROMOSOME I./.4.70E-08//165aa//  
33%//Q09820  
5 C-PLACE1009443//Mus musculus F-box protein FBL8 mRNA, complete cds./.1.00E-173//1367bp//77%//  
AF176523  
C-PLACE1009444//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA (EC 2.7.1.67) (PI4-KINASE) (PTDINS-4-KI-  
NASE) (PI4K-ALPHA).//7.80E-71//82aa//89%//P42356  
C-PLACE1009468//PHOSPHOLIPASE A-2-ACTIVATING PROTEIN (PLAP).//3.10E-289//550aa//93%//P54319  
10 C-PLACE1009476//PUTATIVE ATP-DEPENDENT RNA HELICASE T26G10.1 IN CHROMOSOME III./.3.90E-40//  
179aa//37%//P34580  
C-PLACE1009477//Homo sapiens ubiquitin-fusion degradation protein 2 (UFD2) mRNA, complete cds./.6.60E-  
147//592bp//99%//AF043117  
C-PLACE1009524//ARF NUCLEOTIDE-BINDING SITE OPENER (ARNO PROTEIN) (ARF EXCHANGE FAC-  
15 TOR).//8.10E-99//228aa//75%//Q99418  
C-PLACE1009571//Homo sapiens PTD002 mRNA, complete cds./.5.90E-185//857bp//99%//AF078857  
C-PLACE1009596//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1./.5.10E-54//291aa//40%//Q00808  
C-PLACE1009622//MATERNAL EFFECT PROTEIN STAUFEN./.1.30E-60//209aa//41%//P25159  
20 C-PLACE1009659//MEMBRANE-ASSOCIATED PROTEIN HEM-2 (NAP1 PROTEIN).//1.50E-285//538aa//99%//  
P55161  
C-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds./.0//1854bp//100%//AF062534  
C-PLACE1009708//HYPOTHETICAL 143.3 KD TRP-ASP REPEATS CONTAINING PROTEIN C12G12.13C IN  
CHROMOSOME I./.7.00E-33//166aa//43%//Q09876  
C-PLACE1009721//MSF1 PROTEIN./.1.70E-22//176aa//33%//P35200  
25 C-PLACE1009731//AIG1 PROTEIN./.1.60E-22//274aa//28%//P54120  
C-PLACE1009763//Homo sapiens mRNA for Nedd8-activating enzyme hUba3, complete cds./.4.30E-294//  
1329bp//100%//AB012190  
C-PLACE1009798//RLR1 PROTEIN./.1.60E-18//270aa//23%//P53552  
C-PLACE1009845//WEB1 PROTEIN (PROTEIN TRANSPORT PROTEIN SEC31).//2.30E-59//405aa//33%//  
30 P38968  
C-PLACE1009861//CATHEPSIN B-LIKE CYSTEINE PROTEINASE 6 PRECURSOR (EC 3.4.22.-).//6.50E-28//  
209aa//38%//P43510  
C-PLACE1009908//HYPOTHETICAL GTP-BINDING PROTEIN IN SEH1-PRP20 INTERGENIC REGION./.1.90E-  
108//277aa//43%//P53145  
35 C-PLACE1009925//Homo sapiens RNA helicase (RIG-I) mRNA, complete cds./.0//1730bp//99%//AF038963  
C-PLACE1009992//LIMULUS CLOTTING FACTOR C PRECURSOR (EC 3.4.21.84).//4.60E-59//450aa//34%//  
P28175  
C-PLACE1009997//Rattus norvegicus A-kinase anchoring protein AKAP 220 mRNA, complete cds./.5.20E-70//  
736bp//73 %//U48288  
40 C-PLACE1010053//M.musculus Spnr mRNA for RNA binding protein./.6.00E-279//1402bp//94%//X84692  
C-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds./.0//2019bp//99%//AF065482  
C-PLACE1010096//100 KD PROTEIN (EC 6.3.2.-).//1.40E-268//506aa//98%//Q62671  
C-PLACE1010105//RING CANAL PROTEIN (KELCH PROTEIN).//7.30E-114//537aa//44%//Q04652  
45 C-PLACE1010134//TRANSCRIPTION REGULATORY PROTEIN SNF2 (SWI/SNF COMPLEX COMPONENT  
SNF2) (REGULATORY PROTEIN SWI2) (REGULATORY PROTEIN GAM1) (TRANSCRIPTION FACTOR  
TYE3).//1.70E-20//156aa//42%//P22082  
C-PLACE1010148//CYUCIN I (MULTIPLE-BAND POLYPEPTIDE I).//4.60E-07//431aa//23%//P35662  
C-PLACE1010194//SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35)  
(SPLICING COMPONENT, 35 KD) (PR264 PROTEIN).//9.80E-11//95aa//49%//Q01130  
50 C-PLACE1010231//CELL SURFACE GLYCOPROTEIN EMR1 PRECURSOR (EMR1 HORMONE RECEPTOR).//  
5.1 OE-27//371aa//28%//Q14246  
C-PLACE1010261//SEGREGATION DISTORTER PROTEIN./.1.60E-77//214aa//62%//P25722  
C-PLACE1010310//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).//1.20E-18//467aa//30%//P46804  
C-PLACE1010321//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT).//  
55 1.10E-09//350aa//22%//P52178  
C-PLACE1010362//1-PHOSPHATIDYLINOSITOL PHOSPHODIESTERASE PRECURSOR (EC 3.1.4.10)  
(PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE C) (PI-PLC).//2.00E-09//126aa//29%//P34024  
C-PLACE1010481//Bos taurus C5-glucuronyl epimerase mRNA, partial cds./.0//2082bp//91%//AF003927

C-PLACE1010522//Homo sapiens mRNA for DEPP (decidual protein induced by progesterone), complete cds.//0//1981 bp//99%//AB022718  
 C-PLACE1010529//Homo sapiens TANK binding kinase TBK1 (TBK1) mRNA, complete cds.//0//1750bp//99%//AF191838  
 5 C-PLACE1010547//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1//1.20E-07//616aa//24%//P25386  
 C-PLACE1010579//Homo sapiens CED-6 protein (CED-6) mRNA, complete cds.//8.80E-300//1359bp//99%//AF191771  
 10 C-PLACE1010599//Homo sapiens Pex14 mRNA for peroxisomal membrane anchor protein, complete cds.//0//1904bp//99%//AB017546  
 C-PLACE1010622//TROPONIN T, CARDIAC MUSCLE ISOFORMS (TNTC).//0.00000016//120aa//28%//P02642  
 C-PLACE1010628//Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds.//7.50E-08//324bp//64%//AF109907  
 15 C-PLACE1010661//TESTIS-SPECIFIC PROTEIN PBS 13.//5.70E-75//423aa//39%//Q01755  
 C-PLACE1010662//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT).//1.80E-222//808aa//52%//Q09332  
 C-PLACE1010702//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//5.20E-151//427aa//55%//P28160  
 C-PLACE1010720//Homo sapiens mRNA for chromosome-associated polypeptide-C, complete cds.//4.00E-299//1091bp//99%//AB019987  
 20 C-PLACE1010743//Homo sapiens myosin-IXb splice variant (Myo9b) mRNA, partial cds.//8.90E-91//668bp//82%//AF020267  
 C-PLACE1010761//Homo sapiens mRNA for cisplatin resistance-associated overexpressed protein, complete cds.//0//1448bp//99%//AB034205  
 C-PLACE1010771//M.musculus HCNGP mRNA.//7.40E-168//966bp//89%//X68061  
 25 C-PLACE1010811//Rattus norvegicus mRNA for protein encoded by bdeight gene, partial.//1.60E-217//858bp//87%//AJ010392  
 C-PLACE1010833//CALTRACTIN(CENTRIN).//0.0000001//154aa//28%//P41209  
 C-PLACE1010870//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.30E-143//407aa//58%//Q05481  
 30 C-PLACE1010896//NUF1 PROTEIN (SPINDLE POLY BODY SPACER PROTEIN SPC110).//1.50E-25//583aa//23%//P35580  
 C-PLACE1010926//HYPOTHETICAL 72.2 KD PROTEIN C12C2.05C IN CHROMOSOME II.//7.60E-23//103aa//53%//Q09746  
 C-PLACE1010942//Homo sapiens intersectin long isoform (ITSN) mRNA, complete cds.//0//1440bp//99%//AF114487  
 35 C-PLACE1010960//ACTIN-LIKE PROTEIN 13E.//5.30E-98//297aa//48%//P45890  
 C-PLACE1011041//Homo sapiens mRNA for BAP2-alpha protein, complete cds.//0//1701bp//97%//AB015019  
 C-PLACE1011046//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 1 (EC 3.1.4.11) (PLC-BETA-1) (PHOSPHOLIPASE C-BETA-1) (PLC-I) (PLC-154).//0//646aa//97%//P10894  
 40 C-PLACE1011056//HISTONE H1, GONADAL.//6.80E-13//154aa//37%//P02256  
 C-PLACE1011109//ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEFG).//1.50E-22//63aa//88%//Q07803  
 C-PLACE1011114//PROBABLE ATP-DEPENDENT RNA HELICASE HAS1.//2.90E-71//190aa//44%//Q03532  
 45 C-PLACE1011160//Homo sapiens HFB30 mRNA, complete cds.//0//1691bp//99%//AB022663  
 C-PLACE1011185//INSERTION ELEMENT IS1 PROTEIN INSB.//1.30E-89//167aa//100%//P03830  
 C-PLACE1011219//PROBABLE OXIDOREDUCTASE (EC 1.---).//3.20E-12//212aa//29%//Q03326  
 C-PLACE1011229//Homo sapiens ubiquitin-specific protease homolog (UPH) mRNA, complete cds.//2.30E-152//701bp//99%//AF153604  
 C-PLACE1011310//MYOSIN HEAVY CHAIN, GIZZARD SMOOTH MUSCLE.//3.50E-20//496aa//25%//P10587  
 50 C-PLACE1011332//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//7.20E-151//697bp//99%//AF102265  
 C-PLACE1011340//Homo sapiens IDN3-B mRNA, complete cds.//1.20E-74//380bp//97%//AB019602  
 C-PLACE1011371//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2).//1.70E-78//383aa//39%//Q61703  
 55 C-PLACE1011399//Homo sapiens CGI-72 protein mRNA, complete cds.//3.20E-90//427bp//99%//AF151830  
 C-PLACE1011433//TRANSCRIPTION FACTOR IIIA (FACTOR A) (TFIIIA).//3.00E-10//236aa//25%//P34695  
 C-PLACE1011477//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.//0//2040bp//99%//AF065482  
 C-PLACE1011492//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT).//

4.90E-11//147aa//32%//P52178  
C-PLACE1011576//Human Kruppel related zinc finger protein (HTF10) mRNA, complete cds./0//1791bp//82%//  
L11672  
C-PLACE1011586//Rattus norvegicus clone C53 CDK5 activator-binding protein mRNA, complete cds7/4.10E-  
5 259//1538bp//87%//AF177476  
C-PLACE1011635//Homo sapiens heparan sulfate D-glucosaminyl 3-O-sulfotransferase-3B (3OST3B1) mRNA,  
complete cds./0//1559bp//99%//AF105377  
C-PLACE1011664//CROOKED NECK PROTEIN./1.60E-187//505aa//64%//P17886  
C-PLACE1011858//Homo sapiens BAG-family molecular chaperone regulator-2 mRNA, complete cds./1.30E-  
10 255//1179bp//99%//AF095192  
C-PLACE1011896//Mus musculus Wnt10a mRNA, complete cds./2.60E-287//1820bp//85%//U61969  
C-PLACE1011922//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN, TYPE  
B) (NMMHC-B).//1.30E-15//409aa//27%//P35580  
C-PLACE1011923//Homo sapiens serum-inducible kinase mRNA, complete cds./0//2782bp//99%//AF059617  
15 C-PLACE101-2031//Homo sapiens sorting nexin 13 (SNX13) mRNA, partial cds./0//1701bp//100%//AF121862  
C-PLACE2000014//HYPOTHETICAL HELICASE C28H8.3 IN CHROMOSOME III./2.60E-42//104aa//49%//  
Q09475  
C-PLACE2000015//EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN  
EPS15) (AF-1P PROTEIN).//1.10E-116//364aa//45%//P42566  
20 C-PLACE2000021//Homo sapiens TRF1-interacting ankyrin-related ADP-ribose polymerase mRNA, complete  
cds./2.70E-107//981bp//74%//AF082556  
C-PLACE2000034//LAR PROTEIN PRECURSOR (LEUKOCYTE ANTIGEN RELATED) (EC 3.1.3.48).//2.20E-29//  
212aa//35%//P10586  
C-PLACE2000039//DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC) (MAP 1C).//6.10E-293//388aa//99%//P38650  
25 C-PLACE2000062//Homo sapiens mRNA for type II membrane protein similar to HIV gp120-binding C-type lectin,  
complete cds, clone:HP01347.//6.30E-166//656bp//94%//AB015629  
C-PLACE2000072//Homo sapiens ZNF202 beta (ZNF202) mRNA, complete cds./0//3174bp//99%//AF027219  
C-PLACE2000164//TIPD PROTEIN./2.10E-59//481aa//33%//O15736  
C-PLACE2000216//SPECTRIN BETA CHAIN, BRAIN (SPECTRIN, NON-ERYTHROID BETA CHAIN) (FODRIN  
30 BETA CHAIN) (SPTBN1).//6.60E-115//226aa//99%//Q01082  
C-PLACE2000246//RING CANAL PROTEIN (KELCH PROTEIN).//6.00E-57//239aa//34%//Q04652  
C-PLACE2000274//DYNEIN BETA CHAIN, CILIARY./2.20E-167//880aa//37%//P23098  
C-PLACE2000341//Homo sapiens sodium-dependent multivitamin transporter (SMVT) mRNA, complete cds./0//  
1554bp//99%//AF069307  
35 C-PLACE2000371//TENSIN./2.90E-78//561aa//37%//Q04205  
C-PLACE2000373//F-SPONDIN PRECURSOR./8.60E-16//371aa//28%//P35446  
C-PLACE2000398//LAR PROTEIN PRECURSOR (LEUKOCYTE ANTIGEN RELATED) (EC 3.1.3.48).//6.30E-37//  
90aa//98%//P10586  
C-PLACE2000399//T-CELL SURFACE GLYCOPROTEIN E2 PRECURSOR (E2 ANTIGEN) (CD99) (MIC2 PRO-  
40 TEIN) (12E7).//1.60E-14//180aa//39%//P14209  
C-PLACE2000404//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--T RNA LIGASE)  
(LEURS).//9.90E-229//821aa//54%//Q09996  
C-PLACE2000411//Homo sapiens epsin 2b mRNA, complete cds./3.80E-271//642bp//99%//AF062085  
C-PLACE2000427//PROBABLE HELICASE MOT1./1.20E-26//200aa//27%//P32333  
45 C-PLACE2000438//POLYPEPTIDE N-ACETYLGLACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PROTEIN-  
UDP ACETYLGLACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N- ACETYLGLACTOS-  
AMINYLTRANSFERASE) (GALNAC-T1).//2.10E-86//348aa//41%//Q10472  
C-PLACE2000458//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//2.50E-25//  
165aa//40%//P33450  
50 C-PLACE2000477//Homo sapiens putative secreted protein (ZSIG11) mRNA, complete cds./6.70E-127//671bp//  
94%//AF072733  
C-PLACE3000009//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1)(FRAG-  
MENT).//3.50E-30//400aa//30%//P11414  
C-PLACE3000020//Homo sapiens type III adenylyl cyclase (AC-III) mRNA, complete cds./0//2253bp//99%//  
55 AF033861  
C-PLACE3000059//Mus musculus mRNA for ubiquitin conjugating enzyme./0//1979bp//90%//Y17267  
C-PLACE3000121//VESICULAR TRAFFIC CONTROL PROTEIN SEC157/1.90E-08//281aa//22%//P22224  
C-PLACE3000145//TENSIN./1.00E-108//277aa//75%//Q04205

C-PLACE3000147//Homo sapiens metalloproteinase with thrombospondin type 1 motifs ADAMTS1 (ADAMTS1) mRNA, complete cds.//0//2043bp//99%//AF170084  
 C-PLACE3000169//ZINC FINGER PROTEIN 135.//2.50E-90//358aa//47%//P52742  
 C-PLACE3000218//Homo sapiens putative protein O-mannosyltransferase (POMT2) mRNA, complete cds.//0//1862bp//98%//AF105020  
 5 C-PLACE3000242//Human trophinin mRNA, complete cds.//0//2290bp//99%//U04811  
 C-PLACE3000244//PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR).//0//1435aa//92%//P53995  
 C-PLACE3000254//Homo sapiens transcriptional activator SRCAP (SRCAP) mRNA, complete cds.//0//4583bp//83%//AF143946  
 10 C-PLACE3000339//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//9.60E-08//359aa//23%//P08640  
 C-PLACE3000350//SERINE/THREONINE-PROTEIN KINASE SULU (EC 2.7.1.-).//1.00E-54//418aa//38%//P46549  
 15 C-PLACE3000416//Homo sapiens mRNA for actin binding protein ABP620, complete cds.//1.80E-141//565bp//98%//AB029290  
 C-PLACE3000477//Homo sapiens phosphoprotein pp75 mRNA, partial cds.//0//3012bp//98%//AF153085  
 C-PLACE4000009//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN, TYPE B) (NMMHC-B).//2.90E-54//626aa//29%//P35580  
 20 C-PLACE4000014//X-LINKED HEUCASE II (X-LINKED NUCLEAR PROTEIN) (XNP).//3.10E-111//348aa//41%//P46100  
 C-PLACE4000052//Homo sapiens ATP cassette binding transporter 1 (ABC1) mRNA, complete cds.//0//4661bp//99%//AF165281  
 C-PLACE4000063//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//1.70E-15//740aa//23%//P08640  
 25 C-PLACE4000100//Homo sapiens hydroxypyruvate reductase (GRHPR) gene, complete cds.//0//4199bp//97%//AF146689  
 C-PLACE4000128//Mus musculus putative transcription factor mRNA, complete cds.//1.60E-86//190aabp//88%//AF091234  
 C-PLACE4000156//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.40E-235//516aa//51%//Q05481  
 30 C-PLACE4000192//ZINC FINGER PROTEIN 142 (KIAA0236) (HA4654).//7.00E-22//369aa//25%//P52746  
 C-PLACE4000211//Homo sapiens BAZ2A mRNA for bromodomain adjacent to zinc finger domain 2A, complete cds.//0//5709bp//96%//AB032254  
 C-PLACE4000230//Mus musculus semaphorin VIa mRNA, complete cds.//0//2567bp//88%//AF030430  
 35 C-PLACE4000259//H.sapiens gene for U5 snRNP-specific 200kD protein.//0//5143bp//90%//Z70200  
 C-PLACE4000261//PEREGRIN (BR140 PROTEIN).//9.50E-10//128aa//34%//P55201  
 C-PLACE4000269//Rattus norvegicus rexo70 mRNA, complete cds.//0//2034bp//89%//AF032667  
 C-PLACE4000326//NAM7 PROTEIN (NONSENSE-MEDIATED MRNA DECAY PROTEIN 1) (UP-FRAMESHIFT SUPPRESSOR 1).//8.10E-24//319aa//31%//P30771  
 40 C-PLACE4000369//Homo sapiens thyroid hormone receptor-associated protein complex component TRAP240 mRNA, complete cds.//1.40E-185//1135bp//67%//AF117754  
 C-PLACE4000401//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE-COA LIGASE) (ACYL- ACTIVATING ENZYME).//7.20E-22//54aa//62%//Q01576  
 C-PLACE4000431//H.sapiens gene for U5 snRNP-specific 200kD protein.//0//5142bp//90%//Z70200  
 45 C-PLACE4000450//Homo sapiens BAZ2A mRNA for bromodomain adjacent to zinc finger domain 2A, complete cds.//0//5709bp//96%//AB032254  
 C-PLACE4000489//PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT I-BINDING ACTIVITY) (TRANSCRIPTION FACTOR NTF-1)7//5.70E-60//254aa//44%//P13002  
 C-PLACE4000522//NEUROGENIC LOCUS NOTCH PROTEIN HOMOLOG PRECURSOR (XOTCH PROTEIN).//2.40E-191//828aa//48%//P21783  
 50 C-PLACE4000548//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//8.70E-13//784aa//21%//P08640  
 C-PLACE4000558//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAF (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE FAF) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE FAF) (DEUBIQUITINATING ENZYME FAF) (FAT FACETS PROTEIN).//1.50E-26//252aa//35%//P55824  
 55 C-PLACE4000581//FIBROPELLIN I PRECURSOR (EPIDERMAL GROWTH FACTOR-RELATED PROTEIN 1) (UEGF-1).//9.30E-70//226aa//52%//P10079  
 C-PLACE4000650//TUBERIN (TUBEROUS SCLEROSIS 2 HOMOLOG PROTEIN).//7.90E-17//201aa//34%//

P49816

C-PLACE4000654//Mus musculus mRNA for ubiquitin conjugating enzyme./0//6340bp//87%//Y17267  
 C-SKNMC1000011//PUTATIVE IMPORTIN BETA-4 SUBUNIT (KARYOPHERIN BETA-4 SUBUNIT).//5.50E-35//  
 431aa//29%//O60100

5 C-SKNMC1000013//Homo sapiens ATP-binding cassette protein M-ABC1 mRNA, nuclear gene encoding mitochondrial protein, complete cds.//0//2384bp//99%//AF047690

C-SKNMC1000046//Homo sapiens liprin-alpha3 mRNA, partial cds.//1.90E-162//749bp//99%//AF034800

C-SKNMC1000050//CALPAIN 2, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM-ACTIVATED NEUTRAL PROTEINASE) (CANP) (M-TYPE).//3.20E-41//87aa//98%//P17655

10 C-SKNMC1000091//Homo sapiens mRNA for leucine-zipper protein, complete cds.//6.10E-190//872bp//99%//AB021663

C-THYRO1000034/TRICHOHYALIN./9.40E-10//176aa//30%//P37709

C-THYRO1000072//MYOSIN UGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC 2.7.1.117) (MLCK) [CONTAINS: TELOKIN].//3.40E-16//201aa//29%//P11799

15 C-THYRO1000085//PAIRED BOX PROTEIN PAX-8, ISOFORMS 8A/8B.//2.00E-72//155aa//92%//Q06710

C-THYRO1000121//Rattus norvegicus CTD-binding SR-like protein rA8 mRNA, complete cds.//0//1737bp//87%//U49055

C-THYRO1000132//Homo sapiens echinoderm microtubule-associated protein homolog HuEMAP mRNA, complete cds.//1.10E-159//824bp//95%//U97018

20 C-THYRO1000173//Homo sapiens AP-mu chain family member mulB (HSMU1B) mRNA, complete cds.//0//1713bp//99%//AF020797

C-THYRO1000197//Homo sapiens mRNA for poly(A)-specific ribonuclease./0//2362bp//99%//AJ005698

C-THYRO1000242//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//5.00E-118//239aa//66%//P51523

25 C-THYRO1000288//Homo sapiens mRNA for Hs Ste24p, complete cds.//0//2161bp//99%//AB016068

C-THY-RO1000327//Homo sapiens autocrine motility factor receptor (AMFR) mRNA, complete cds.//0//1567bp//99%//AF124145

C-THYRO1000343//ATROPHIN-1 (DENTATORUBRAL-PALUDOLUYSIAN ATROPHY PROTEIN).//4.90E-06//280aa//31%//P54259

30 C-THYRO1000358//SELENIUM-BINDING LIVER PROTEIN./2.30E-229//237aa//79%//P17563

C-THYRO1000394//Homo sapiens peroxisomal membrane protein PMP 24 mRNA, complete cds.//1.20E-299//1325bp//99%//AF072864

C-THYRO1000395//Homo sapiens actin-binding protein (IPP) mRNA, complete cds.//0//2092bp//99%//AF156857

C-THYRO1000401//Human TcD37 homolog (HTcD37) mRNA, partial cds.//1.10E-90//430bp//99%//U67085

35 C-THYRO1000488//Homo sapiens HFB30 mRNA, complete cds.//0//2254bp//100%//AB022663

C-THYRO1000501//52 KD RO PROTEIN (SJOGEN SYNDROME TYPE A ANTIGEN (SS-A))(RO(SS-A)).//4.20E-98//408aa//42%//P19474

C-THYRO1000569//Mus musculus hematopoietic zinc finger protein mRNA, complete cds.//0//1557bp//91%//AF118566

40 C-THYRO1000585//Homo sapiens protein associated with Myc mRNA, complete cds.//0//1901bp//99%//AF075587

C-THYRO1000605//Homo sapiens histone acetyltransferase (HBOa) mRNA, complete cds.//0//3080bp//99%//AF140360

C-THYRO1000662//Homo sapiens XPV mRNA for DNA polymerase eta, complete cds.//0//2341 bp//99%//AB024313

C-THYRO1000666//Mus musculus mRNA for kinesin like protein 9./0//2001bp//86%//AJ132889

C-THYRO1000684//Homo sapiens BAG-family molecular chaperone regulator-5 mRNA, complete cds.//0//3347bp//99%//AF095195

45 C-THYRO1000748//RHO-GAP HEMATOPOIETIC PROTEIN C1 (P115) (KIAA0131).//3.30E-96//335aa//52%//P98171

C-THYRO1000756//ALPHA-N-ACETYLGLUCOSAMINIDE ALPHA-2,6-SIALYLTRANSFERASE (EC 2.4.99.-) (ST6GALNACIII)(STY).//1.80E-55//243aa//42%//Q64686

C-THYRO1000783//Xenopus laevis tail-specific thyroid hormone up-regulated (gene 5) mRNA, complete cds.//2.40E-157//1656bp//70%//U37373

50 C-THYRO1000852//Human branched-chain amino acid aminotransferase (ECA40) mRNA, complete cds.//1.40E-137//689bp//96%//U62739

C-THYRO1000926//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds.//0//2387bp//99%//AF079529

C-THYRO11000934//PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2) (P5CR) (P5C REDUCTASE).//  
7.50E-57//315aa/43%//P32322

C-THYRO1000951//DIHYDROXYACETONE KINASE 2 (EC 2.7.1.29) (GLYCERONE KINASE).//5.00E-83//  
566aa/37%//P43550

5 C-THYRO1000983//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (EC 6.3.2.19) (UBIQUITIN-PROTEIN  
LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B).//6.30E-17//143aa/39%//P35132

C-THYRO1001003//UBIQUITIN-CONJUGATING ENZYME E2-21.2 KD (EC 6.3.2.19) (UBIQUITIN-PROTEIN  
UGASE) (UBIQUITIN CARRIER PROTEIN).//5.90E-14//84aa/41%//P52491

C-THYRO1001033//TRANSFORMATION-SENSITIVE PROTEIN IEF SSP 3521.//8.40E-12//167aa/29%//P31948

10 C-THYRO1001100//ZINC FINGER X-UNKED PROTEIN ZXDA (FRAGMENT).//1.20E-67//245aa/62%//P98168

C-THYRO1001120//Homo sapiens deltex (Dx) mRNA, complete cds.//1.30E-110//1947bp//65%//AF053700

C-THYRO1001134//Homo sapiens CGI-78 protein mRNA, complete cds.//0//1898bp//99%//AF151835

C-THYRO1001189//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.10E-200//546aa//  
62%//Q05481

15 C-THYRO1001204//Homo sapiens cathepsin Z precursor (CTSZ) gene, exons 4, 5, and 6 and complete cds; and  
TH1 gene partial sequence.//3.80E-100//478bp//99%//AF136276

C-THYRO1001287//MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE (EC 3.2.1.113) (MAN(9)-  
ALPHA-MANNOSIDASE) (FRAGMENT).//3.40E-51//429aa/33%//P45701

C-THYRO1001313//Homo sapiens sorting nexin 11 (SNX11) mRNA, complete cds.//0//2330bp//94%//AF121861

20 C-THYRO1001347//Homo sapiens RAN binding protein 16 mRNA, complete cds.//2.00E-263//3101bp//68%//  
AF064729

C-THYRO1001374//CYTOSOLIC ACYL COENZYME A THIOESTER HYDROLASE (EC 3.1.2.2) (LONG CHAIN  
ACYL-COA THIOESTER HYDROLASE) (CTE-II).//1.80E-13//361aa/22%//O00154

C-THYRO1001405//PLECTIN.//6.90E-19//450aa/27%//P30427

25 C-THYRO1001406//PUTATIVE STEROID DEHYDROGENASE KIK-I (EC 1.1.1.-).//1.10E-131//219aa/81%//  
O70503

C-THYRO1001458//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN,  
TYPE B) (NMMHC-B).//2.70E-171//559aa/59%//P35580

C-THYRO1001617//Homo sapiens cDNA for dihydroxyacetone phosphate acyltransferase (DAP-AT).//0//1784bp//  
99%//AJ002190

30 C-THYRO1001656//Homo sapiens Leman coiled-coil protein (LCCP) mRNA, complete cds.//4.10E-273//1947bp//  
82%//AF175968

C-THYRO1001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59 kDa isoform.//0//1820bp//99%//  
AJ225089

35 C-THYRO1001703//NIFR3-LIKEPROTEIN.//2.90E-32//282aa/32%//P45672

C-THYRO1001721//RING CANAL PROTEIN (KELCH PROTEIN).//9.30E-34//220aa/38%//Q04652

C-THYRO1001738//TUBULIN--TYROSINE LIGASE (EC 6.3.2.25) (TTL).//2.40E-20//217aa/30%//P38584

C-THYRO1001809//MYOCYTE NUCLEAR FACTOR (MNF).//1.40E-74//158aa/89%//P42128

40 C-Y79AA1000013//Mus musculus RING finger protein A07 mRNA, complete cds.//8.90E-205//1435bp//81%//  
AF171060

C-Y79AA1000033//Homo sapiens CARD4 mRNA, complete cds.//0//2929bp//96%//AF126484

C-Y79AA1000037//DNA-BINDING PROTEIN BMI-1.//2.40E-30//80aa/60%//P25916

C-Y79AA1000059//Homo sapiens aryl-hydrocarbon interacting protein-like 1 (AIPL1) gene, complete cds.//0//  
980bp//96%//AF180472

45 C-Y79AA1000181//Homo sapiens CGI-01 protein mRNA, complete cds.//0//1858bp//99%//AF132936

C-Y79AA1000214//Homo sapiens histone H2A.F/Z variant (H2AV) mRNA, complete cds.//7.10E-71//345bp//  
100%//AF081192

C-Y79AA1000231//Homo sapiens nucleolar protein NOP5/NOP58 mRNA, complete cds.//0//1515bp//99%//  
AF123534

50 C-Y79AA1000268//Mus musculus Nip21 mRNA, complete cds.//2.10E-50//648bp//64%//AF035207

C-Y79AA1000313//CALPHOTIN.//0.000011//336aa/23%//Q02910

C-Y79AA1000328//SEL-10 PROTEIN.//0.00000067//219aa/25%//Q93794

C-Y79AA1000342//Homo sapiens Ciz1 mRNA, complete cds.//0//2644bp//81%//AB030835

55 C-Y79AA1000346//Homo sapiens nonclathrin coat protein gamma2-COP mRNA, complete cds.//0//2520bp//99%//  
AF157833

C-Y79AA1000349//M.musculus Spnr mRNA for RNA binding protein.//0//2048bp//93%//X84692

C-Y79AA1000368//REDUCED VIABILITY UPON STARVATION PROTEIN 161.//4.00E-20//261aa/27%//P25343

C-Y79AA1000469//Mus musculus ancient ubiquitous 46 kDa protein AUP1 precursor (Aup1) mRNA, complete

cds./.8.30E-252//1207bp//85%//U41736  
 C-Y79AA1000540//CELL POLARITY PROTEIN TEA1./.2.10E-12//211aa//33%//P87061  
 C-Y79AA1000560//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT)7/0//652aa//98%//P17427  
 C-Y79AA1000589//32.3 KD PROTEIN IN CWP1-MBR1 INTERGENIC REGION./.2.40E-27//216aa//34%//P28320  
 C-Y79AA1000627//Homo sapiens zinc finger protein (ZF5128) mRNA, complete cds./.2.00E-287//2031bp//82%//AF060503  
 C-Y79AA1000705//M.musculus mRNA of enhancer-trap-locus 1./.5.80E-254//1477bp//84%//X69942  
 C-Y79AA1000734//Homo sapiens peroxisomal biogenesis factor (PEX11b) mRNA, complete cds./.0//1594bp//99%//AF093670  
 C-Y79AA1000748//Rattus norvegicus clone C42 CDK5 activator-binding protein mRNA, complete cds./.6.60E-286//1832bp//84%//AF177477  
 C-Y79AA1000752//PUTATIVE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN X (HNRNP X) (CBP).//4.90E-91//200aa//64%//Q61990  
 C-Y79AA1000782//CYTOSOLIC PURINE 5'-NUCLEOTIDASE (EC 3.1.3.5).//3.00E-37//469aa//27%//P49902  
 C-Y79AA1000784//Homo sapiens RanBP7/importin 7 mRNA, complete cds./.1.10E-236//1076bp//99%//AF098799  
 C-Y79AA1000794//Homo sapiens actin-associated protein 2E4/kaptin (2E4) mRNA, 2E4-1 allele, complete cds./.0//1610bp//99%//AF105369  
 C-Y79AA1000800//Homo sapiens putative secreted protein (ZSIG11) mRNA, complete cds./.1.60E-284//1288bp//99%//AF072733  
 C-Y79AA1000833//TUBULIN ALPHA-1 CHAIN./.5.00E-173//220aa//79%//P05209  
 C-Y79AA1000962//MYOSIN HEAVY CHAIN, NON-MUSCLE (ZIPPER PROTEIN) (MYOSIN II)7/4.20E-17//430aa//27%//Q99323  
 C-Y79AA1000966//Homo sapiens COP9 complex subunit 4 mRNA, complete cds./.0//1586bp//99%//AF100757  
 C-Y79AA1000968//Rattus norvegicus initiation factor eIF-2B gamma subunit (eIF-2B gamma) mRNA, complete cds./.3.90E-248//1468bp//87%//U38253  
 C-Y79AA1000985//Human centrosomal protein kendrin mRNA, complete cds./.4.70E-151//985bp//87%//U52962  
 C-Y79AA1001048//ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (VLCAD).//3.10E-138//583aa//47%//P45953  
 C-Y79AA1001211//Homo sapiens origin recognition complex subunit 6 (ORC6) mRNA, complete cds./.0//1435bp//99%//AF139658  
 C-Y79AA1001233//ESTRADIOL 17 BETA-DEHYDROGENASE 1 (EC 1.1.1.62) (17-BETA-HSD 1) (17-BETA-HYDROXYSTEROID DEHYDROGENASE 1).//7.70E-50//228aa//42%//P51657  
 C-Y79AA1001236//Homo sapiens cell division protein mRNA, complete cds./.0//1612bp//99%//AF063015  
 C-Y79AA1001299//Homo sapiens mRNA for integrase interactor 1b protein (INI1B).//0//996bp//99%//AJ011738  
 C-Y79AA1001312//ZINC FINGER PROTEIN MLZ-4 (ZINC FINGER PROTEIN 46).//0.000000023//193aa//30%//Q03309  
 C-Y79AA1001323//Mus musculus mRNA for GSG1, complete cds./.3.30E-172//1171bp//83%//D87325  
 C-Y79AA1001384//Homo sapiens very large G-protein coupled receptor-1 (VLGR1) mRNA, complete cds./.0//4708bp//99%//AF055084  
 C-Y79AA1001391//HOMEobox PROTEIN HOX-A13 (HOX-1J).//1.20E-58//178aa//66%//P31271  
 C-Y79AA1001394//CELL DIVISION PROTEIN FTSH HOMOLOG (EC 3.4.24.-).//1.20E-13//230aa//32%//O83746  
 C-Y79AA1001402//Homo sapiens paraneoplastic cancer-testis-brain antigen (MA4) mRNA, partial cds./.8.50E-65//784bp//62%//AF083115  
 C-Y79AA1001493//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B).//3.80E-18//151aa//38%//P35132  
 C-Y79AA1001533//Mouse mRNA for RNA polymerase I associated factor (PAF53), complete cds./.4.50E-193//1333bp//80%//D14336  
 C-Y79AA1001548//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA (EC 2.7.1.67) (PI4-KINASE) (PTDINS-4-KINASE) (PI4K-ALPHA).//7.50E-76//85aa//90%//P42356  
 C-Y79AA1001581//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME).//1.90E-40//482aa//27%//P27550  
 C-Y79AA1001594//HYALURONAN-MEDIATED MOTILITY RECEPTOR (HYALURONIC ACID RECEPTOR).//2.50E-14//410aa//24%//Q00547  
 C-Y79AA1001603//POLYPEPTIDE N-ACETYLGLACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PROTEIN-UDP ACETYLGLACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N- ACETYLGLACTOS-

AMINYLTRANSFERASE) (GALNAC-T1).//1.70E-84//313aa//48%//Q07537  
 C-Y79AA1001613//ZINC FINGER PROTEIN 132.//3.80E-91//209aa//41%//P52740  
 C-Y79AA1001679//Homo sapiens lambda-crystallin mRNA, complete cds.//3.4e-310//1430bp//98%//AF077049  
 C-Y79AA1001692//Mus musculus strain C57BL/J germ cell-less protein (Gc1) mRNA, complete cds.//1.40E-78//  
 5 227aa//40%//Q01820  
 C-Y79AA1001705//Homo sapiens p53 regulated PA26-T2 nuclear protein (PA26) mRNA, complete cds.//3.40E-  
 47//626bp//68%//AF033120  
 C-Y79AA1001711//Human 60-kdal ribonucleoprotein (Ro) mRNA, complete cds.//1.20E-258//1185bp//99%//  
 J04137  
 10 C-Y79AA1001827//Homo sapiens mammalian inositol hexakisphosphate kinase 2 (IP6K2) mRNA, complete cds.//  
 0//1689bp//98%//AF177145  
 C-Y79AA1001866//Homo sapiens zinc finger protein ZNF180 (ZNF180) mRNA, complete cds.//0//2927bp//97%//  
 AF192913  
 15 C-Y79AA1001874//OX40L RECEPTOR PRECURSOR (ACT35 ANTIGEN) (TAX-TRANSCRIPTIONALLY ACTI-  
 VATED GLYCOPROTEIN 1 RECEPTOR) (CD134 ANTIGEN).//4.50E-08//135aa//31%//P43489  
 C-Y79AA1001875//RAS-RELATED PROTEIN RAB-7.//9.40E-12//34aa//97%//P51149  
 C-Y79AA1001923//Homo sapiens F-box protein Fbx22 (FBX22) gene, partial cds.//7.10E-52//279bp//97%//  
 AF174602  
 20 C-Y79AA1001963//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE  
 SPAC10F6.02C.//1.00E-10//94aa//47%//O42643  
 C-Y79AA1002027//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN  
 LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42).//9.90E-39//143aa//52%//P42743  
 C-Y79AA1002083//H.sapiens mRNA for MUF1 protein.//5.00E-163//752bp//99%//X86018  
 C-Y79AA1002103//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//3.00E-257//549aa//76%//P16415  
 25 C-Y79AA1002139//DNAJ PROTEIN HOMOLOG 1 (DROJ1).//9.00E-17//120aa//45%//Q24133  
 C-Y79AA1002204//COMPLEXIN 2 (SYNAPHIN 1) (921-L).//7.50E-09//131aa//35%//Q13329  
 C-Y79AA1002208//ANKYRIN.//8.10E-34//188aa//38%//Q02357  
 C-Y79AA1002209//TYROSYL-TRNA SYNTHETASE (EC 6.1.1.1) (TYROSINE--TRNA LIGASE) (TYRRS).//1.60E-  
 72//437aa//39%//P00952  
 30 C-Y79AA1002210//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PRO-  
 TEIN).//0.0000018//140aa//25%//Q13829  
 C-Y79AA1002211//PHOSPHATIDYLETHANOLAMINE-BINDING PROTEIN HOMOLOG F40A3.3.//1.70E-17//  
 146aa//35%//O16264  
 C-Y79AA1002229//DNA CROSS-LINK REPAIR PROTEIN PSO2/SNM1.//7.10E-17//213aa//31%//P30620  
 35 C-Y79AA1002246//SYNAPTOTAGMIN V.//1.60E-28//286aa//32%//O00445  
 C-Y79AA1002258//Homo sapiens mRNA for HIP1R, complete cds.//0//2106bp//99%//AB013384  
 C-Y79AA1002307//Homo sapiens astrotactin2 (ASTN2) mRNA, complete cds.//0//1209bp//99%//AF116574  
 C-Y79AA1002311//R.norvegicus mRNA for cytosolic resiniferatoxin-binding protein.//2.90E-186//1130bp//82%//  
 X67877  
 40 C-Y79AA1002361//Rattus norvegicus mRNA for protein phosphatase 1 (GL-subunit).//6.90E-140//966bp//82%//  
 Y18208  
 C-Y79AA1002399//Homo sapiens mRNA for sperm protein.//0//1163bp//95%//X91879  
 C-Y79AA1002416//Mus musculus CTP synthetase homolog (CTPsH) mRNA, complete cds.//3.9e-317//1902bp//  
 86%//U49385  
 45 C-Y79AA1002431//TRANSDUCIN-LIKE ENHANCER PROTEIN 2 (ESG2).//9.80E-62//318aa//35%//Q04725  
 C-Y79AA1002433//Homo sapiens chromatin- specific transcription elongation factor FACT 140 kDa subunit mR-  
 NA, complete cds.//0//1545bp//96%//AF152961  
 C-Y79AA1002472//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.50E-136//472aa//  
 49%//Q05481  
 50 C-Y79AA1002482//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.70E-137//340aa//  
 51%//Q05481  
 C-Y79AA1002487//Homo sapiens chromosome 5 F-box protein Fbx4 (FBX4) mRNA, complete cds.//7.3e-311//  
 1444bp//98%//AF129534

55

**Claims**

1. Use of an oligonucleotide as a primer for synthesizing the polynucleotide comprising the nucleotide sequence set

forth in any one of SEQ ID NOs: 1-5547 and SEQ ID NOs: 16111-16164, or the complementary strand thereof, wherein said oligonucleotide is complementary to said polynucleotide or the complementary strand thereof and comprises at least 15 nucleotides.

- 5 2. A primer set for synthesizing polynucleotides, the primer set comprising an oligo-dT primer and an oligonucleotide complementary to the complementary strand of the polynucleotide comprising the nucleotide sequence set forth in any one of SEQ ID NOs: 1-5547 and SEQ ID NOs: 16111-16164, wherein said oligonucleotide comprises at least 15 nucleotides.
- 10 3. A primer set for synthesizing polynucleotides, the primer set comprising a combination of an oligonucleotide comprising a nucleotide sequence complementary to the complementary strand of the polynucleotide comprising a 5'-end nucleotide sequence and an oligonucleotide comprising a nucleotide sequence complementary to the polynucleotide comprising a 3'-end nucleotide sequence, wherein said oligonucleotides comprise at least 15 nucleotides and wherein said combination of 5'-end nucleotide sequence 3'-end nucleotide sequence is selected from the group consisting of:
- 15

SEQ ID NO: 1 / SEQ ID NO: 5548, SEQ ID NO: 4 / SEQ ID NO: 5549, SEQ ID NO: 5 / SEQ —  
 ID NO: 5550, SEQ ID NO: 6 / SEQ ID NO: 5551, SEQ ID NO: 7 / SEQ ID NO: 5552, SEQ ID  
 20 NO: 8 / SEQ ID NO: 5553, SEQ ID NO: 9 / SEQ ID NO: 5554, SEQ ID NO: 10 / SEQ ID NO:  
 5555, SEQ ID NO: 11 / SEQ ID NO: 5556, SEQ ID NO: 12 / SEQ ID NO: 5557, SEQ ID NO: .  
 13 / SEQ ID NO: 5558, SEQ ID NO: 14 / SEQ ID NO: 5559, SEQ ID NO: 15 / SEQ ID NO:  
 5560, SEQ ID NO: 16 / SEQ ID NO: 5561, SEQ ID NO: 17 / SEQ ID NO: 5562, SEQ ID NO:  
 25 18 / SEQ ID NO: 5563, SEQ ID NO: 19 / SEQ ID NO: 5564, SEQ ID NO: 20 / SEQ ID NO:  
 5565, SEQ ID NO: 21 / SEQ ID NO: 5566, SEQ ID NO: 22 / SEQ ID NO: 5567, SEQ ID NO:  
 23 / SEQ ID NO: 5568, SEQ ID NO: 24 / SEQ ID NO: 5569, SEQ ID NO: 25 / SEQ ID NO:  
 5570, SEQ ID NO: 26 / SEQ ID NO: 5571, SEQ ID NO: 27 / SEQ ID NO: 5572, SEQ ID NO:  
 30 28 / SEQ ID NO: 5573, SEQ ID NO: 29 / SEQ ID NO: 5574, SEQ ID NO: 30 / SEQ ID NO:  
 5575, SEQ ID NO: 31 / SEQ ID NO: 5576, SEQ ID NO: 32 / SEQ ID NO: 5577, SEQ ID NO:  
 33 / SEQ ID NO: 5578, SEQ ID NO: 34 / SEQ ID NO: 5579, SEQ ID NO: 35 / SEQ ID NO:  
 5580, SEQ ID NO: 37 / SEQ ID NO: 5581, SEQ ID NO: 38 / SEQ ID NO: 5582, SEQ ID NO:  
 39 / SEQ ID NO: 5583, SEQ ID NO: 40 / SEQ ID NO: 5584, SEQ ID NO: 42 / SEQ ID NO:  
 35 5585, SEQ ID NO: 43 / SEQ ID NO: 5586, SEQ ID NO: 44 / SEQ ID NO: 5587, SEQ ID NO:  
 45 / SEQ ID NO: 5588, SEQ ID NO: 46 / SEQ ID NO: 5589, SEQ ID NO: 47 / SEQ ID NO:  
 5590, SEQ ID NO: 48 / SEQ ID NO: 5591, SEQ ID NO: 49 / SEQ ID NO: 5592, SEQ ID NO:  
 50 / SEQ ID NO: 5593, SEQ ID NO: 51 / SEQ ID NO: 5594, SEQ ID NO: 52 / SEQ ID NO:  
 5595, SEQ ID NO: 53 / SEQ ID NO: 5596, SEQ ID NO: 54 / SEQ ID NO: 5597, SEQ ID NO:  
 40 55 / SEQ ID NO: 5598, SEQ ID NO: 56 / SEQ ID NO: 5599, SEQ ID NO: 57 / SEQ ID NO:  
 5600, SEQ ID NO: 58 / SEQ ID NO: 5601, SEQ ID NO: 59 / SEQ ID NO: 5602, SEQ ID NO:  
 60 / SEQ ID NO: 5603, SEQ ID NO: 61 / SEQ ID NO: 5604, SEQ ID NO: 62 / SEQ ID NO:  
 5605, SEQ ID NO: 63 / SEQ ID NO: 5606, SEQ ID NO: 65 / SEQ ID NO: 5607, SEQ ID NO:  
 45 66 / SEQ ID NO: 5608, SEQ ID NO: 67 / SEQ ID NO: 5609, SEQ ID NO: 68 / SEQ ID NO:  
 5610, SEQ ID NO: 69 / SEQ ID NO: 5611, SEQ ID NO: 70 / SEQ ID NO: 5612, SEQ ID NO:  
 71 / SEQ ID NO: 5613, SEQ ID NO: 72 / SEQ ID NO: 5614, SEQ ID NO: 74 / SEQ ID NO:  
 5615, SEQ ID NO: 76 / SEQ ID NO: 5616, SEQ ID NO: 77 / SEQ ID NO: 5617, SEQ ID NO:  
 50 78 / SEQ ID NO: 5618, SEQ ID NO: 79 / SEQ ID NO: 5619, SEQ ID NO: 80 / SEQ ID NO:  
 5620, SEQ ID NO: 81 / SEQ ID NO: 5621, SEQ ID NO: 82 / SEQ ID NO: 5622, SEQ ID NO:  
 83 / SEQ ID NO: 5623, SEQ ID NO: 84 / SEQ ID NO: 5624, SEQ ID NO: 85 / SEQ ID NO:  
 5625, SEQ ID NO: 86 / SEQ ID NO: 5626, SEQ ID NO: 87 / SEQ ID NO: 5627, SEQ ID NO:  
 88 / SEQ ID NO: 5628, SEQ ID NO: 89 / SEQ ID NO: 5629, SEQ ID NO: 90 / SEQ ID NO:  
 55 5630, SEQ ID NO: 91 / SEQ ID NO: 5631, SEQ ID NO: 92 / SEQ ID NO: 5632, SEQ ID NO:







































NO: 2919 / SEQ ID NO: 7990, SEQ ID NO: 2920 / SEQ ID NO: 7991, SEQ ID NO: 2921 /  
 SEQ ID NO: 7992, SEQ ID NO: 2922 / SEQ ID NO: 7993, SEQ ID NO: 2923 / SEQ ID NO:  
 5 7994, SEQ ID NO: 2924 / SEQ ID NO: 7995, SEQ ID NO: 2925 / SEQ ID NO: 7996, SEQ ID  
 NO: 2927 / SEQ ID NO: 7997, SEQ ID NO: 2928 / SEQ ID NO: 7998, SEQ ID NO: 2929 /  
 SEQ ID NO: 7999, SEQ ID NO: 2930 / SEQ ID NO: 8000, SEQ ID NO: 2931 / SEQ ID NO:  
 10 8001, SEQ ID NO: 2932 / SEQ ID NO: 8002, SEQ ID NO: 2933 / SEQ ID NO: 8003, SEQ ID  
 NO: 2934 / SEQ ID NO: 8004, SEQ ID NO: 2935 / SEQ ID NO: 8005, SEQ ID NO: 2936 /  
 SEQ ID NO: 8006, SEQ ID NO: 2937 / SEQ ID NO: 8007, SEQ ID NO: 2938 / SEQ ID NO:  
 15 8008, SEQ ID NO: 2939 / SEQ ID NO: 8009, SEQ ID NO: 2941 / SEQ ID NO: 8010, SEQ ID  
 NO: 2942 / SEQ ID NO: 8011, SEQ ID NO: 2943 / SEQ ID NO: 8012, SEQ ID NO: 2944 /  
 SEQ ID NO: 8013, SEQ ID NO: 2945 / SEQ ID NO: 8014, SEQ ID NO: 2946 / SEQ ID NO:  
 20 8015, SEQ ID NO: 2947 / SEQ ID NO: 8016, SEQ ID NO: 2948 / SEQ ID NO: 8017, SEQ ID  
 NO: 2949 / SEQ ID NO: 8018, SEQ ID NO: 2950 / SEQ ID NO: 8019, SEQ ID NO: 2951 /  
 SEQ ID NO: 8020, SEQ ID NO: 2952 / SEQ ID NO: 8021, SEQ ID NO: 2953 / SEQ ID NO:  
 25 8022, SEQ ID NO: 2954 / SEQ ID NO: 8023, SEQ ID NO: 2955 / SEQ ID NO: 8024, SEQ ID  
 NO: 2956 / SEQ ID NO: 8025, SEQ ID NO: 2957 / SEQ ID NO: 8026, SEQ ID NO: 2958 /  
 SEQ ID NO: 8027, SEQ ID NO: 2959 / SEQ ID NO: 8028, SEQ ID NO: 2960 / SEQ ID NO:  
 30 8029, SEQ ID NO: 2961 / SEQ ID NO: 8030, SEQ ID NO: 2962 / SEQ ID NO: 8031, SEQ ID  
 NO: 2963 / SEQ ID NO: 8032, SEQ ID NO: 2964 / SEQ ID NO: 8033, SEQ ID NO: 2965 /  
 SEQ ID NO: 8034, SEQ ID NO: 2966 / SEQ ID NO: 8035, SEQ ID NO: 2967 / SEQ ID NO:  
 35 8036, SEQ ID NO: 2968 / SEQ ID NO: 8037, SEQ ID NO: 2969 / SEQ ID NO: 8038, SEQ ID  
 NO: 2970 / SEQ ID NO: 8039, SEQ ID NO: 2971 / SEQ ID NO: 8040, SEQ ID NO: 2972 /  
 SEQ ID NO: 8041, SEQ ID NO: 2973 / SEQ ID NO: 8042, SEQ ID NO: 2974 / SEQ ID NO:  
 40 8043, SEQ ID NO: 2975 / SEQ ID NO: 8044, SEQ ID NO: 2976 / SEQ ID NO: 8045, SEQ ID  
 NO: 2977 / SEQ ID NO: 8046, SEQ ID NO: 2978 / SEQ ID NO: 8047,  
 SEQ ID NO: 2979 / SEQ ID NO: 8048, SEQ ID NO: 2981 / SEQ ID NO: 8049, SEQ ID NO:  
 45 2982 / SEQ ID NO: 8050, SEQ ID NO: 2983 / SEQ ID NO: 8051, SEQ ID NO: 2984 / SEQ ID  
 NO: 8052, SEQ ID NO: 2985 / SEQ ID NO: 8053, SEQ ID NO: 2986 / SEQ ID NO: 8054, SEQ  
 ID NO: 2987 / SEQ ID NO: 8055, SEQ ID NO: 2988 / SEQ ID NO: 8056, SEQ ID NO: 2989 /  
 SEQ ID NO: 8057, SEQ ID NO: 2990 / SEQ ID NO: 8058, SEQ ID NO: 2991 / SEQ ID NO:  
 50 8059, SEQ ID NO: 2992 / SEQ ID NO: 8060, SEQ ID NO: 2993 / SEQ ID NO: 8061, SEQ ID  
 NO: 2994 / SEQ ID NO: 8062, SEQ ID NO: 2995 / SEQ ID NO: 8063, SEQ ID NO: 2996 /  
 SEQ ID NO: 8064, SEQ ID NO: 2997 / SEQ ID NO: 8065, SEQ ID NO: 2998 / SEQ ID NO:  
 55 8066, SEQ ID NO: 2999 / SEQ ID NO: 8067, SEQ ID NO: 3000 / SEQ ID NO: 8068, SEQ ID  
 NO: 3001 / SEQ ID NO: 8069, SEQ ID NO: 3002 / SEQ ID NO: 8070, SEQ ID NO: 3003 /  
 SEQ ID NO: 8071, SEQ ID NO: 3005 / SEQ ID NO: 8072, SEQ ID NO: 3006 / SEQ ID NO:  
 60 8073, SEQ ID NO: 3007 / SEQ ID NO: 8074, SEQ ID NO: 3008 / SEQ ID NO: 8075, SEQ ID  
 NO: 3009 / SEQ ID NO: 8076, SEQ ID NO: 3010 / SEQ ID NO: 8077, SEQ ID NO: 3011 /  
 SEQ ID NO: 8078, SEQ ID NO: 3012 / SEQ ID NO: 8079, SEQ ID NO: 3014 / SEQ ID NO:  
 65 8080, SEQ ID NO: 3015 / SEQ ID NO: 8081, SEQ ID NO: 3016 / SEQ ID NO: 8082, SEQ ID  
 NO: 3017 / SEQ ID NO: 8083, SEQ ID NO: 3018 / SEQ ID NO: 8084, SEQ ID NO: 3019 /  
 SEQ ID NO: 8085, SEQ ID NO: 3020 / SEQ ID NO: 8086, SEQ ID NO: 3021 / SEQ ID NO:  
 70 8087, SEQ ID NO: 3022 / SEQ ID NO: 8088, SEQ ID NO: 3023 / SEQ ID NO: 8089, SEQ ID  
 NO: 3024 / SEQ ID NO: 8090, SEQ ID NO: 3025 / SEQ ID NO: 8091, SEQ ID NO: 3026 /  
 SEQ ID NO: 8092, SEQ ID NO: 3027 / SEQ ID NO: 8093, SEQ ID NO: 3028 / SEQ ID NO:  
 75 8094, SEQ ID NO: 3030 / SEQ ID NO: 8095, SEQ ID NO: 3031 / SEQ ID NO: 8096, SEQ ID  
 NO: 3032 / SEQ ID NO: 8097, SEQ ID NO: 3033 / SEQ ID NO: 8098, SEQ ID NO: 3034 /  
 SEQ ID NO: 8099, SEQ ID NO: 3035 / SEQ ID NO: 8100, SEQ ID NO: 3036 / SEQ ID NO:  
 80 8101, SEQ ID NO: 3037 / SEQ ID NO: 8102, SEQ ID NO: 3038 / SEQ ID NO: 8103, SEQ ID  
 NO: 3039 / SEQ ID NO: 8104, SEQ ID NO: 3040 / SEQ ID NO: 8105, SEQ ID NO: 3041 /  
 SEQ ID NO: 8106, SEQ ID NO: 3042 / SEQ ID NO: 8107, SEQ ID NO: 3043 / SEQ ID NO:  
 85 8108, SEQ ID NO: 3044 / SEQ ID NO: 8109, SEQ ID NO: 3045 / SEQ ID NO: 8110, SEQ ID









8594, SEQ ID NO: 3557 / SEQ ID NO: 8595, SEQ ID NO: 3558 / SEQ ID NO: 8596, SEQ ID  
 NO: 3559 / SEQ ID NO: 8597, SEQ ID NO: 3560 / SEQ ID NO: 8598, SEQ ID NO: 3561 /  
 5 SEQ ID NO: 8599, SEQ ID NO: 3562 / SEQ ID NO: 8600, SEQ ID NO: 3563 / SEQ ID NO:  
 8601, SEQ ID NO: 3564 / SEQ ID NO: 8602, SEQ ID NO: 3565 / SEQ ID NO: 8603, SEQ ID  
 NO: 3566 / SEQ ID NO: 8604, SEQ ID NO: 3567 / SEQ ID NO: 8605, SEQ ID NO: 3568 /  
 SEQ ID NO: 8606, SEQ ID NO: 3569 / SEQ ID NO: 8607, SEQ ID NO: 3570 / SEQ ID NO:  
 10 8608, SEQ ID NO: 3571 / SEQ ID NO: 8609, SEQ ID NO: 3572 / SEQ ID NO: 8610, SEQ ID  
 NO: 3573 / SEQ ID NO: 8611, SEQ ID NO: 3574 / SEQ ID NO: 8612, SEQ ID NO: 3575 /  
 SEQ ID NO: 8613, SEQ ID NO: 3576 / SEQ ID NO: 8614, SEQ ID NO: 3577 / SEQ ID NO:  
 15 8615, SEQ ID NO: 3579 / SEQ ID NO: 8616, SEQ ID NO: 3580 / SEQ ID NO: 8617, SEQ ID  
 NO: 3581 / SEQ ID NO: 8618, SEQ ID NO: 3582 / SEQ ID NO: 8619, SEQ ID NO: 3583 /  
 SEQ ID NO: 8620, SEQ ID NO: 3584 / SEQ ID NO: 8621, SEQ ID NO: 3585 / SEQ ID NO:  
 20 8622, SEQ ID NO: 3586 / SEQ ID NO: 8623, SEQ ID NO: 3587 / SEQ ID NO: 8624, SEQ ID  
 NO: 3590 / SEQ ID NO: 8625, SEQ ID NO: 3591 / SEQ ID NO: 8626, SEQ ID NO: 3592 /  
 SEQ ID NO: 8627, SEQ ID NO: 3593 / SEQ ID NO: 8628, SEQ ID NO: 3594 / SEQ ID NO:  
 25 8629, SEQ ID NO: 3595 / SEQ ID NO: 8630, SEQ ID NO: 3596 / SEQ ID NO: 8631, SEQ ID  
 NO: 3597 / SEQ ID NO: 8632, SEQ ID NO: 3598 / SEQ ID NO: 8633, SEQ ID NO: 3599 /  
 SEQ ID NO: 8634, SEQ ID NO: 3600 / SEQ ID NO: 8635, SEQ ID NO: 3601 / SEQ ID NO:  
 30 8636, SEQ ID NO: 3602 / SEQ ID NO: 8637, SEQ ID NO: 3603 / SEQ ID NO: 8638, SEQ ID  
 NO: 3604 / SEQ ID NO: 8639, SEQ ID NO: 3605 / SEQ ID NO: 8640, SEQ ID NO: 3606 /  
 SEQ ID NO: 8641, SEQ ID NO: 3607 / SEQ ID NO: 8642, SEQ ID NO: 3608 / SEQ ID NO:  
 35 8643, SEQ ID NO: 3609 / SEQ ID NO: 8644, SEQ ID NO: 3610 / SEQ ID NO: 8645, SEQ ID  
 NO: 3611 / SEQ ID NO: 8646, SEQ ID NO: 3613 / SEQ ID NO: 8647,  
 SEQ ID NO: 3614 / SEQ ID NO: 8648, SEQ ID NO: 3615 / SEQ ID NO: 8649, SEQ ID NO:  
 40 3616 / SEQ ID NO: 8650, SEQ ID NO: 3617 / SEQ ID NO: 8651, SEQ ID NO: 3618 / SEQ ID  
 NO: 8652, SEQ ID NO: 3619 / SEQ ID NO: 8653, SEQ ID NO: 3620 / SEQ ID NO: 8654, SEQ  
 ID NO: 3622 / SEQ ID NO: 8655, SEQ ID NO: 3623 / SEQ ID NO: 8656, SEQ ID NO: 3624 /  
 45 SEQ ID NO: 8657, SEQ ID NO: 3625 / SEQ ID NO: 8658, SEQ ID NO: 3626 / SEQ ID NO:  
 50 8659, SEQ ID NO: 3627 / SEQ ID NO: 8660, SEQ ID NO: 3628 / SEQ ID NO: 8661, SEQ ID  
 NO: 3629 / SEQ ID NO: 8662, SEQ ID NO: 3630 / SEQ ID NO: 8663, SEQ ID NO: 3632 /  
 SEQ ID NO: 8664, SEQ ID NO: 3633 / SEQ ID NO: 8665, SEQ ID NO: 3634 / SEQ ID NO:  
 55 8666, SEQ ID NO: 3635 / SEQ ID NO: 8667, SEQ ID NO: 3636 / SEQ ID NO: 8668, SEQ ID  
 NO: 3637 / SEQ ID NO: 8669, SEQ ID NO: 3638 / SEQ ID NO: 8670, SEQ ID NO: 3639 /  
 SEQ ID NO: 8671, SEQ ID NO: 3640 / SEQ ID NO: 8672, SEQ ID NO: 3641 / SEQ ID NO:  
 60 8673, SEQ ID NO: 3642 / SEQ ID NO: 8674, SEQ ID NO: 3643 / SEQ ID NO: 8675, SEQ ID  
 NO: 3644 / SEQ ID NO: 8676, SEQ ID NO: 3645 / SEQ ID NO: 8677, SEQ ID NO: 3646 /  
 SEQ ID NO: 8678, SEQ ID NO: 3647 / SEQ ID NO: 8679, SEQ ID NO: 3648 / SEQ ID NO:  
 65 8680, SEQ ID NO: 3649 / SEQ ID NO: 8681, SEQ ID NO: 3650 / SEQ ID NO: 8682, SEQ ID  
 NO: 3651 / SEQ ID NO: 8683, SEQ ID NO: 3652 / SEQ ID NO: 8684, SEQ ID NO: 3653 /  
 SEQ ID NO: 8685, SEQ ID NO: 3654 / SEQ ID NO: 8686, SEQ ID NO: 3655 / SEQ ID NO:  
 70 8687, SEQ ID NO: 3656 / SEQ ID NO: 8688, SEQ ID NO: 3658 / SEQ ID NO: 8689, SEQ ID  
 NO: 3659 / SEQ ID NO: 8690, SEQ ID NO: 3660 / SEQ ID NO: 8691, SEQ ID NO: 3661 /  
 SEQ ID NO: 8692, SEQ ID NO: 3662 / SEQ ID NO: 8693, SEQ ID NO: 3663 / SEQ ID NO:  
 75 8694, SEQ ID NO: 3664 / SEQ ID NO: 8695, SEQ ID NO: 3665 / SEQ ID NO: 8696, SEQ ID  
 NO: 3666 / SEQ ID NO: 8697, SEQ ID NO: 3668 / SEQ ID NO: 8698, SEQ ID NO: 3669 /  
 SEQ ID NO: 8699, SEQ ID NO: 3670 / SEQ ID NO: 8700, SEQ ID NO: 3671 / SEQ ID NO:  
 80 8701, SEQ ID NO: 3672 / SEQ ID NO: 8702, SEQ ID NO: 3673 / SEQ ID NO: 8703, SEQ ID  
 NO: 3674 / SEQ ID NO: 8704, SEQ ID NO: 3675 / SEQ ID NO: 8705, SEQ ID NO: 3676 /  
 SEQ ID NO: 8706, SEQ ID NO: 3678 / SEQ ID NO: 8707, SEQ ID NO: 3679 / SEQ ID NO:  
 85 8708, SEQ ID NO: 3680 / SEQ ID NO: 8709, SEQ ID NO: 3681 / SEQ ID NO: 8710, SEQ ID  
 NO: 3682 / SEQ ID NO: 8711, SEQ ID NO: 3683 / SEQ ID NO: 8712, SEQ ID NO: 3685 /  
 90 8713, SEQ ID NO: 3686 / SEQ ID NO: 8714, SEQ ID NO: 3688 / SEQ ID NO:





SEQ ID NO: 8957, SEQ ID NO: 3957 / SEQ ID NO: 8958, SEQ ID NO: 3958 / SEQ ID NO:  
 5 SEQ ID NO: 8959, SEQ ID NO: 3959 / SEQ ID NO: 8960, SEQ ID NO: 3960 / SEQ ID NO: 8961, SEQ ID  
 NO: 3961 / SEQ ID NO: 8962, SEQ ID NO: 3962 / SEQ ID NO: 8963, SEQ ID NO: 3963 /  
 SEQ ID NO: 8964, SEQ ID NO: 3964 / SEQ ID NO: 8965, SEQ ID NO: 3966 / SEQ ID NO:  
 10 8966, SEQ ID NO: 3967 / SEQ ID NO: 8967, SEQ ID NO: 3968 / SEQ ID NO: 8968, SEQ ID  
 NO: 3969 / SEQ ID NO: 8969, SEQ ID NO: 3970 / SEQ ID NO: 8970, SEQ ID NO: 3972 /  
 SEQ ID NO: 8971, SEQ ID NO: 3973 / SEQ ID NO: 8972, SEQ ID NO: 3974 / SEQ ID NO:  
 15 8973, SEQ ID NO: 3975 / SEQ ID NO: 8974, SEQ ID NO: 3977 / SEQ ID NO: 8975, SEQ ID  
 NO: 3978 / SEQ ID NO: 8976, SEQ ID NO: 3979 / SEQ ID NO: 8977, SEQ ID NO: 3980 /  
 SEQ ID NO: 8978, SEQ ID NO: 3981 / SEQ ID NO: 8979, SEQ ID NO: 3983 / SEQ ID NO:  
 20 8980, SEQ ID NO: 3985 / SEQ ID NO: 8981, SEQ ID NO: 3986 / SEQ ID NO: 8982, SEQ ID  
 NO: 3987 / SEQ ID NO: 8983, SEQ ID NO: 3988 / SEQ ID NO: 8984, SEQ ID NO: 3989 /  
 SEQ ID NO: 8985, SEQ ID NO: 3990 / SEQ ID NO: 8986, SEQ ID NO: 3992 / SEQ ID NO:  
 25 8987, SEQ ID NO: 3993 / SEQ ID NO: 8988, SEQ ID NO: 3994 / SEQ ID NO: 8989, SEQ ID  
 NO: 3995 / SEQ ID NO: 8990, SEQ ID NO: 3996 / SEQ ID NO: 8991, SEQ ID NO: 3997 /  
 SEQ ID NO: 8992, SEQ ID NO: 3998 / SEQ ID NO: 8993, SEQ ID NO: 3999 / SEQ ID NO:  
 30 8994, SEQ ID NO: 4000 / SEQ ID NO: 8995, SEQ ID NO: 4001 / SEQ ID NO: 8996, SEQ ID  
 NO: 4002 / SEQ ID NO: 8997, SEQ ID NO: 4003 / SEQ ID NO: 8998, SEQ ID NO: 4004 /  
 SEQ ID NO: 8999, SEQ ID NO: 4005 / SEQ ID NO: 9000, SEQ ID NO: 4006 / SEQ ID NO:  
 35 9001, SEQ ID NO: 4007 / SEQ ID NO: 9002, SEQ ID NO: 4008 / SEQ ID NO: 9003, SEQ ID  
 NO: 4009 / SEQ ID NO: 9004, SEQ ID NO: 4010 / SEQ ID NO: 9005, SEQ ID NO: 4011 /  
 SEQ ID NO: 9006, SEQ ID NO: 4012 / SEQ ID NO: 9007, SEQ ID NO: 4013 / SEQ ID NO:  
 40 9008, SEQ ID NO: 4014 / SEQ ID NO: 9009, SEQ ID NO: 4015 / SEQ ID NO: 9010, SEQ ID  
 NO: 4016 / SEQ ID NO: 9011, SEQ ID NO: 4017 / SEQ ID NO: 9012, SEQ ID NO: 4018 /  
 SEQ ID NO: 9013, SEQ ID NO: 4019 / SEQ ID NO: 9014, SEQ ID NO: 4020 / SEQ ID NO:  
 45 9015, SEQ ID NO: 4021 / SEQ ID NO: 9016, SEQ ID NO: 4022 / SEQ ID NO: 9017, SEQ ID  
 NO: 4023 / SEQ ID NO: 9018, SEQ ID NO: 4024 / SEQ ID NO: 9019, SEQ ID NO: 4025 /  
 50 9020, SEQ ID NO: 4026 / SEQ ID NO: 9021, SEQ ID NO: 4028 / SEQ ID NO:  
 SEQ ID NO: 9022, SEQ ID NO: 4029 / SEQ ID NO: 9023, SEQ ID NO: 4030 / SEQ ID NO: 9024, SEQ ID  
 NO: 4031 / SEQ ID NO: 9025, SEQ ID NO: 4032 / SEQ ID NO: 9026, SEQ ID NO: 4033 /  
 55 9027, SEQ ID NO: 4034 / SEQ ID NO: 9028, SEQ ID NO: 4035 / SEQ ID NO:  
 SEQ ID NO: 9029, SEQ ID NO: 4036 / SEQ ID NO: 9030, SEQ ID NO: 4038 / SEQ ID NO: 9031, SEQ ID  
 NO: 4039 / SEQ ID NO: 9032, SEQ ID NO: 4040 / SEQ ID NO: 9033, SEQ ID NO: 4041 /  
 SEQ ID NO: 9034, SEQ ID NO: 4042 / SEQ ID NO: 9035, SEQ ID NO: 4043 / SEQ ID NO:  
 SEQ ID NO: 9036, SEQ ID NO: 4044 / SEQ ID NO: 9037, SEQ ID NO: 4045 / SEQ ID NO: 9038, SEQ ID  
 NO: 4046 / SEQ ID NO: 9039, SEQ ID NO: 4047 / SEQ ID NO: 9040, SEQ ID NO: 4048 /  
 SEQ ID NO: 9041, SEQ ID NO: 4050 / SEQ ID NO: 9042, SEQ ID NO: 4051 / SEQ ID NO:  
 SEQ ID NO: 9043, SEQ ID NO: 4052 / SEQ ID NO: 9044, SEQ ID NO: 4053 / SEQ ID NO: 9045, SEQ ID  
 NO: 4054 / SEQ ID NO: 9046, SEQ ID NO: 4055 / SEQ ID NO: 9047,  
 SEQ ID NO: 4056 / SEQ ID NO: 9048, SEQ ID NO: 4057 / SEQ ID NO: 9049, SEQ ID NO:  
 4058 / SEQ ID NO: 9050, SEQ ID NO: 4059 / SEQ ID NO: 9051, SEQ ID NO: 4060 / SEQ ID  
 NO: 9052, SEQ ID NO: 4061 / SEQ ID NO: 9053, SEQ ID NO: 4062 / SEQ ID NO: 9054, SEQ  
 ID NO: 4063 / SEQ ID NO: 9055, SEQ ID NO: 4064 / SEQ ID NO: 9056, SEQ ID NO: 4065 /  
 SEQ ID NO: 9057, SEQ ID NO: 4066 / SEQ ID NO: 9058, SEQ ID NO: 4067 / SEQ ID NO:  
 4059, SEQ ID NO: 4068 / SEQ ID NO: 9060, SEQ ID NO: 4069 / SEQ ID NO: 9061, SEQ ID  
 NO: 4070 / SEQ ID NO: 9062, SEQ ID NO: 4071 / SEQ ID NO: 9063, SEQ ID NO: 4072 /  
 SEQ ID NO: 9064, SEQ ID NO: 4073 / SEQ ID NO: 9065, SEQ ID NO: 4074 / SEQ ID NO:  
 4066, SEQ ID NO: 4075 / SEQ ID NO: 9067, SEQ ID NO: 4077 / SEQ ID NO: 9068, SEQ ID  
 NO: 4078 / SEQ ID NO: 9069, SEQ ID NO: 4079 / SEQ ID NO: 9070, SEQ ID NO: 4080 /  
 SEQ ID NO: 9071, SEQ ID NO: 4081 / SEQ ID NO: 9072, SEQ ID NO: 4082 / SEQ ID NO:  
 4073, SEQ ID NO: 4083 / SEQ ID NO: 9074, SEQ ID NO: 4084 / SEQ ID NO: 9075, SEQ ID  
 NO: 4085 / SEQ ID NO: 9076, SEQ ID NO: 4086 / SEQ ID NO: 9077, SEQ ID NO: 4087 /

SEQ ID NO: 9078, SEQ ID NO: 4088 / SEQ ID NO: 9079, SEQ ID NO: 4089 / SEQ ID NO:  
 5 SEQ ID NO: 9080, SEQ ID NO: 4090 / SEQ ID NO: 9081, SEQ ID NO: 4091 / SEQ ID NO: 9082, SEQ ID  
 NO: 4092 / SEQ ID NO: 9083, SEQ ID NO: 4093 / SEQ ID NO: 9084, SEQ ID NO: 4094 /  
 SEQ ID NO: 9085, SEQ ID NO: 4095 / SEQ ID NO: 9086, SEQ ID NO: 4096 / SEQ ID NO:  
 10 9087, SEQ ID NO: 4097 / SEQ ID NO: 9088, SEQ ID NO: 4098 / SEQ ID NO: 9089, SEQ ID  
 NO: 4099 / SEQ ID NO: 9090, SEQ ID NO: 4100 / SEQ ID NO: 9091, SEQ ID NO: 4101 /  
 SEQ ID NO: 9092, SEQ ID NO: 4102 / SEQ ID NO: 9093, SEQ ID NO: 4103 / SEQ ID NO:  
 15 9094, SEQ ID NO: 4104 / SEQ ID NO: 9095, SEQ ID NO: 4105 / SEQ ID NO: 9096, SEQ ID  
 NO: 4107 / SEQ ID NO: 9097, SEQ ID NO: 4108 / SEQ ID NO: 9098, SEQ ID NO: 4109 /  
 SEQ ID NO: 9099, SEQ ID NO: 4110 / SEQ ID NO: 9100, SEQ ID NO: 4111 / SEQ ID NO:  
 20 9101, SEQ ID NO: 4112 / SEQ ID NO: 9102, SEQ ID NO: 4113 / SEQ ID NO: 9103, SEQ ID  
 NO: 4114 / SEQ ID NO: 9104, SEQ ID NO: 4115 / SEQ ID NO: 9105, SEQ ID NO: 4116 /  
 SEQ ID NO: 9106, SEQ ID NO: 4117 / SEQ ID NO: 9107, SEQ ID NO: 4118 / SEQ ID NO:  
 25 9108, SEQ ID NO: 4119 / SEQ ID NO: 9109, SEQ ID NO: 4120 / SEQ ID NO: 9110, SEQ ID  
 NO: 4121 / SEQ ID NO: 9111, SEQ ID NO: 4122 / SEQ ID NO: 9112, SEQ ID NO: 4123 /  
 SEQ ID NO: 9113, SEQ ID NO: 4124 / SEQ ID NO: 9114, SEQ ID NO: 4125 / SEQ ID NO:  
 30 9115, SEQ ID NO: 4126 / SEQ ID NO: 9116, SEQ ID NO: 4127 / SEQ ID NO: 9117, SEQ ID  
 NO: 4128 / SEQ ID NO: 9118, SEQ ID NO: 4129 / SEQ ID NO: 9119, SEQ ID NO: 4130 /  
 SEQ ID NO: 9120, SEQ ID NO: 4132 / SEQ ID NO: 9121, SEQ ID NO: 4133 / SEQ ID NO:  
 35 9122, SEQ ID NO: 4134 / SEQ ID NO: 9123, SEQ ID NO: 4135 / SEQ ID NO: 9124, SEQ ID  
 NO: 4136 / SEQ ID NO: 9125, SEQ ID NO: 4137 / SEQ ID NO: 9126, SEQ ID NO: 4138 /  
 SEQ ID NO: 9127, SEQ ID NO: 4139 / SEQ ID NO: 9128, SEQ ID NO: 4140 / SEQ ID NO:  
 40 9129, SEQ ID NO: 4141 / SEQ ID NO: 9130, SEQ ID NO: 4142 / SEQ ID NO: 9131, SEQ ID  
 NO: 4143 / SEQ ID NO: 9132, SEQ ID NO: 4144 / SEQ ID NO: 9133, SEQ ID NO: 4145 /  
 SEQ ID NO: 9134, SEQ ID NO: 4146 / SEQ ID NO: 9135, SEQ ID NO: 4147 / SEQ ID NO:  
 45 9136, SEQ ID NO: 4148 / SEQ ID NO: 9137, SEQ ID NO: 4149 / SEQ ID NO: 9138, SEQ ID  
 NO: 4150 / SEQ ID NO: 9139, SEQ ID NO: 4151 / SEQ ID NO: 9140, SEQ ID NO: 4152 /  
 SEQ ID NO: 9141, SEQ ID NO: 4153 / SEQ ID NO: 9142, SEQ ID NO: 4154 / SEQ ID NO:  
 50 9143, SEQ ID NO: 4155 / SEQ ID NO: 9144, SEQ ID NO: 4157 / SEQ ID NO: 9145, SEQ ID  
 NO: 4158 / SEQ ID NO: 9146, SEQ ID NO: 4159 / SEQ ID NO: 9147,  
 SEQ ID NO: 4160 / SEQ ID NO: 9148, SEQ ID NO: 4161 / SEQ ID NO: 9149, SEQ ID NO:  
 55 4162 / SEQ ID NO: 9150, SEQ ID NO: 4164 / SEQ ID NO: 9151, SEQ ID NO: 4165 / SEQ ID  
 NO: 9152, SEQ ID NO: 4166 / SEQ ID NO: 9153, SEQ ID NO: 4167 / SEQ ID NO: 9154, SEQ  
 ID NO: 4168 / SEQ ID NO: 9155, SEQ ID NO: 4169 / SEQ ID NO: 9156, SEQ ID NO: 4170 /  
 SEQ ID NO: 9157, SEQ ID NO: 4171 / SEQ ID NO: 9158, SEQ ID NO: 4172 / SEQ ID NO:  
 60 9159, SEQ ID NO: 4173 / SEQ ID NO: 9160, SEQ ID NO: 4174 / SEQ ID NO: 9161, SEQ ID  
 NO: 4175 / SEQ ID NO: 9162, SEQ ID NO: 4176 / SEQ ID NO: 9163, SEQ ID NO: 4177 /  
 SEQ ID NO: 9164, SEQ ID NO: 4178 / SEQ ID NO: 9165, SEQ ID NO: 4179 / SEQ ID NO:  
 65 9166, SEQ ID NO: 4180 / SEQ ID NO: 9167, SEQ ID NO: 4181 / SEQ ID NO: 9168, SEQ ID  
 NO: 4182 / SEQ ID NO: 9169, SEQ ID NO: 4183 / SEQ ID NO: 9170, SEQ ID NO: 4184 /  
 SEQ ID NO: 9171, SEQ ID NO: 4185 / SEQ ID NO: 9172, SEQ ID NO: 4186 / SEQ ID NO:  
 70 9173, SEQ ID NO: 4187 / SEQ ID NO: 9174, SEQ ID NO: 4188 / SEQ ID NO: 9175, SEQ ID  
 NO: 4189 / SEQ ID NO: 9176, SEQ ID NO: 4190 / SEQ ID NO: 9177, SEQ ID NO: 4191 /  
 SEQ ID NO: 9178, SEQ ID NO: 4192 / SEQ ID NO: 9179, SEQ ID NO: 4193 / SEQ ID NO:  
 75 9180, SEQ ID NO: 4194 / SEQ ID NO: 9181, SEQ ID NO: 4195 / SEQ ID NO: 9182, SEQ ID  
 NO: 4196 / SEQ ID NO: 9183, SEQ ID NO: 4197 / SEQ ID NO: 9184, SEQ ID NO: 4198 /  
 SEQ ID NO: 9185, SEQ ID NO: 4199 / SEQ ID NO: 9186, SEQ ID NO: 4200 / SEQ ID NO:  
 80 9187, SEQ ID NO: 4201 / SEQ ID NO: 9188, SEQ ID NO: 4202 / SEQ ID NO: 9189, SEQ ID  
 NO: 4203 / SEQ ID NO: 9190, SEQ ID NO: 4204 / SEQ ID NO: 9191, SEQ ID NO: 4205 /  
 SEQ ID NO: 9192, SEQ ID NO: 4206 / SEQ ID NO: 9193, SEQ ID NO: 4208 / SEQ ID NO:  
 85 9194, SEQ ID NO: 4209 / SEQ ID NO: 9195, SEQ ID NO: 4210 / SEQ ID NO: 9196, SEQ ID  
 NO: 4211 / SEQ ID NO: 9197, SEQ ID NO: 4212 / SEQ ID NO: 9198, SEQ ID NO: 4213 /

SEQ ID NO: 9199, SEQ ID NO: 4214 / SEQ ID NO: 9200, SEQ ID NO: 4215 / SEQ ID NO:  
 9201, SEQ ID NO: 4216 / SEQ ID NO: 9202, SEQ ID NO: 4217 / SEQ ID NO: 9203, SEQ ID  
 5 NO: 4218 / SEQ ID NO: 9204, SEQ ID NO: 4219 / SEQ ID NO: 9205, SEQ ID NO: 4220 /  
 SEQ ID NO: 9206, SEQ ID NO: 4221 / SEQ ID NO: 9207, SEQ ID NO: 4222 / SEQ ID NO:  
 9208, SEQ ID NO: 4223 / SEQ ID NO: 9209, SEQ ID NO: 4224 / SEQ ID NO: 9210, SEQ ID  
 10 NO: 4225 / SEQ ID NO: 9211, SEQ ID NO: 4226 / SEQ ID NO: 9212, SEQ ID NO: 4227 /  
 SEQ ID NO: 9213, SEQ ID NO: 4228 / SEQ ID NO: 9214, SEQ ID NO: 4229 / SEQ ID NO:  
 15 9215, SEQ ID NO: 4231 / SEQ ID NO: 9216, SEQ ID NO: 4232 / SEQ ID NO: 9217, SEQ ID  
 NO: 4234 / SEQ ID NO: 9218, SEQ ID NO: 4235 / SEQ ID NO: 9219, SEQ ID NO: 4236 /  
 SEQ ID NO: 9220, SEQ ID NO: 4237 / SEQ ID NO: 9221, SEQ ID NO: 4238 / SEQ ID NO:  
 20 9222, SEQ ID NO: 4239 / SEQ ID NO: 9223, SEQ ID NO: 4240 / SEQ ID NO: 9224, SEQ ID  
 NO: 4241 / SEQ ID NO: 9225, SEQ ID NO: 4243 / SEQ ID NO: 9226, SEQ ID NO: 4244 /  
 SEQ ID NO: 9227, SEQ ID NO: 4245 / SEQ ID NO: 9228, SEQ ID NO: 4246 / SEQ ID NO:  
 25 9229, SEQ ID NO: 4247 / SEQ ID NO: 9230, SEQ ID NO: 4248 / SEQ ID NO: 9231, SEQ ID  
 NO: 4249 / SEQ ID NO: 9232, SEQ ID NO: 4250 / SEQ ID NO: 9233, SEQ ID NO: 4251 /  
 SEQ ID NO: 9234, SEQ ID NO: 4252 / SEQ ID NO: 9235, SEQ ID NO: 4253 / SEQ ID NO:  
 30 9236, SEQ ID NO: 4254 / SEQ ID NO: 9237, SEQ ID NO: 4256 / SEQ ID NO: 9238, SEQ ID  
 NO: 4257 / SEQ ID NO: 9239, SEQ ID NO: 4258 / SEQ ID NO: 9240, SEQ ID NO: 4259 /  
 SEQ ID NO: 9241, SEQ ID NO: 4260 / SEQ ID NO: 9242, SEQ ID NO: 4261 / SEQ ID NO:  
 35 9243, SEQ ID NO: 4262 / SEQ ID NO: 9244, SEQ ID NO: 4263 / SEQ ID NO: 9245, SEQ ID  
 NO: 4264 / SEQ ID NO: 9246, SEQ ID NO: 4265 / SEQ ID NO: 9247,  
 SEQ ID NO: 4266 / SEQ ID NO: 9248, SEQ ID NO: 4267 / SEQ ID NO: 9249, SEQ ID NO:  
 40 4268 / SEQ ID NO: 9250, SEQ ID NO: 4269 / SEQ ID NO: 9251, SEQ ID NO: 4270 / SEQ ID  
 NO: 9252, SEQ ID NO: 4271 / SEQ ID NO: 9253, SEQ ID NO: 4272 / SEQ ID NO: 9254, SEQ  
 ID NO: 4273 / SEQ ID NO: 9255, SEQ ID NO: 4274 / SEQ ID NO: 9256, SEQ ID NO: 4275 /  
 45 4276 / SEQ ID NO: 9258, SEQ ID NO: 4277 / SEQ ID NO:  
 50 9259, SEQ ID NO: 4278 / SEQ ID NO: 9260, SEQ ID NO: 4279 / SEQ ID NO: 9261, SEQ ID  
 NO: 4280 / SEQ ID NO: 9262, SEQ ID NO: 4281 / SEQ ID NO: 9263, SEQ ID NO: 4282 /  
 SEQ ID NO: 9264, SEQ ID NO: 4283 / SEQ ID NO: 9265, SEQ ID NO: 4284 / SEQ ID NO:  
 55 9266, SEQ ID NO: 4285 / SEQ ID NO: 9267, SEQ ID NO: 4286 / SEQ ID NO: 9268, SEQ ID  
 NO: 4288 / SEQ ID NO: 9269, SEQ ID NO: 4289 / SEQ ID NO: 9270, SEQ ID NO: 4290 /  
 SEQ ID NO: 9271, SEQ ID NO: 4291 / SEQ ID NO: 9272, SEQ ID NO: 4292 / SEQ ID NO:  
 60 9273, SEQ ID NO: 4293 / SEQ ID NO: 9274, SEQ ID NO: 4295 / SEQ ID NO: 9275, SEQ ID  
 NO: 4296 / SEQ ID NO: 9276, SEQ ID NO: 4297 / SEQ ID NO: 9277, SEQ ID NO: 4298 /  
 SEQ ID NO: 9278, SEQ ID NO: 4299 / SEQ ID NO: 9279, SEQ ID NO: 4300 / SEQ ID NO:  
 65 9280, SEQ ID NO: 4301 / SEQ ID NO: 9281, SEQ ID NO: 4302 / SEQ ID NO: 9282, SEQ ID  
 NO: 4303 / SEQ ID NO: 9283, SEQ ID NO: 4304 / SEQ ID NO: 9284, SEQ ID NO: 4305 /  
 70 4306 / SEQ ID NO: 9286, SEQ ID NO: 4307 / SEQ ID NO:  
 75 9287, SEQ ID NO: 4308 / SEQ ID NO: 9288, SEQ ID NO: 4309 / SEQ ID NO: 9289, SEQ ID  
 NO: 4310 / SEQ ID NO: 9290, SEQ ID NO: 4311 / SEQ ID NO: 9291, SEQ ID NO: 4312 /  
 80 4313 / SEQ ID NO: 9293, SEQ ID NO: 4314 / SEQ ID NO:  
 85 9294, SEQ ID NO: 4316 / SEQ ID NO: 9295, SEQ ID NO: 4317 / SEQ ID NO: 9296, SEQ ID  
 NO: 4318 / SEQ ID NO: 9297, SEQ ID NO: 4319 / SEQ ID NO: 9298, SEQ ID NO: 4320 /  
 90 4321 / SEQ ID NO: 9300, SEQ ID NO: 4322 / SEQ ID NO:  
 95 9301, SEQ ID NO: 4323 / SEQ ID NO: 9302, SEQ ID NO: 4324 / SEQ ID NO: 9303, SEQ ID  
 NO: 4325 / SEQ ID NO: 9304, SEQ ID NO: 4326 / SEQ ID NO: 9305, SEQ ID NO: 4327 /  
 100 4328 / SEQ ID NO: 9306, SEQ ID NO: 4329 / SEQ ID NO:  
 105 9308, SEQ ID NO: 4330 / SEQ ID NO: 9309, SEQ ID NO: 4331 / SEQ ID NO: 9310, SEQ ID  
 NO: 4332 / SEQ ID NO: 9311, SEQ ID NO: 4333 / SEQ ID NO: 9312, SEQ ID NO: 4334 /  
 110 4335 / SEQ ID NO: 9314, SEQ ID NO: 4336 / SEQ ID NO:  
 115 9315, SEQ ID NO: 4337 / SEQ ID NO: 9316, SEQ ID NO: 4338 / SEQ ID NO: 9317, SEQ ID  
 NO: 4339 / SEQ ID NO: 9318, SEQ ID NO: 4340 / SEQ ID NO: 9319, SEQ ID NO: 4341 /





NO: 4589 / SEQ ID NO: 9562, SEQ ID NO: 4590 / SEQ ID NO: 9563, SEQ ID NO: 4591 /  
 5 SEQ ID NO: 9564, SEQ ID NO: 4592 / SEQ ID NO: 9565, SEQ ID NO: 4593 / SEQ ID NO:  
 9566, SEQ ID NO: 4594 / SEQ ID NO: 9567, SEQ ID NO: 4595 / SEQ ID NO: 9568, SEQ ID  
 NO: 4596 / SEQ ID NO: 9569, SEQ ID NO: 4597 / SEQ ID NO: 9570, SEQ ID NO: 4598 /  
 SEQ ID NO: 9571, SEQ ID NO: 4599 / SEQ ID NO: 9572, SEQ ID NO: 4600 / SEQ ID NO:  
 10 9573, SEQ ID NO: 4601 / SEQ ID NO: 9574, SEQ ID NO: 4602 / SEQ ID NO: 9575, SEQ ID  
 NO: 4603 / SEQ ID NO: 9576, SEQ ID NO: 4604 / SEQ ID NO: 9577, SEQ ID NO: 4605 /  
 SEQ ID NO: 9578, SEQ ID NO: 4606 / SEQ ID NO: 9579, SEQ ID NO: 4607 / SEQ ID NO:  
 15 9580, SEQ ID NO: 4608 / SEQ ID NO: 9581, SEQ ID NO: 4609 / SEQ ID NO: 9582, SEQ ID  
 NO: 4610 / SEQ ID NO: 9583, SEQ ID NO: 4611 / SEQ ID NO: 9584, SEQ ID NO: 4612 /  
 SEQ ID NO: 9585, SEQ ID NO: 4613 / SEQ ID NO: 9586, SEQ ID NO: 4614 / SEQ ID NO:  
 20 9587, SEQ ID NO: 4615 / SEQ ID NO: 9588, SEQ ID NO: 4616 / SEQ ID NO: 9589, SEQ ID  
 NO: 4617 / SEQ ID NO: 9590, SEQ ID NO: 4618 / SEQ ID NO: 9591, SEQ ID NO: 4619 /  
 SEQ ID NO: 9592, SEQ ID NO: 4621 / SEQ ID NO: 9593, SEQ ID NO: 4622 / SEQ ID NO:  
 25 9594, SEQ ID NO: 4623 / SEQ ID NO: 9595, SEQ ID NO: 4624 / SEQ ID NO: 9596, SEQ ID  
 NO: 4625 / SEQ ID NO: 9597, SEQ ID NO: 4626 / SEQ ID NO: 9598, SEQ ID NO: 4627 /  
 SEQ ID NO: 9599, SEQ ID NO: 4628 / SEQ ID NO: 9600, SEQ ID NO: 4629 / SEQ ID NO:  
 30 9601, SEQ ID NO: 4630 / SEQ ID NO: 9602, SEQ ID NO: 4631 / SEQ ID NO: 9603, SEQ ID  
 NO: 4632 / SEQ ID NO: 9604, SEQ ID NO: 4633 / SEQ ID NO: 9605, SEQ ID NO: 4634 /  
 SEQ ID NO: 9606, SEQ ID NO: 4635 / SEQ ID NO: 9607, SEQ ID NO: 4636 / SEQ ID NO:  
 35 9608, SEQ ID NO: 4637 / SEQ ID NO: 9609, SEQ ID NO: 4638 / SEQ ID NO: 9610, SEQ ID  
 NO: 4639 / SEQ ID NO: 9611, SEQ ID NO: 4640 / SEQ ID NO: 9612, SEQ ID NO: 4641 /  
 SEQ ID NO: 9613, SEQ ID NO: 4642 / SEQ ID NO: 9614, SEQ ID NO: 4643 / SEQ ID NO:  
 40 9615, SEQ ID NO: 4644 / SEQ ID NO: 9616, SEQ ID NO: 4645 / SEQ ID NO: 9617, SEQ ID  
 NO: 4646 / SEQ ID NO: 9618, SEQ ID NO: 4647 / SEQ ID NO: 9619, SEQ ID NO: 4648 /  
 SEQ ID NO: 9620, SEQ ID NO: 4649 / SEQ ID NO: 9621, SEQ ID NO: 4650 / SEQ ID NO:  
 45 9622, SEQ ID NO: 4651 / SEQ ID NO: 9623, SEQ ID NO: 4652 / SEQ ID NO: 9624, SEQ ID  
 NO: 4653 / SEQ ID NO: 9625, SEQ ID NO: 4654 / SEQ ID NO: 9626, SEQ ID NO: 4655 /  
 SEQ ID NO: 9627, SEQ ID NO: 4656 / SEQ ID NO: 9628, SEQ ID NO: 4657 / SEQ ID NO:  
 50 9629, SEQ ID NO: 4659 / SEQ ID NO: 9630, SEQ ID NO: 4660 / SEQ ID NO: 9631, SEQ ID  
 NO: 4661 / SEQ ID NO: 9632, SEQ ID NO: 4662 / SEQ ID NO: 9633, SEQ ID NO: 4663 /  
 SEQ ID NO: 9634, SEQ ID NO: 4664 / SEQ ID NO: 9635, SEQ ID NO: 4665 / SEQ ID NO:  
 55 9636, SEQ ID NO: 4666 / SEQ ID NO: 9637, SEQ ID NO: 4667 / SEQ ID NO: 9638, SEQ ID  
 NO: 4669 / SEQ ID NO: 9639, SEQ ID NO: 4670 / SEQ ID NO: 9640, SEQ ID NO: 4671 /  
 SEQ ID NO: 9641, SEQ ID NO: 4672 / SEQ ID NO: 9642, SEQ ID NO: 4673 / SEQ ID NO:  
 60 9643, SEQ ID NO: 4674 / SEQ ID NO: 9644, SEQ ID NO: 4675 / SEQ ID NO: 9645, SEQ ID  
 NO: 4676 / SEQ ID NO: 9646, SEQ ID NO: 4677 / SEQ ID NO: 9647,  
 SEQ ID NO: 4678 / SEQ ID NO: 9648, SEQ ID NO: 4679 / SEQ ID NO: 9649, SEQ ID NO:  
 65 4680 / SEQ ID NO: 9650, SEQ ID NO: 4681 / SEQ ID NO: 9651, SEQ ID NO: 4682 / SEQ ID  
 NO: 9652, SEQ ID NO: 4683 / SEQ ID NO: 9653, SEQ ID NO: 4684 / SEQ ID NO: 9654, SEQ  
 ID NO: 4685 / SEQ ID NO: 9655, SEQ ID NO: 4686 / SEQ ID NO: 9656, SEQ ID NO: 4687 /  
 70 SEQ ID NO: 9657, SEQ ID NO: 4688 / SEQ ID NO: 9658, SEQ ID NO: 4689 / SEQ ID NO:  
 75 9659, SEQ ID NO: 4690 / SEQ ID NO: 9660, SEQ ID NO: 4691 / SEQ ID NO: 9661, SEQ ID  
 NO: 4692 / SEQ ID NO: 9662, SEQ ID NO: 4693 / SEQ ID NO: 9663, SEQ ID NO: 4694 /  
 SEQ ID NO: 9664, SEQ ID NO: 4695 / SEQ ID NO: 9665, SEQ ID NO: 4696 / SEQ ID NO:  
 80 9666, SEQ ID NO: 4697 / SEQ ID NO: 9667, SEQ ID NO: 4699 / SEQ ID NO: 9668, SEQ ID  
 NO: 4700 / SEQ ID NO: 9669, SEQ ID NO: 4701 / SEQ ID NO: 9670, SEQ ID NO: 4702 /  
 SEQ ID NO: 9671, SEQ ID NO: 4703 / SEQ ID NO: 9672, SEQ ID NO: 4704 / SEQ ID NO:  
 85 9673, SEQ ID NO: 4705 / SEQ ID NO: 9674, SEQ ID NO: 4706 / SEQ ID NO: 9675, SEQ ID  
 NO: 4708 / SEQ ID NO: 9676, SEQ ID NO: 4709 / SEQ ID NO: 9677, SEQ ID NO: 4710 /  
 SEQ ID NO: 9678, SEQ ID NO: 4711 / SEQ ID NO: 9679, SEQ ID NO: 4712 / SEQ ID NO:  
 90 9680, SEQ ID NO: 4713 / SEQ ID NO: 9681, SEQ ID NO: 4714 / SEQ ID NO: 9682, SEQ ID



NO: 4839 / SEQ ID NO: 9804, SEQ ID NO: 4840 / SEQ ID NO: 9805, SEQ ID NO: 4841 /  
 SEQ ID NO: 9806, SEQ ID NO: 4842 / SEQ ID NO: 9807, SEQ ID NO: 4843 / SEQ ID NO:  
 5 9808, SEQ ID NO: 4844 / SEQ ID NO: 9809, SEQ ID NO: 4845 / SEQ ID NO: 9810, SEQ ID  
 NO: 4846 / SEQ ID NO: 9811, SEQ ID NO: 4847 / SEQ ID NO: 9812, SEQ ID NO: 4848 /  
 SEQ ID NO: 9813, SEQ ID NO: 4849 / SEQ ID NO: 9814, SEQ ID NO: 4851 / SEQ ID NO:  
 10 9815, SEQ ID NO: 4852 / SEQ ID NO: 9816, SEQ ID NO: 4853 / SEQ ID NO: 9817, SEQ ID  
 NO: 4854 / SEQ ID NO: 9818, SEQ ID NO: 4855 / SEQ ID NO: 9819, SEQ ID NO: 4856 /  
 SEQ ID NO: 9820, SEQ ID NO: 4857 / SEQ ID NO: 9821, SEQ ID NO: 4858 / SEQ ID NO:  
 15 9822, SEQ ID NO: 4859 / SEQ ID NO: 9823, SEQ ID NO: 4860 / SEQ ID NO: 9824, SEQ ID  
 NO: 4861 / SEQ ID NO: 9825, SEQ ID NO: 4862 / SEQ ID NO: 9826, SEQ ID NO: 4863 /  
 SEQ ID NO: 9827, SEQ ID NO: 4864 / SEQ ID NO: 9828, SEQ ID NO: 4865 / SEQ ID NO:  
 20 9829, SEQ ID NO: 4867 / SEQ ID NO: 9830, SEQ ID NO: 4868 / SEQ ID NO: 9831, SEQ ID  
 NO: 4869 / SEQ ID NO: 9832, SEQ ID NO: 4870 / SEQ ID NO: 9833, SEQ ID NO: 4871 /  
 25 SEQ ID NO: 9834, SEQ ID NO: 4872 / SEQ ID NO: 9835, SEQ ID NO: 4873 / SEQ ID NO:  
 9836, SEQ ID NO: 4874 / SEQ ID NO: 9837, SEQ ID NO: 4875 / SEQ ID NO: 9838, SEQ ID  
 NO: 4876 / SEQ ID NO: 9839, SEQ ID NO: 4877 / SEQ ID NO: 9840, SEQ ID NO: 4878 /  
 SEQ ID NO: 9841, SEQ ID NO: 4879 / SEQ ID NO: 9842, SEQ ID NO: 4880 / SEQ ID NO:  
 30 9843, SEQ ID NO: 4881 / SEQ ID NO: 9844, SEQ ID NO: 4882 / SEQ ID NO: 9845, SEQ ID  
 NO: 4883 / SEQ ID NO: 9846, SEQ ID NO: 4884 / SEQ ID NO: 9847,  
 SEQ ID NO: 4885 / SEQ ID NO: 9848, SEQ ID NO: 4886 / SEQ ID NO: 9849, SEQ ID NO:  
 35 4887 / SEQ ID NO: 9850, SEQ ID NO: 4888 / SEQ ID NO: 9851, SEQ ID NO: 4889 / SEQ ID  
 NO: 9852, SEQ ID NO: 4890 / SEQ ID NO: 9853, SEQ ID NO: 4891 / SEQ ID NO: 9854, SEQ  
 ID NO: 4892 / SEQ ID NO: 9855, SEQ ID NO: 4894 / SEQ ID NO: 9856, SEQ ID NO: 4895 /  
 40 SEQ ID NO: 9857, SEQ ID NO: 4896 / SEQ ID NO: 9858, SEQ ID NO: 4897 / SEQ ID NO:  
 45 9859, SEQ ID NO: 4898 / SEQ ID NO: 9860, SEQ ID NO: 4899 / SEQ ID NO: 9861, SEQ ID  
 NO: 4900 / SEQ ID NO: 9862, SEQ ID NO: 4901 / SEQ ID NO: 9863, SEQ ID NO: 4902 /  
 SEQ ID NO: 9864, SEQ ID NO: 4903 / SEQ ID NO: 9865, SEQ ID NO: 4904 / SEQ ID NO:  
 50 9866, SEQ ID NO: 4905 / SEQ ID NO: 9867, SEQ ID NO: 4906 / SEQ ID NO: 9868, SEQ ID  
 NO: 4907 / SEQ ID NO: 9869, SEQ ID NO: 4908 / SEQ ID NO: 9870, SEQ ID NO: 4909 /  
 55 SEQ ID NO: 9871, SEQ ID NO: 4910 / SEQ ID NO: 9872, SEQ ID NO: 4911 / SEQ ID NO:  
 9873, SEQ ID NO: 4912 / SEQ ID NO: 9874, SEQ ID NO: 4913 / SEQ ID NO: 9875, SEQ ID  
 NO: 4914 / SEQ ID NO: 9876, SEQ ID NO: 4915 / SEQ ID NO: 9877, SEQ ID NO: 4916 /  
 SEQ ID NO: 9878, SEQ ID NO: 4917 / SEQ ID NO: 9879, SEQ ID NO: 4918 / SEQ ID NO:  
 60 9880, SEQ ID NO: 4919 / SEQ ID NO: 9881, SEQ ID NO: 4920 / SEQ ID NO: 9882, SEQ ID  
 NO: 4921 / SEQ ID NO: 9883, SEQ ID NO: 4922 / SEQ ID NO: 9884, SEQ ID NO: 4923 /  
 SEQ ID NO: 9885, SEQ ID NO: 4924 / SEQ ID NO: 9886, SEQ ID NO: 4925 / SEQ ID NO:  
 65 9887, SEQ ID NO: 4926 / SEQ ID NO: 9888, SEQ ID NO: 4927 / SEQ ID NO: 9889, SEQ ID  
 NO: 4928 / SEQ ID NO: 9890, SEQ ID NO: 4929 / SEQ ID NO: 9891, SEQ ID NO: 4931 /  
 SEQ ID NO: 9892, SEQ ID NO: 4932 / SEQ ID NO: 9893, SEQ ID NO: 4933 / SEQ ID NO:  
 70 9894, SEQ ID NO: 4934 / SEQ ID NO: 9895, SEQ ID NO: 4935 / SEQ ID NO: 9896, SEQ ID  
 NO: 4936 / SEQ ID NO: 9897, SEQ ID NO: 4937 / SEQ ID NO: 9898, SEQ ID NO: 4938 /  
 SEQ ID NO: 9899, SEQ ID NO: 4939 / SEQ ID NO: 9900, SEQ ID NO: 4940 / SEQ ID NO:  
 75 9901, SEQ ID NO: 4941 / SEQ ID NO: 9902, SEQ ID NO: 4942 / SEQ ID NO: 9903, SEQ ID  
 NO: 4944 / SEQ ID NO: 9904, SEQ ID NO: 4945 / SEQ ID NO: 9905, SEQ ID NO: 4946 /  
 SEQ ID NO: 9906, SEQ ID NO: 4947 / SEQ ID NO: 9907, SEQ ID NO: 4948 / SEQ ID NO:  
 80 9908, SEQ ID NO: 4949 / SEQ ID NO: 9909, SEQ ID NO: 4950 / SEQ ID NO: 9910, SEQ ID  
 NO: 4951 / SEQ ID NO: 9911, SEQ ID NO: 4952 / SEQ ID NO: 9912, SEQ ID NO: 4953 /  
 SEQ ID NO: 9913, SEQ ID NO: 4954 / SEQ ID NO: 9914, SEQ ID NO: 4955 / SEQ ID NO:  
 85 9915, SEQ ID NO: 4956 / SEQ ID NO: 9916, SEQ ID NO: 4957 / SEQ ID NO: 9917, SEQ ID  
 NO: 4958 / SEQ ID NO: 9918, SEQ ID NO: 4959 / SEQ ID NO: 9919, SEQ ID NO: 4960 /  
 SEQ ID NO: 9920, SEQ ID NO: 4961 / SEQ ID NO: 9921, SEQ ID NO: 4962 / SEQ ID NO:  
 90 9922, SEQ ID NO: 4963 / SEQ ID NO: 9923, SEQ ID NO: 4964 / SEQ ID NO: 9924, SEQ ID

NO: 4965 / SEQ ID NO: 9925, SEQ ID NO: 4966 / SEQ ID NO: 9926, SEQ ID NO: 4967 /  
 SEQ ID NO: 9927, SEQ ID NO: 4968 / SEQ ID NO: 9928, SEQ ID NO: 4969 / SEQ ID NO:  
 5 9929, SEQ ID NO: 4970 / SEQ ID NO: 9930, SEQ ID NO: 4971 / SEQ ID NO: 9931, SEQ ID  
 NO: 4972 / SEQ ID NO: 9932, SEQ ID NO: 4973 / SEQ ID NO: 9933, SEQ ID NO: 4974 /  
 SEQ ID NO: 9934, SEQ ID NO: 4975 / SEQ ID NO: 9935, SEQ ID NO: 4976 / SEQ ID NO:  
 10 9936, SEQ ID NO: 4977 / SEQ ID NO: 9937, SEQ ID NO: 4978 / SEQ ID NO: 9938, SEQ ID  
 NO: 4979 / SEQ ID NO: 9939, SEQ ID NO: 4980 / SEQ ID NO: 9940, SEQ ID NO: 4981 /  
 SEQ ID NO: 9941, SEQ ID NO: 4982 / SEQ ID NO: 9942, SEQ ID NO: 4983 / SEQ ID NO:  
 15 9943, SEQ ID NO: 4984 / SEQ ID NO: 9944, SEQ ID NO: 4985 / SEQ ID NO: 9945, SEQ ID  
 NO: 4986 / SEQ ID NO: 9946, SEQ ID NO: 4987 / SEQ ID NO: 9947,  
 SEQ ID NO: 4988 / SEQ ID NO: 9948, SEQ ID NO: 4989 / SEQ ID NO: 9949, SEQ ID NO:  
 20 4990 / SEQ ID NO: 9950, SEQ ID NO: 4991 / SEQ ID NO: 9951, SEQ ID NO: 4992 / SEQ ID  
 NO: 9952, SEQ ID NO: 4993 / SEQ ID NO: 9953, SEQ ID NO: 4994 / SEQ ID NO: 9954, SEQ  
 ID NO: 4995 / SEQ ID NO: 9955, SEQ ID NO: 4996 / SEQ ID NO: 9956, SEQ ID NO: 4997 /  
 25 9957, SEQ ID NO: 4998 / SEQ ID NO: 9958, SEQ ID NO: 4999 / SEQ ID NO:  
 9959, SEQ ID NO: 5000 / SEQ ID NO: 9960, SEQ ID NO: 5001 / SEQ ID NO: 9961, SEQ ID  
 NO: 5002 / SEQ ID NO: 9962, SEQ ID NO: 5004 / SEQ ID NO: 9963, SEQ ID NO: 5005 /  
 30 9964, SEQ ID NO: 5006 / SEQ ID NO: 9965, SEQ ID NO: 5007 / SEQ ID NO:  
 9966, SEQ ID NO: 5008 / SEQ ID NO: 9967, SEQ ID NO: 5009 / SEQ ID NO: 9968, SEQ ID  
 NO: 5010 / SEQ ID NO: 9969, SEQ ID NO: 5011 / SEQ ID NO: 9970, SEQ ID NO: 5012 /  
 SEQ ID NO: 9971, SEQ ID NO: 5013 / SEQ ID NO: 9972, SEQ ID NO: 5014 / SEQ ID NO:  
 35 9973, SEQ ID NO: 5016 / SEQ ID NO: 9974, SEQ ID NO: 5017 / SEQ ID NO: 9975, SEQ ID  
 NO: 5018 / SEQ ID NO: 9976, SEQ ID NO: 5019 / SEQ ID NO: 9977, SEQ ID NO: 5020 /  
 40 9978, SEQ ID NO: 5021 / SEQ ID NO: 9979, SEQ ID NO: 5022 / SEQ ID NO:  
 9980, SEQ ID NO: 5024 / SEQ ID NO: 9981, SEQ ID NO: 5025 / SEQ ID NO: 9982, SEQ ID  
 NO: 5026 / SEQ ID NO: 9983, SEQ ID NO: 5027 / SEQ ID NO: 9984, SEQ ID NO: 5028 /  
 45 9985, SEQ ID NO: 5029 / SEQ ID NO: 9986, SEQ ID NO: 5030 / SEQ ID NO:  
 9987, SEQ ID NO: 5031 / SEQ ID NO: 9988, SEQ ID NO: 5032 / SEQ ID NO: 9989, SEQ ID  
 NO: 5033 / SEQ ID NO: 9990, SEQ ID NO: 5035 / SEQ ID NO: 9991, SEQ ID NO: 5036 /  
 50 9992, SEQ ID NO: 5037 / SEQ ID NO: 9993, SEQ ID NO: 5038 / SEQ ID NO:  
 9994, SEQ ID NO: 5039 / SEQ ID NO: 9995, SEQ ID NO: 5040 / SEQ ID NO: 9996, SEQ ID  
 NO: 5041 / SEQ ID NO: 9997, SEQ ID NO: 5042 / SEQ ID NO: 9998, SEQ ID NO: 5043 /  
 55 9999, SEQ ID NO: 5044 / SEQ ID NO: 10000, SEQ ID NO: 5045 / SEQ ID NO:  
 10001, SEQ ID NO: 5046 / SEQ ID NO: 10002, SEQ ID NO: 5047 / SEQ ID NO: 10003, SEQ  
 ID NO: 5048 / SEQ ID NO: 10004, SEQ ID NO: 5049 / SEQ ID NO: 10005, SEQ ID NO: 5050  
 / SEQ ID NO: 10006, SEQ ID NO: 5051 / SEQ ID NO: 10007, SEQ ID NO: 5052 / SEQ ID  
 NO: 10008, SEQ ID NO: 5053 / SEQ ID NO: 10009, SEQ ID NO: 5054 / SEQ ID NO: 10010,  
 SEQ ID NO: 5055 / SEQ ID NO: 10011, SEQ ID NO: 5056 / SEQ ID NO: 10012, SEQ ID NO:  
 60 5057 / SEQ ID NO: 10013, SEQ ID NO: 5058 / SEQ ID NO: 10014, SEQ ID NO: 5059 / SEQ  
 ID NO: 10015, SEQ ID NO: 5061 / SEQ ID NO: 10016, SEQ ID NO: 5062 / SEQ ID NO:  
 65 10017, SEQ ID NO: 5064 / SEQ ID NO: 10018, SEQ ID NO: 5065 / SEQ ID NO: 10019, SEQ  
 ID NO: 5066 / SEQ ID NO: 10020, SEQ ID NO: 5068 / SEQ ID NO: 10021, SEQ ID NO: 5069  
 / SEQ ID NO: 10022, SEQ ID NO: 5070 / SEQ ID NO: 10023, SEQ ID NO: 5071 / SEQ ID  
 NO: 10024, SEQ ID NO: 5072 / SEQ ID NO: 10025, SEQ ID NO: 5073 / SEQ ID NO: 10026,  
 70 SEQ ID NO: 5074 / SEQ ID NO: 10027, SEQ ID NO: 5075 / SEQ ID NO: 10028, SEQ ID NO:  
 75 5076 / SEQ ID NO: 10029, SEQ ID NO: 5077 / SEQ ID NO: 10030, SEQ ID NO: 5078 / SEQ  
 ID NO: 10031, SEQ ID NO: 5079 / SEQ ID NO: 10032, SEQ ID NO: 5080 / SEQ ID NO:  
 80 10033, SEQ ID NO: 5082 / SEQ ID NO: 10034, SEQ ID NO: 5083 / SEQ ID NO: 10035, SEQ  
 ID NO: 5084 / SEQ ID NO: 10036, SEQ ID NO: 5085 / SEQ ID NO: 10037, SEQ ID NO: 5086  
 / SEQ ID NO: 10038, SEQ ID NO: 5087 / SEQ ID NO: 10039, SEQ ID NO: 5088 / SEQ ID  
 NO: 10040, SEQ ID NO: 5089 / SEQ ID NO: 10041, SEQ ID NO: 5090 / SEQ ID NO: 10042,  
 85 SEQ ID NO: 5091 / SEQ ID NO: 10043, SEQ ID NO: 5092 / SEQ ID NO: 10044, SEQ ID NO:  
 90

5093 / SEQ ID NO: 10045, SEQ ID NO: 5094 / SEQ ID NO: 10046, SEQ ID NO: 5095 / SEQ  
 ID NO: 10047,  
 SEQ ID NO: 5096 / SEQ ID NO: 10048, SEQ ID NO: 5097 / SEQ ID NO: 10049, SEQ ID NO:  
 5098 / SEQ ID NO: 10050, SEQ ID NO: 5099 / SEQ ID NO: 10051, SEQ ID NO: 5101 / SEQ  
 ID NO: 10052, SEQ ID NO: 5102 / SEQ ID NO: 10053, SEQ ID NO: 5103 / SEQ ID NO:  
 10054, SEQ ID NO: 5104 / SEQ ID NO: 10055, SEQ ID NO: 5105 / SEQ ID NO: 10056, SEQ  
 ID NO: 5106 / SEQ ID NO: 10057, SEQ ID NO: 5107 / SEQ ID NO: 10058, SEQ ID NO: 5108  
 / SEQ ID NO: 10059, SEQ ID NO: 5109 / SEQ ID NO: 10060, SEQ ID NO: 5110 / SEQ ID  
 10 NO: 10061, SEQ ID NO: 5111 / SEQ ID NO: 10062, SEQ ID NO: 5112 / SEQ ID NO: 10063,  
 SEQ ID NO: 5113 / SEQ ID NO: 10064, SEQ ID NO: 5114 / SEQ ID NO: 10065, SEQ ID NO:  
 15 5115 / SEQ ID NO: 10066, SEQ ID NO: 5116 / SEQ ID NO: 10067, SEQ ID NO: 5117 / SEQ  
 ID NO: 10068, SEQ ID NO: 5118 / SEQ ID NO: 10069, SEQ ID NO: 5119 / SEQ ID NO:  
 10070, SEQ ID NO: 5120 / SEQ ID NO: 10071, SEQ ID NO: 5121 / SEQ ID NO: 10072, SEQ  
 ID NO: 5122 / SEQ ID NO: 10073, SEQ ID NO: 5123 / SEQ ID NO: 10074, SEQ ID NO: 5124  
 / SEQ ID NO: 10075, SEQ ID NO: 5127 / SEQ ID NO: 10076, SEQ ID NO: 5128 / SEQ ID  
 NO: 10077, SEQ ID NO: 5129 / SEQ ID NO: 10078, SEQ ID NO: 5130 / SEQ ID NO: 10079,  
 SEQ ID NO: 5131 / SEQ ID NO: 10080, SEQ ID NO: 5133 / SEQ ID NO: 10081, SEQ ID NO:  
 20 5134 / SEQ ID NO: 10082, SEQ ID NO: 5135 / SEQ ID NO: 10083, SEQ ID NO: 5137 / SEQ  
 ID NO: 10084, SEQ ID NO: 5138 / SEQ ID NO: 10085, SEQ ID NO: 5139 / SEQ ID NO:  
 10086, SEQ ID NO: 5140 / SEQ ID NO: 10087, SEQ ID NO: 5141 / SEQ ID NO: 10088, SEQ  
 ID NO: 5142 / SEQ ID NO: 10089, SEQ ID NO: 5143 / SEQ ID NO: 10090, SEQ ID NO: 5144  
 / SEQ ID NO: 10091, SEQ ID NO: 5145 / SEQ ID NO: 10092, SEQ ID NO: 5146 / SEQ ID  
 NO: 10093, SEQ ID NO: 5147 / SEQ ID NO: 10094, SEQ ID NO: 5148 / SEQ ID NO: 10095,  
 SEQ ID NO: 5149 / SEQ ID NO: 10096, SEQ ID NO: 5150 / SEQ ID NO: 10097, SEQ ID NO:  
 25 5151 / SEQ ID NO: 10098, SEQ ID NO: 5153 / SEQ ID NO: 10099, SEQ ID NO: 5154 / SEQ  
 ID NO: 10100, SEQ ID NO: 5155 / SEQ ID NO: 10101, SEQ ID NO: 5156 / SEQ ID NO:  
 10102, SEQ ID NO: 5157 / SEQ ID NO: 10103, SEQ ID NO: 5158 / SEQ ID NO: 10104, SEQ  
 ID NO: 5159 / SEQ ID NO: 10105, SEQ ID NO: 5160 / SEQ ID NO: 10106, SEQ ID NO: 5161  
 / SEQ ID NO: 10107, SEQ ID NO: 5162 / SEQ ID NO: 10108, SEQ ID NO: 5163 / SEQ ID  
 NO: 10109, SEQ ID NO: 5164 / SEQ ID NO: 10110, SEQ ID NO: 5165 / SEQ ID NO: 10111,  
 SEQ ID NO: 5166 / SEQ ID NO: 10112, SEQ ID NO: 5167 / SEQ ID NO: 10113, SEQ ID NO:  
 30 5168 / SEQ ID NO: 10114, SEQ ID NO: 5169 / SEQ ID NO: 10115, SEQ ID NO: 5170 / SEQ  
 ID NO: 10116, SEQ ID NO: 5171 / SEQ ID NO: 10117, SEQ ID NO: 5172 / SEQ ID NO:  
 10118, SEQ ID NO: 5173 / SEQ ID NO: 10119, SEQ ID NO: 5174 / SEQ ID NO: 10120, SEQ  
 ID NO: 5175 / SEQ ID NO: 10121, SEQ ID NO: 5176 / SEQ ID NO: 10122, SEQ ID NO: 5177  
 / SEQ ID NO: 10123, SEQ ID NO: 5178 / SEQ ID NO: 10124, SEQ ID NO: 5179 / SEQ ID  
 NO: 10125, SEQ ID NO: 5180 / SEQ ID NO: 10126, SEQ ID NO: 5181 / SEQ ID NO: 10127,  
 35 SEQ ID NO: 5182 / SEQ ID NO: 10128, SEQ ID NO: 5183 / SEQ ID NO: 10129, SEQ ID NO:  
 5184 / SEQ ID NO: 10130, SEQ ID NO: 5185 / SEQ ID NO: 10131, SEQ ID NO: 5186 / SEQ  
 ID NO: 10132, SEQ ID NO: 5187 / SEQ ID NO: 10133, SEQ ID NO: 5188 / SEQ ID NO:  
 10134, SEQ ID NO: 5189 / SEQ ID NO: 10135, SEQ ID NO: 5190 / SEQ ID NO: 10136, SEQ  
 ID NO: 5191 / SEQ ID NO: 10137, SEQ ID NO: 5192 / SEQ ID NO: 10138, SEQ ID NO: 5193  
 / SEQ ID NO: 10139, SEQ ID NO: 5194 / SEQ ID NO: 10140, SEQ ID NO: 5195 / SEQ ID  
 NO: 10141, SEQ ID NO: 5196 / SEQ ID NO: 10142, SEQ ID NO: 5197 / SEQ ID NO: 10143,  
 SEQ ID NO: 5198 / SEQ ID NO: 10144, SEQ ID NO: 5200 / SEQ ID NO: 10145, SEQ ID NO:  
 40 5201 / SEQ ID NO: 10146, SEQ ID NO: 5202 / SEQ ID NO: 10147,  
 SEQ ID NO: 5204 / SEQ ID NO: 10148, SEQ ID NO: 5206 / SEQ ID NO: 10149, SEQ ID NO:  
 5207 / SEQ ID NO: 10150, SEQ ID NO: 5208 / SEQ ID NO: 10151, SEQ ID NO: 5209 / SEQ  
 ID NO: 10152, SEQ ID NO: 5211 / SEQ ID NO: 10153, SEQ ID NO: 5212 / SEQ ID NO:  
 45 10154, SEQ ID NO: 5213 / SEQ ID NO: 10155, SEQ ID NO: 5214 / SEQ ID NO: 10156, SEQ  
 ID NO: 5215 / SEQ ID NO: 10157, SEQ ID NO: 5216 / SEQ ID NO: 10158, SEQ ID NO: 5217  
 / SEQ ID NO: 10159, SEQ ID NO: 5218 / SEQ ID NO: 10160, SEQ ID NO: 5219 / SEQ ID  
 50  
 55

NO: 10161, SEQ ID NO: 5220 / SEQ ID NO: 10162, SEQ ID NO: 5221 / SEQ ID NO: 10163,  
 SEQ ID NO: 5222 / SEQ ID NO: 10164, SEQ ID NO: 5223 / SEQ ID NO: 10165, SEQ ID NO:  
 5 5224 / SEQ ID NO: 10166, SEQ ID NO: 5225 / SEQ ID NO: 10167, SEQ ID NO: 5227 / SEQ  
 ID NO: 10168, SEQ ID NO: 5229 / SEQ ID NO: 10169, SEQ ID NO: 5231 / SEQ ID NO:  
 10 10170, SEQ ID NO: 5232 / SEQ ID NO: 10171, SEQ ID NO: 5234 / SEQ ID NO: 10172, SEQ  
 ID NO: 5235 / SEQ ID NO: 10173, SEQ ID NO: 5236 / SEQ ID NO: 10174, SEQ ID NO: 5251  
 15 / SEQ ID NO: 10175, SEQ ID NO: 5252 / SEQ ID NO: 10176, SEQ ID NO: 5253 / SEQ ID  
 NO: 10177, SEQ ID NO: 5254 / SEQ ID NO: 10178, SEQ ID NO: 5255 / SEQ ID NO: 10179,  
 SEQ ID NO: 5256 / SEQ ID NO: 10180, SEQ ID NO: 5257 / SEQ ID NO: 10181, SEQ ID NO:  
 20 5258 / SEQ ID NO: 10182, SEQ ID NO: 5259 / SEQ ID NO: 10183, SEQ ID NO: 5260 / SEQ  
 ID NO: 10184, SEQ ID NO: 5261 / SEQ ID NO: 10185, SEQ ID NO: 5262 / SEQ ID NO:  
 25 10186, SEQ ID NO: 5263 / SEQ ID NO: 10187, SEQ ID NO: 5264 / SEQ ID NO: 10188, SEQ  
 ID NO: 5265 / SEQ ID NO: 10189, SEQ ID NO: 5266 / SEQ ID NO: 10190, SEQ ID NO: 5267  
 / SEQ ID NO: 10191, SEQ ID NO: 5268 / SEQ ID NO: 10192, SEQ ID NO: 5269 / SEQ ID  
 NO: 10193, SEQ ID NO: 5270 / SEQ ID NO: 10194, SEQ ID NO: 5271 / SEQ ID NO: 10195,  
 SEQ ID NO: 5272 / SEQ ID NO: 10196, SEQ ID NO: 5273 / SEQ ID NO: 10197, SEQ ID NO:  
 30 5274 / SEQ ID NO: 10198, SEQ ID NO: 5275 / SEQ ID NO: 10199, SEQ ID NO: 5276 / SEQ  
 ID NO: 10200, SEQ ID NO: 5277 / SEQ ID NO: 10201, SEQ ID NO: 5278 / SEQ ID NO:  
 35 10202, SEQ ID NO: 5279 / SEQ ID NO: 10203, SEQ ID NO: 5280 / SEQ ID NO: 10204, SEQ  
 ID NO: 5281 / SEQ ID NO: 10205, SEQ ID NO: 5282 / SEQ ID NO: 10206, SEQ ID NO: 5283  
 / SEQ ID NO: 10207, SEQ ID NO: 5284 / SEQ ID NO: 10208, SEQ ID NO: 5285 / SEQ ID  
 NO: 10209, SEQ ID NO: 5286 / SEQ ID NO: 10210, SEQ ID NO: 5287 / SEQ ID NO: 10211,  
 SEQ ID NO: 5288 / SEQ ID NO: 10212, SEQ ID NO: 5289 / SEQ ID NO: 10213, SEQ ID NO:  
 40 5290 / SEQ ID NO: 10214, SEQ ID NO: 5291 / SEQ ID NO: 10215, SEQ ID NO: 5292 / SEQ  
 ID NO: 10216, SEQ ID NO: 5293 / SEQ ID NO: 10217, SEQ ID NO: 5294 / SEQ ID NO:  
 45 10218, SEQ ID NO: 5295 / SEQ ID NO: 10219, SEQ ID NO: 5296 / SEQ ID NO: 10220, SEQ  
 ID NO: 5297 / SEQ ID NO: 10221, SEQ ID NO: 5298 / SEQ ID NO: 10222, SEQ ID NO: 5299  
 / SEQ ID NO: 10223, SEQ ID NO: 5300 / SEQ ID NO: 10224, SEQ ID NO: 5301 / SEQ ID  
 NO: 10225, SEQ ID NO: 5302 / SEQ ID NO: 10226, SEQ ID NO: 5303 / SEQ ID NO: 10227,  
 SEQ ID NO: 5304 / SEQ ID NO: 10228, SEQ ID NO: 5305 / SEQ ID NO: 10229, SEQ ID NO:  
 50 5306 / SEQ ID NO: 10230, SEQ ID NO: 5307 / SEQ ID NO: 10231, SEQ ID NO: 5308 / SEQ  
 ID NO: 10232, SEQ ID NO: 5309 / SEQ ID NO: 10233, SEQ ID NO: 5310 / SEQ ID NO:  
 55 10234, SEQ ID NO: 5311 / SEQ ID NO: 10235, SEQ ID NO: 5312 / SEQ ID NO: 10236, SEQ  
 ID NO: 5313 / SEQ ID NO: 10237, SEQ ID NO: 5314 / SEQ ID NO: 10238, SEQ ID NO: 5315  
 / SEQ ID NO: 10239, SEQ ID NO: 5317 / SEQ ID NO: 10240, SEQ ID NO: 5318 / SEQ ID  
 NO: 10241, SEQ ID NO: 5319 / SEQ ID NO: 10242, SEQ ID NO: 5320 / SEQ ID NO: 10243,  
 SEQ ID NO: 5321 / SEQ ID NO: 10244, SEQ ID NO: 5322 / SEQ ID NO: 10245, SEQ ID NO:  
 60 5323 / SEQ ID NO: 10246, SEQ ID NO: 5324 / SEQ ID NO: 10247,  
 SEQ ID NO: 5325 / SEQ ID NO: 10248, SEQ ID NO: 5326 / SEQ ID NO: 10249, SEQ ID NO:  
 65 5327 / SEQ ID NO: 10250, SEQ ID NO: 5328 / SEQ ID NO: 10251, SEQ ID NO: 5329 / SEQ  
 ID NO: 10252, SEQ ID NO: 5330 / SEQ ID NO: 10253, SEQ ID NO: 5331 / SEQ ID NO:  
 70 10254, SEQ ID NO: 5332 / SEQ ID NO: 10255, SEQ ID NO: 5333 / SEQ ID NO: 10256, SEQ  
 ID NO: 5334 / SEQ ID NO: 10257, SEQ ID NO: 5335 / SEQ ID NO: 10258, SEQ ID NO: 5336  
 / SEQ ID NO: 10259, SEQ ID NO: 5337 / SEQ ID NO: 10260, SEQ ID NO: 5338 / SEQ ID  
 NO: 10261, SEQ ID NO: 5339 / SEQ ID NO: 10262, SEQ ID NO: 5340 / SEQ ID NO: 10263,  
 SEQ ID NO: 5341 / SEQ ID NO: 10264, SEQ ID NO: 5342 / SEQ ID NO: 10265, SEQ ID NO:  
 75 5343 / SEQ ID NO: 10266, SEQ ID NO: 5344 / SEQ ID NO: 10267, SEQ ID NO: 5345 / SEQ  
 ID NO: 10268, SEQ ID NO: 5346 / SEQ ID NO: 10269, SEQ ID NO: 5347 / SEQ ID NO:  
 80 10270, SEQ ID NO: 5348 / SEQ ID NO: 10271, SEQ ID NO: 5349 / SEQ ID NO: 10272, SEQ  
 ID NO: 5350 / SEQ ID NO: 10273, SEQ ID NO: 5351 / SEQ ID NO: 10274, SEQ ID NO: 5352  
 / SEQ ID NO: 10275, SEQ ID NO: 5353 / SEQ ID NO: 10276, SEQ ID NO: 5354 / SEQ ID  
 NO: 10277, SEQ ID NO: 5355 / SEQ ID NO: 10278, SEQ ID NO: 5356 / SEQ ID NO: 10279,

SEQ ID NO: 5357 / SEQ ID NO: 10280, SEQ ID NO: 5358 / SEQ ID NO: 10281, SEQ ID NO:  
 5 5359 / SEQ ID NO: 10282, SEQ ID NO: 5360 / SEQ ID NO: 10283, SEQ ID NO: 5362 / SEQ  
 ID NO: 10284, SEQ ID NO: 5363 / SEQ ID NO: 10285, SEQ ID NO: 5364 / SEQ ID NO:  
 10 10286, SEQ ID NO: 5365 / SEQ ID NO: 10287, SEQ ID NO: 5366 / SEQ ID NO: 10288, SEQ  
 ID NO: 5367 / SEQ ID NO: 10289, SEQ ID NO: 5368 / SEQ ID NO: 10290, SEQ ID NO: 5369  
 / SEQ ID NO: 10291, SEQ ID NO: 5370 / SEQ ID NO: 10292, SEQ ID NO: 5371 / SEQ ID  
 NO: 10293, SEQ ID NO: 5372 / SEQ ID NO: 10294, SEQ ID NO: 5373 / SEQ ID NO: 10295,  
 15 SEQ ID NO: 5374 / SEQ ID NO: 10296, SEQ ID NO: 5375 / SEQ ID NO: 10297, SEQ ID NO:  
 10 5376 / SEQ ID NO: 10298, SEQ ID NO: 5377 / SEQ ID NO: 10299, SEQ ID NO: 5378 / SEQ  
 ID NO: 10300, SEQ ID NO: 5379 / SEQ ID NO: 10301, SEQ ID NO: 5380 / SEQ ID NO:  
 20 10302, SEQ ID NO: 5381 / SEQ ID NO: 10303, SEQ ID NO: 5382 / SEQ ID NO: 10304, SEQ  
 ID NO: 5383 / SEQ ID NO: 10305, SEQ ID NO: 5384 / SEQ ID NO: 10306, SEQ ID NO: 5385  
 / SEQ ID NO: 10307, SEQ ID NO: 5386 / SEQ ID NO: 10308, SEQ ID NO: 5387 / SEQ ID  
 NO: 10309, SEQ ID NO: 5388 / SEQ ID NO: 10310, SEQ ID NO: 5389 / SEQ ID NO: 10311,  
 25 SEQ ID NO: 5390 / SEQ ID NO: 10312, SEQ ID NO: 5391 / SEQ ID NO: 10313, SEQ ID NO:  
 20 5392 / SEQ ID NO: 10314, SEQ ID NO: 5393 / SEQ ID NO: 10315, SEQ ID NO: 5394 / SEQ  
 ID NO: 10316, SEQ ID NO: 5395 / SEQ ID NO: 10317, SEQ ID NO: 5396 / SEQ ID NO:  
 25 10318, SEQ ID NO: 5397 / SEQ ID NO: 10319, SEQ ID NO: 5398 / SEQ ID NO: 10320, SEQ  
 ID NO: 5399 / SEQ ID NO: 10321, SEQ ID NO: 5400 / SEQ ID NO: 10322, SEQ ID NO: 5401  
 / SEQ ID NO: 10323, SEQ ID NO: 5402 / SEQ ID NO: 10324, SEQ ID NO: 5403 / SEQ ID  
 NO: 10325, SEQ ID NO: 5404 / SEQ ID NO: 10326, SEQ ID NO: 5405 / SEQ ID NO: 10327,  
 30 SEQ ID NO: 5407 / SEQ ID NO: 10328, SEQ ID NO: 5408 / SEQ ID NO: 10329, SEQ ID NO:  
 25 5409 / SEQ ID NO: 10330, SEQ ID NO: 5410 / SEQ ID NO: 10331, SEQ ID NO: 5411 / SEQ  
 ID NO: 10332, SEQ ID NO: 5412 / SEQ ID NO: 10333, SEQ ID NO: 5413 / SEQ ID NO:  
 30 10334, SEQ ID NO: 5414 / SEQ ID NO: 10335, SEQ ID NO: 5415 / SEQ ID NO: 10336, SEQ  
 ID NO: 5416 / SEQ ID NO: 10337, SEQ ID NO: 5417 / SEQ ID NO: 10338, SEQ ID NO: 5418  
 / SEQ ID NO: 10339, SEQ ID NO: 5419 / SEQ ID NO: 10340, SEQ ID NO: 5420 / SEQ ID  
 NO: 10341, SEQ ID NO: 5421 / SEQ ID NO: 10342, SEQ ID NO: 5422 / SEQ ID NO: 10343,  
 35 SEQ ID NO: 5423 / SEQ ID NO: 10344, SEQ ID NO: 5424 / SEQ ID NO: 10345, SEQ ID NO:  
 30 5425 / SEQ ID NO: 10346, SEQ ID NO: 5426 / SEQ ID NO: 10347,  
 SEQ ID NO: 5427 / SEQ ID NO: 10348, SEQ ID NO: 5428 / SEQ ID NO: 10349, SEQ ID NO:  
 35 5429 / SEQ ID NO: 10350, SEQ ID NO: 5430 / SEQ ID NO: 10351, SEQ ID NO: 5431 / SEQ  
 ID NO: 10352, SEQ ID NO: 5432 / SEQ ID NO: 10353, SEQ ID NO: 5433 / SEQ ID NO:  
 40 10354, SEQ ID NO: 5434 / SEQ ID NO: 10355, SEQ ID NO: 5435 / SEQ ID NO: 10356, SEQ  
 ID NO: 5436 / SEQ ID NO: 10357, SEQ ID NO: 5437 / SEQ ID NO: 10358, SEQ ID NO: 5438  
 / SEQ ID NO: 10359, SEQ ID NO: 5439 / SEQ ID NO: 10360, SEQ ID NO: 5440 / SEQ ID  
 NO: 10361, SEQ ID NO: 5442 / SEQ ID NO: 10362, SEQ ID NO: 5443 / SEQ ID NO: 10363,  
 45 SEQ ID NO: 5444 / SEQ ID NO: 10364, SEQ ID NO: 5445 / SEQ ID NO: 10365, SEQ ID NO:  
 40 5446 / SEQ ID NO: 10366, SEQ ID NO: 5447 / SEQ ID NO: 10367, SEQ ID NO: 5448 / SEQ  
 ID NO: 10368, SEQ ID NO: 5449 / SEQ ID NO: 10369, SEQ ID NO: 5450 / SEQ ID NO:  
 45 10370, SEQ ID NO: 5451 / SEQ ID NO: 10371, SEQ ID NO: 5452 / SEQ ID NO: 10372, SEQ  
 ID NO: 5453 / SEQ ID NO: 10373, SEQ ID NO: 5454 / SEQ ID NO: 10374, SEQ ID NO: 5455  
 / SEQ ID NO: 10375, SEQ ID NO: 5457 / SEQ ID NO: 10376, SEQ ID NO: 5458 / SEQ ID  
 NO: 10377, SEQ ID NO: 5460 / SEQ ID NO: 10378, SEQ ID NO: 5461 / SEQ ID NO: 10379,  
 50 SEQ ID NO: 5462 / SEQ ID NO: 10380, SEQ ID NO: 5463 / SEQ ID NO: 10381, SEQ ID NO:  
 45 5464 / SEQ ID NO: 10382, SEQ ID NO: 5465 / SEQ ID NO: 10383, SEQ ID NO: 5466 / SEQ  
 ID NO: 10384, SEQ ID NO: 5467 / SEQ ID NO: 10385, SEQ ID NO: 5468 / SEQ ID NO:  
 50 10386, SEQ ID NO: 5469 / SEQ ID NO: 10387, SEQ ID NO: 5470 / SEQ ID NO: 10388, SEQ  
 ID NO: 5471 / SEQ ID NO: 10389, SEQ ID NO: 5472 / SEQ ID NO: 10390, SEQ ID NO: 5473  
 / SEQ ID NO: 10391, SEQ ID NO: 5474 / SEQ ID NO: 10392, SEQ ID NO: 5475 / SEQ ID  
 NO: 10393, SEQ ID NO: 5476 / SEQ ID NO: 10394, SEQ ID NO: 5477 / SEQ ID NO: 10395,  
 55 SEQ ID NO: 5478 / SEQ ID NO: 10396, SEQ ID NO: 5479 / SEQ ID NO: 10397, SEQ ID NO:

5 5480 / SEQ ID NO: 10398, SEQ ID NO: 5481 / SEQ ID NO: 10399, SEQ ID NO: 5482 / SEQ  
 ID NO: 10400, SEQ ID NO: 5483 / SEQ ID NO: 10401, SEQ ID NO: 5484 / SEQ ID NO:  
 10402, SEQ ID NO: 5485 / SEQ ID NO: 10403, SEQ ID NO: 5486 / SEQ ID NO: 10404, SEQ  
 ID NO: 5487 / SEQ ID NO: 10405, SEQ ID NO: 5488 / SEQ ID NO: 10406, SEQ ID NO: 5489  
 / SEQ ID NO: 10407, SEQ ID NO: 5490 / SEQ ID NO: 10408, SEQ ID NO: 5491 / SEQ ID  
 NO: 10409, SEQ ID NO: 5492 / SEQ ID NO: 10410, SEQ ID NO: 5493 / SEQ ID NO: 10411,  
 SEQ ID NO: 5494 / SEQ ID NO: 10412, SEQ ID NO: 5496 / SEQ ID NO: 10413, SEQ ID NO:  
 10 5497 / SEQ ID NO: 10414, SEQ ID NO: 5498 / SEQ ID NO: 10415, SEQ ID NO: 5499 / SEQ  
 ID NO: 10416, SEQ ID NO: 5500 / SEQ ID NO: 10417, SEQ ID NO: 5501 / SEQ ID NO:  
 10418, SEQ ID NO: 5502 / SEQ ID NO: 10419, SEQ ID NO: 5503 / SEQ ID NO: 10420, SEQ  
 ID NO: 5504 / SEQ ID NO: 10421, SEQ ID NO: 5505 / SEQ ID NO: 10422, SEQ ID NO: 5506  
 / SEQ ID NO: 10423, SEQ ID NO: 5507 / SEQ ID NO: 10424, SEQ ID NO: 5508 / SEQ ID  
 NO: 10425, SEQ ID NO: 5509 / SEQ ID NO: 10426, SEQ ID NO: 5510 / SEQ ID NO: 10427,  
 15 SEQ ID NO: 5511 / SEQ ID NO: 10428, SEQ ID NO: 5512 / SEQ ID NO: 10429, SEQ ID NO:  
 5513 / SEQ ID NO: 10430, SEQ ID NO: 5514 / SEQ ID NO: 10431, SEQ ID NO: 5515 / SEQ  
 ID NO: 10432, SEQ ID NO: 5517 / SEQ ID NO: 10433, SEQ ID NO: 5518 / SEQ ID NO:  
 10434, SEQ ID NO: 5519 / SEQ ID NO: 10435, SEQ ID NO: 5520 / SEQ ID NO: 10436, SEQ  
 ID NO: 5521 / SEQ ID NO: 10437, SEQ ID NO: 5522 / SEQ ID NO: 10438, SEQ ID NO: 5523  
 20 / SEQ ID NO: 10439, SEQ ID NO: 5524 / SEQ ID NO: 10440, SEQ ID NO: 5525 / SEQ ID  
 NO: 10441, SEQ ID NO: 5526 / SEQ ID NO: 10442, SEQ ID NO: 5527 / SEQ ID NO: 10443,  
 SEQ ID NO: 5528 / SEQ ID NO: 10444, SEQ ID NO: 5529 / SEQ ID NO: 10445, SEQ ID NO:  
 5530 / SEQ ID NO: 10446, SEQ ID NO: 5531 / SEQ ID NO: 10447,  
 25 SEQ ID NO: 5532 / SEQ ID NO: 10448, SEQ ID NO: 5533 / SEQ ID NO: 10449, SEQ ID NO:  
 5534 / SEQ ID NO: 10450, SEQ ID NO: 5535 / SEQ ID NO: 10451, SEQ ID NO: 5536 / SEQ  
 ID NO: 10452, SEQ ID NO: 5537 / SEQ ID NO: 10453, SEQ ID NO: 5538 / SEQ ID NO:  
 10454, SEQ ID NO: 5539 / SEQ ID NO: 10455, SEQ ID NO: 5540 / SEQ ID NO: 10456, SEQ  
 ID NO: 5541 / SEQ ID NO: 10457, SEQ ID NO: 5542 / SEQ ID NO: 10458, SEQ ID NO: 5543  
 30 / SEQ ID NO: 10459, SEQ ID NO: 5544 / SEQ ID NO: 10460, SEQ ID NO: 5545 / SEQ ID  
 NO: 10461, SEQ ID NO: 5546 / SEQ ID NO: 10462, SEQ ID NO: 5547 / SEQ ID NO: 10463  
 SEQ ID NO: 16111 / SEQ ID NO: 16165, SEQ ID NO: 16112 / SEQ ID NO: 16166, SEQ ID  
 NO: 16113 / SEQ ID NO: 16167, SEQ ID NO: 16114 / SEQ ID NO: 16168, SEQ ID NO: 16115  
 / SEQ ID NO: 16169, SEQ ID NO: 16116 / SEQ ID NO: 16170, SEQ ID NO: 16117 / SEQ ID  
 NO: 16171, SEQ ID NO: 16118 / SEQ ID NO: 16172, SEQ ID NO: 16119 / SEQ ID NO: 16173,  
 35 SEQ ID NO: 16120 / SEQ ID NO: 16174, SEQ ID NO: 16121 / SEQ ID NO: 16175, SEQ ID  
 NO: 16122 / SEQ ID NO: 16176, SEQ ID NO: 16123 / SEQ ID NO: 16177, SEQ ID NO: 16124  
 / SEQ ID NO: 16178, SEQ ID NO: 16125 / SEQ ID NO: 16179, SEQ ID NO: 16126 / SEQ ID  
 NO: 16180, SEQ ID NO: 16127 / SEQ ID NO: 16181, SEQ ID NO: 16128 / SEQ ID NO: 16182,  
 40 SEQ ID NO: 16129 / SEQ ID NO: 16183, SEQ ID NO: 16130 / SEQ ID NO: 16184, SEQ ID  
 NO: 16131 / SEQ ID NO: 16185, SEQ ID NO: 16132 / SEQ ID NO: 16186, SEQ ID NO: 16133  
 / SEQ ID NO: 16187, SEQ ID NO: 16134 / SEQ ID NO: 16188, SEQ ID NO: 16135 / SEQ ID  
 NO: 16189, SEQ ID NO: 16136 / SEQ ID NO: 16190, SEQ ID NO: 16137 / SEQ ID NO: 16191,  
 45 SEQ ID NO: 16138 / SEQ ID NO: 16192, SEQ ID NO: 16139 / SEQ ID NO: 16193, SEQ ID  
 NO: 16140 / SEQ ID NO: 16194, SEQ ID NO: 16141 / SEQ ID NO: 16195, SEQ ID NO: 16142  
 / SEQ ID NO: 16196, SEQ ID NO: 16143 / SEQ ID NO: 16197, SEQ ID NO: 16144 / SEQ ID  
 NO: 16198, SEQ ID NO: 16145 / SEQ ID NO: 16199, SEQ ID NO: 16146 / SEQ ID NO: 16200,  
 50 SEQ ID NO: 16147 / SEQ ID NO: 16201, SEQ ID NO: 16148 / SEQ ID NO: 16202, SEQ ID  
 NO: 16149 / SEQ ID NO: 16203, SEQ ID NO: 16150 / SEQ ID NO: 16204, SEQ ID NO: 16151  
 / SEQ ID NO: 16205, SEQ ID NO: 16152 / SEQ ID NO: 16206, SEQ ID NO: 16153 / SEQ ID  
 NO: 16207, SEQ ID NO: 16154 / SEQ ID NO: 16208, SEQ ID NO: 16155 / SEQ ID NO: 16209,  
 SEQ ID NO: 16156 / SEQ ID NO: 16210, SEQ ID NO: 16157 / SEQ ID NO: 16211, SEQ ID  
 NO: 16158 / SEQ ID NO: 16212, SEQ ID NO: 16159 / SEQ ID NO: 16213, SEQ ID NO: 16160  
 / SEQ ID NO: 16214, SEQ ID NO: 16161 / SEQ ID NO: 16215, SEQ ID NO: 16162 / SEQ ID

NO: 16216, SEQ ID NO: 16163 / SEQ ID NO: 16217, and SEQ ID NO: 16164 / SEQ ID NO:  
16218

- 5      4. A polynucleotide which can be synthesized with the primer set of claim 2 or 3.
5. A polynucleotide comprising a coding region in the polynucleotide of claim 4.
- 10     6. A substantially pure protein encoded by polynucleotide of claim 4.
7. A partial peptide of the protein of claim 6.
- 15     8. An isolated polynucleotide selected from the group consisting of  
              (a) a polynucleotide comprising a coding region of the nucleotide sequence set forth in any one of the following  
              SEQ ID NOs:

20

25

30

35

40

45

50

55

SEQ ID NO: 10468, SEQ ID NO: 10470, SEQ ID NO: 10471, SEQ ID NO: 10472, SEQ ID  
NO: 10473, SEQ ID NO: 10475, SEQ ID NO: 10477, SEQ ID NO: 10479, SEQ ID NO: 10481,  
5 SEQ ID NO: 10483, SEQ ID NO: 10485, SEQ ID NO: 10487, SEQ ID NO: 10488, SEQ ID  
NO: 10489, SEQ ID NO: 10491, SEQ ID NO: 10493, SEQ ID NO: 10495, SEQ ID NO: 10496,  
SEQ ID NO: 10497, SEQ ID NO: 10498, SEQ ID NO: 10500, SEQ ID NO: 10502, SEQ ID  
NO: 10503, SEQ ID NO: 10504, SEQ ID NO: 10505, SEQ ID NO: 10507, SEQ ID NO: 10508,  
10 SEQ ID NO: 10510, SEQ ID NO: 10511, SEQ ID NO: 10512, SEQ ID NO: 10514, SEQ ID  
NO: 10516, SEQ ID NO: 10517, SEQ ID NO: 10519, SEQ ID NO: 10521, SEQ ID NO: 10523,  
SEQ ID NO: 10524, SEQ ID NO: 10526, SEQ ID NO: 10528, SEQ ID NO: 10529, SEQ ID  
NO: 10530, SEQ ID NO: 10532, SEQ ID NO: 10534, SEQ ID NO: 10535, SEQ ID NO: 10537,  
15 SEQ ID NO: 10539, SEQ ID NO: 10540, SEQ ID NO: 10542, SEQ ID NO: 10543, SEQ ID  
NO: 10545, SEQ ID NO: 10546, SEQ ID NO: 10548, SEQ ID NO: 10550, SEQ ID NO: 10551,  
SEQ ID NO: 10553, SEQ ID NO: 10555, SEQ ID NO: 10556, SEQ ID NO: 10557, SEQ ID  
NO: 10558, SEQ ID NO: 10560, SEQ ID NO: 10562, SEQ ID NO: 10564, SEQ ID NO: 10566,  
20 SEQ ID NO: 10567, SEQ ID NO: 10569, SEQ ID NO: 10571, SEQ ID NO: 10573, SEQ ID  
NO: 10574, SEQ ID NO: 10576, SEQ ID NO: 10578, SEQ ID NO: 10580, SEQ ID NO: 10582,  
SEQ ID NO: 10584, SEQ ID NO: 10586, SEQ ID NO: 10588, SEQ ID NO: 10590, SEQ ID  
NO: 10592, SEQ ID NO: 10594, SEQ ID NO: 10596, SEQ ID NO: 10597, SEQ ID NO: 10599,  
25 SEQ ID NO: 10601, SEQ ID NO: 10603, SEQ ID NO: 10604, SEQ ID NO: 10606, SEQ ID  
NO: 10607, SEQ ID NO: 10609, SEQ ID NO: 10611, SEQ ID NO: 10613, SEQ ID NO: 10614,  
SEQ ID NO: 10615, SEQ ID NO: 10616, SEQ ID NO: 10618, SEQ ID NO: 10619, SEQ ID  
NO: 10620, SEQ ID NO: 10622, SEQ ID NO: 10624, SEQ ID NO: 10625, SEQ ID NO: 10627,  
30 SEQ ID NO: 10629,  
SEQ ID NO: 10630, SEQ ID NO: 10632, SEQ ID NO: 10633, SEQ ID NO: 10635, SEQ ID  
NO: 10637, SEQ ID NO: 10639, SEQ ID NO: 10641, SEQ ID NO: 10642, SEQ ID NO: 10644,  
SEQ ID NO: 10646, SEQ ID NO: 10647, SEQ ID NO: 10648, SEQ ID NO: 10649, SEQ ID  
NO: 10650, SEQ ID NO: 10652, SEQ ID NO: 10654, SEQ ID NO: 10655, SEQ ID NO: 10656,  
35 SEQ ID NO: 10658, SEQ ID NO: 10659, SEQ ID NO: 10661, SEQ ID NO: 10663, SEQ ID  
NO: 10665, SEQ ID NO: 10667, SEQ ID NO: 10669, SEQ ID NO: 10670, SEQ ID NO: 10671,  
SEQ ID NO: 10673, SEQ ID NO: 10674, SEQ ID NO: 10676, SEQ ID NO: 10678, SEQ ID  
NO: 10680, SEQ ID NO: 10682, SEQ ID NO: 10683, SEQ ID NO: 10685, SEQ ID NO: 10687,  
40 SEQ ID NO: 10689, SEQ ID NO: 10691, SEQ ID NO: 10693, SEQ ID NO: 10695, SEQ ID  
NO: 10696, SEQ ID NO: 10698, SEQ ID NO: 10700, SEQ ID NO: 10702, SEQ ID NO: 10704,  
SEQ ID NO: 10706, SEQ ID NO: 10708, SEQ ID NO: 10710, SEQ ID NO: 10711, SEQ ID  
NO: 10713, SEQ ID NO: 10715, SEQ ID NO: 10717, SEQ ID NO: 10718, SEQ ID NO: 10720,  
45 SEQ ID NO: 10722, SEQ ID NO: 10723, SEQ ID NO: 10725, SEQ ID NO: 10727, SEQ ID  
NO: 10728, SEQ ID NO: 10730, SEQ ID NO: 10732, SEQ ID NO: 10734, SEQ ID NO: 10736,  
SEQ ID NO: 10738, SEQ ID NO: 10740, SEQ ID NO: 10742, SEQ ID NO: 10744, SEQ ID  
NO: 10746, SEQ ID NO: 10748, SEQ ID NO: 10750, SEQ ID NO: 10752, SEQ ID NO: 10753,  
50 SEQ ID NO: 10754, SEQ ID NO: 10756, SEQ ID NO: 10757, SEQ ID NO: 10758, SEQ ID  
NO: 10760, SEQ ID NO: 10761, SEQ ID NO: 10763, SEQ ID NO: 10765, SEQ ID NO: 10767,  
SEQ ID NO: 10769, SEQ ID NO: 10771, SEQ ID NO: 10773, SEQ ID NO: 10774, SEQ ID  
NO: 10776, SEQ ID NO: 10778, SEQ ID NO: 10780, SEQ ID NO: 10781, SEQ ID NO: 10783,





















SEQ ID NO: 14798, SEQ ID NO: 14800, SEQ ID NO: 14802, SEQ ID NO: 14804, SEQ ID  
 NO: 14806, SEQ ID NO: 14808, SEQ ID NO: 14809, SEQ ID NO: 14811, SEQ ID NO: 14812,  
 SEQ ID NO: 14814,  
 5 SEQ ID NO: 14816, SEQ ID NO: 14818, SEQ ID NO: 14820, SEQ ID NO: 14822, SEQ ID  
 NO: 14823, SEQ ID NO: 14824, SEQ ID NO: 14826, SEQ ID NO: 14828, SEQ ID NO: 14830,  
 SEQ ID NO: 14831, SEQ ID NO: 14833, SEQ ID NO: 14835, SEQ ID NO: 14837, SEQ ID  
 NO: 14839, SEQ ID NO: 14841, SEQ ID NO: 14843, SEQ ID NO: 14845, SEQ ID NO: 14847,  
 SEQ ID NO: 14849, SEQ ID NO: 14850, SEQ ID NO: 14852, SEQ ID NO: 14854, SEQ ID  
 10 NO: 14856, SEQ ID NO: 14858, SEQ ID NO: 14860, SEQ ID NO: 14862, SEQ ID NO: 14864,  
 SEQ ID NO: 14865, SEQ ID NO: 14867, SEQ ID NO: 14869, SEQ ID NO: 14871, SEQ ID  
 NO: 14872, SEQ ID NO: 14874, SEQ ID NO: 14876, SEQ ID NO: 14878, SEQ ID NO: 14880,  
 SEQ ID NO: 14882, SEQ ID NO: 14884, SEQ ID NO: 14886, SEQ ID NO: 14888, SEQ ID  
 15 NO: 14890, SEQ ID NO: 14892, SEQ ID NO: 14894, SEQ ID NO: 14896, SEQ ID NO: 14898,  
 SEQ ID NO: 14900, SEQ ID NO: 14902, SEQ ID NO: 14904, SEQ ID NO: 14906, SEQ ID  
 NO: 14908, SEQ ID NO: 14910, SEQ ID NO: 14912, SEQ ID NO: 14914, SEQ ID NO: 14916,  
 SEQ ID NO: 14918, SEQ ID NO: 14919, SEQ ID NO: 14921, SEQ ID NO: 14923, SEQ ID  
 20 NO: 14924, SEQ ID NO: 14925, SEQ ID NO: 14927, SEQ ID NO: 14929, SEQ ID NO: 14931,  
 SEQ ID NO: 14933, SEQ ID NO: 14935, SEQ ID NO: 14937, SEQ ID NO: 14938, SEQ ID  
 NO: 14940, SEQ ID NO: 14942, SEQ ID NO: 14944, SEQ ID NO: 14946, SEQ ID NO: 14948,  
 SEQ ID NO: 14950, SEQ ID NO: 14952, SEQ ID NO: 14954, SEQ ID NO: 14956, SEQ ID  
 NO: 14958, SEQ ID NO: 14960, SEQ ID NO: 14961, SEQ ID NO: 14963, SEQ ID NO: 14965,  
 SEQ ID NO: 14967, SEQ ID NO: 14969, SEQ ID NO: 14971, SEQ ID NO: 14973, SEQ ID  
 25 NO: 14975, SEQ ID NO: 14977, SEQ ID NO: 14979, SEQ ID NO: 14981, SEQ ID NO: 14982,  
 SEQ ID NO: 14984, SEQ ID NO: 14986, SEQ ID NO: 14987, SEQ ID NO: 14988, SEQ ID  
 NO: 14990, SEQ ID NO: 14992, SEQ ID NO: 14993, SEQ ID NO: 14994, SEQ ID NO: 14996,  
 SEQ ID NO: 14998,  
 SEQ ID NO: 15000, SEQ ID NO: 15002, SEQ ID NO: 15004, SEQ ID NO: 15005, SEQ ID  
 30 NO: 15006, SEQ ID NO: 15007, SEQ ID NO: 15009, SEQ ID NO: 15011, SEQ ID NO: 15012,  
 SEQ ID NO: 15013, SEQ ID NO: 15015, SEQ ID NO: 15017, SEQ ID NO: 15019, SEQ ID  
 NO: 15021, SEQ ID NO: 15023, SEQ ID NO: 15025, SEQ ID NO: 15026, SEQ ID NO: 15028,  
 SEQ ID NO: 15029, SEQ ID NO: 15031, SEQ ID NO: 15033, SEQ ID NO: 15035, SEQ ID  
 35 NO: 15037, SEQ ID NO: 15039, SEQ ID NO: 15040, SEQ ID NO: 15042, SEQ ID NO: 15044,  
 SEQ ID NO: 15046, SEQ ID NO: 15048, SEQ ID NO: 15050, SEQ ID NO: 15051, SEQ ID  
 NO: 15053, SEQ ID NO: 15055, SEQ ID NO: 15057, SEQ ID NO: 15059, SEQ ID NO: 15060,  
 SEQ ID NO: 15062, SEQ ID NO: 15064, SEQ ID NO: 15066, SEQ ID NO: 15067, SEQ ID  
 40 NO: 15069, SEQ ID NO: 15071, SEQ ID NO: 15073, SEQ ID NO: 15075, SEQ ID NO: 15077,  
 SEQ ID NO: 15078, SEQ ID NO: 15080, SEQ ID NO: 15082, SEQ ID NO: 15084, SEQ ID  
 NO: 15086, SEQ ID NO: 15088, SEQ ID NO: 15090, SEQ ID NO: 15091, SEQ ID NO: 15093;  
 SEQ ID NO: 15095, SEQ ID NO: 15096, SEQ ID NO: 15098, SEQ ID NO: 15099, SEQ ID  
 45 NO: 15101, SEQ ID NO: 15103, SEQ ID NO: 15105, SEQ ID NO: 15107, SEQ ID NO: 15109,  
 SEQ ID NO: 15111, SEQ ID NO: 15113, SEQ ID NO: 15115, SEQ ID NO: 15117, SEQ ID  
 NO: 15119, SEQ ID NO: 15121, SEQ ID NO: 15123, SEQ ID NO: 15125, SEQ ID NO: 15127,  
 SEQ ID NO: 15129, SEQ ID NO: 15130, SEQ ID NO: 15132, SEQ ID NO: 15134, SEQ ID  
 NO: 15136, SEQ ID NO: 15138, SEQ ID NO: 15140, SEQ ID NO: 15142, SEQ ID NO: 15144,  
 SEQ ID NO: 15146, SEQ ID NO: 15147, SEQ ID NO: 15148, SEQ ID NO: 15150, SEQ ID  
 50 NO: 15152, SEQ ID NO: 15154, SEQ ID NO: 15155, SEQ ID NO: 15157, SEQ ID NO: 15159,  
 SEQ ID NO: 15161, SEQ ID NO: 15163, SEQ ID NO: 15165, SEQ ID NO: 15167, SEQ ID  
 NO: 15168, SEQ ID NO: 15169, SEQ ID NO: 15171, SEQ ID NO: 15173, SEQ ID NO: 15175,  
 SEQ ID NO: 15177,  
 SEQ ID NO: 15179, SEQ ID NO: 15181, SEQ ID NO: 15183, SEQ ID NO: 15185, SEQ ID  
 55 NO: 15187, SEQ ID NO: 15189, SEQ ID NO: 15191, SEQ ID NO: 15192, SEQ ID NO: 15194,  
 SEQ ID NO: 15196, SEQ ID NO: 15198, SEQ ID NO: 15200, SEQ ID NO: 15201, SEQ ID













SEQ ID NO: 17420, SEQ ID NO: 17422, SEQ ID NO: 17424, SEQ ID NO: 17426, SEQ ID  
 NO: 17427, SEQ ID NO: 17429, SEQ ID NO: 17430, SEQ ID NO: 17432, SEQ ID NO: 17433,  
 5 SEQ ID NO: 17434, SEQ ID NO: 17436, SEQ ID NO: 17437, SEQ ID NO: 17438, SEQ ID  
 NO: 17440, SEQ ID NO: 17442, SEQ ID NO: 17443, SEQ ID NO: 17445, SEQ ID NO: 17447,  
 SEQ ID NO: 17449, SEQ ID NO: 17450, SEQ ID NO: 17452, SEQ ID NO: 17454, SEQ ID  
 10 NO: 17456, SEQ ID NO: 17457, SEQ ID NO: 17459, SEQ ID NO: 17460, SEQ ID NO: 17461,  
 SEQ ID NO: 17463, SEQ ID NO: 17465, SEQ ID NO: 17467, SEQ ID NO: 17468, SEQ ID  
 15 NO: 17470, SEQ ID NO: 17472, SEQ ID NO: 17474, SEQ ID NO: 17475, SEQ ID NO: 17477,  
 SEQ ID NO: 17479, SEQ ID NO: 17480, SEQ ID NO: 17482, SEQ ID NO: 17484, SEQ ID  
 NO: 17485, SEQ ID NO: 17487, SEQ ID NO: 17489, SEQ ID NO: 17490, SEQ ID NO: 17492,  
 20 SEQ ID NO: 17494, SEQ ID NO: 17496, SEQ ID NO: 17498, SEQ ID NO: 17500, SEQ ID  
 NO: 17502, SEQ ID NO: 17504, SEQ ID NO: 17506, SEQ ID NO: 17508, SEQ ID NO: 17510,  
 SEQ ID NO: 17512, SEQ ID NO: 17514, SEQ ID NO: 17516, SEQ ID NO: 17518, SEQ ID  
 25 NO: 17520, SEQ ID NO: 17522, SEQ ID NO: 17524, SEQ ID NO: 17526, SEQ ID NO: 17527,  
 SEQ ID NO: 17529,  
 SEQ ID NO: 17531, SEQ ID NO: 17532, SEQ ID NO: 17533, SEQ ID NO: 17535, SEQ ID  
 30 NO: 17537, SEQ ID NO: 17539, SEQ ID NO: 17541, SEQ ID NO: 17543, SEQ ID NO: 17545,  
 SEQ ID NO: 17547, SEQ ID NO: 17549, SEQ ID NO: 17551, SEQ ID NO: 17553, SEQ ID  
 NO: 17555, SEQ ID NO: 17557, SEQ ID NO: 17559, SEQ ID NO: 17561, SEQ ID NO: 17563,  
 35 SEQ ID NO: 17565, SEQ ID NO: 17567, SEQ ID NO: 17569, SEQ ID NO: 17571, SEQ ID  
 NO: 17572, SEQ ID NO: 17574, SEQ ID NO: 17576, SEQ ID NO: 17578, SEQ ID NO: 17579,  
 SEQ ID NO: 17581, SEQ ID NO: 17583, SEQ ID NO: 17585, SEQ ID NO: 17586, SEQ ID  
 40 NO: 17588, SEQ ID NO: 17589, SEQ ID NO: 17591, SEQ ID NO: 17593, SEQ ID NO: 17594,  
 SEQ ID NO: 17596, SEQ ID NO: 17598, SEQ ID NO: 17600, SEQ ID NO: 17602, SEQ ID  
 NO: 17604, SEQ ID NO: 17606, SEQ ID NO: 17608, SEQ ID NO: 17610, SEQ ID NO: 17612,  
 45 SEQ ID NO: 17614, SEQ ID NO: 17616, SEQ ID NO: 17618, SEQ ID NO: 17620, SEQ ID  
 NO: 17622, SEQ ID NO: 17624, SEQ ID NO: 17626, SEQ ID NO: 17628, SEQ ID NO: 17630,  
 SEQ ID NO: 17632, SEQ ID NO: 17634, SEQ ID NO: 17636, SEQ ID NO: 17638, SEQ ID  
 NO: 17640, SEQ ID NO: 17642, SEQ ID NO: 17644, SEQ ID NO: 17646, SEQ ID NO: 17648,  
 50 SEQ ID NO: 17649, SEQ ID NO: 17650, SEQ ID NO: 17652, SEQ ID NO: 17654, SEQ ID  
 NO: 17656, SEQ ID NO: 17657, SEQ ID NO: 17659, SEQ ID NO: 17660, SEQ ID NO: 17662,  
 SEQ ID NO: 17663, SEQ ID NO: 17665, SEQ ID NO: 17666, SEQ ID NO: 17668, SEQ ID  
 NO: 17670, SEQ ID NO: 17672, SEQ ID NO: 17674, SEQ ID NO: 17676, SEQ ID NO: 17678,  
 55 SEQ ID NO: 17680, SEQ ID NO: 17681, SEQ ID NO: 17682, SEQ ID NO: 17683, SEQ ID  
 NO: 17685, SEQ ID NO: 17687, SEQ ID NO: 17689, SEQ ID NO: 17691, SEQ ID NO: 17693,  
 SEQ ID NO: 17695, SEQ ID NO: 17697, SEQ ID NO: 17699, SEQ ID NO: 17701, SEQ ID  
 NO: 17703, SEQ ID NO: 17705, SEQ ID NO: 17706, SEQ ID NO: 17708, SEQ ID NO: 17710,  
 60 SEQ ID NO: 17712,  
 SEQ ID NO: 17714, SEQ ID NO: 17716, SEQ ID NO: 17717, SEQ ID NO: 17718, SEQ ID  
 NO: 17720, SEQ ID NO: 17721, SEQ ID NO: 17722, SEQ ID NO: 17723, SEQ ID NO: 17724,  
 SEQ ID NO: 17726, SEQ ID NO: 17728, SEQ ID NO: 17729, SEQ ID NO: 17730, SEQ ID  
 65 NO: 17732, SEQ ID NO: 17733, SEQ ID NO: 17735, SEQ ID NO: 17737, SEQ ID NO: 17739,  
 SEQ ID NO: 17740, SEQ ID NO: 17742, SEQ ID NO: 17744, SEQ ID NO: 17746, SEQ ID  
 NO: 17747, SEQ ID NO: 17748, SEQ ID NO: 17750, SEQ ID NO: 17751, SEQ ID NO: 17753,  
 70 SEQ ID NO: 17754, SEQ ID NO: 17756, SEQ ID NO: 17758, SEQ ID NO: 17759, SEQ ID  
 NO: 17761, SEQ ID NO: 17762, SEQ ID NO: 17763, SEQ ID NO: 17764, SEQ ID NO: 17765,  
 SEQ ID NO: 17767, SEQ ID NO: 17768, SEQ ID NO: 17769, SEQ ID NO: 17770, SEQ ID  
 75 NO: 17771, SEQ ID NO: 17773, SEQ ID NO: 17774, SEQ ID NO: 17776, SEQ ID NO: 17778,  
 SEQ ID NO: 17780, SEQ ID NO: 17781, SEQ ID NO: 17783, SEQ ID NO: 17785, SEQ ID  
 NO: 17787, SEQ ID NO: 17789, SEQ ID NO: 17790, SEQ ID NO: 17792, SEQ ID NO: 17794,  
 80 SEQ ID NO: 17795, SEQ ID NO: 17797, SEQ ID NO: 17799, SEQ ID NO: 17801, SEQ ID  
 NO: 17802, SEQ ID NO: 17803, SEQ ID NO: 17805, SEQ ID NO: 17806, SEQ ID NO: 17807,







SEQ ID NO: 18938, SEQ ID NO: 18940, SEQ ID NO: 18941, SEQ ID NO: 18943, SEQ ID  
NO: 18944, SEQ ID NO: 18946, SEQ ID NO: 18947, SEQ ID NO: 18949, SEQ ID NO: 18951,  
5 SEQ ID NO: 18953, SEQ ID NO: 18955, SEQ ID NO: 18956, SEQ ID NO: 18957, SEQ ID  
NO: 18958, SEQ ID NO: 18959, SEQ ID NO: 18960, SEQ ID NO: 18962, SEQ ID NO: 18964,  
SEQ ID NO: 18966, SEQ ID NO: 18968, SEQ ID NO: 18969, SEQ ID NO: 18970, SEQ ID  
NO: 18972, SEQ ID NO: 18973, SEQ ID NO: 18975, SEQ ID NO: 18976, SEQ ID NO: 18978,  
10 SEQ ID NO: 18980,  
SEQ ID NO: 18981, SEQ ID NO: 18982, SEQ ID NO: 18983, SEQ ID NO: 18984, SEQ ID  
NO: 18985, SEQ ID NO: 18986, SEQ ID NO: 18987, SEQ ID NO: 18988, SEQ ID NO: 18989,  
SEQ ID NO: 18990, SEQ ID NO: 18992, SEQ ID NO: 18993, SEQ ID NO: 18995, SEQ ID  
NO: 18997, SEQ ID NO: 18998, SEQ ID NO: 18999, SEQ ID NO: 19000, SEQ ID NO: 19001,  
15 SEQ ID NO: 19002, SEQ ID NO: 19004, SEQ ID NO: 19006  
SEQ ID NO: 19007, SEQ ID NO: 19009, SEQ ID NO: 19011, SEQ ID NO: 19012, SEQ ID  
NO: 19013, SEQ ID NO: 19014, SEQ ID NO: 19016, SEQ ID NO: 19018, SEQ ID NO: 19020,  
SEQ ID NO: 19022, SEQ ID NO: 19024, and SEQ ID NO: 19025

20 (b) a polynucleotide comprising a nucleotide sequence encoding a protein comprising the amino acid sequence  
set forth in any one of the following SEQ ID NOs:

25

30

35

40

45

50

55

SEQ ID NO:10469, SEQ ID NO:10474, SEQ ID NO:10476, SEQ ID NO:10478, SEQ ID  
NO:10480, SEQ ID NO:10482, SEQ ID NO:10484, SEQ ID NO:10486, SEQ ID NO:10490,  
SEQ ID NO:10492, SEQ ID NO:10494, SEQ ID NO:10499, SEQ ID NO:10501, SEQ ID  
5 NO:10506, SEQ ID NO:10509, SEQ ID NO:10513, SEQ ID NO:10515, SEQ ID NO:10518,  
SEQ ID NO:10520, SEQ ID NO:10522, SEQ ID NO:10525, SEQ ID NO:10527, SEQ ID  
NO:10531, SEQ ID NO:10533, SEQ ID NO:10536, SEQ ID NO:10538, SEQ ID NO:10541,  
10 SEQ ID NO:10544, SEQ ID NO:10547, SEQ ID NO:10549, SEQ ID NO:10552, SEQ ID  
NO:10554, SEQ ID NO:10559, SEQ ID NO:10561, SEQ ID NO:10563, SEQ ID NO:10565,  
SEQ ID NO:10568, SEQ ID NO:10570, SEQ ID NO:10572, SEQ ID NO:10575, SEQ ID  
NO:10577, SEQ ID NO:10579, SEQ ID NO:10581, SEQ ID NO:10583, SEQ ID NO:10585,  
15 SEQ ID NO:10587, SEQ ID NO:10589, SEQ ID NO:10591, SEQ ID NO:10593, SEQ ID  
NO:10595, SEQ ID NO:10598, SEQ ID NO:10600, SEQ ID NO:10602, SEQ ID NO:10605,  
SEQ ID NO:10608, SEQ ID NO:10610, SEQ ID NO:10612, SEQ ID NO:10617, SEQ ID  
NO:10621, SEQ ID NO:10623, SEQ ID NO:10626, SEQ ID NO:10628, SEQ ID NO:10631,  
20 SEQ ID NO:10634, SEQ ID NO:10636, SEQ ID NO:10638, SEQ ID NO:10640, SEQ ID  
NO:10643, SEQ ID NO:10645, SEQ ID NO:10651, SEQ ID NO:10653, SEQ ID NO:10657,  
SEQ ID NO:10660, SEQ ID NO:10662, SEQ ID NO:10664, SEQ ID NO:10666, SEQ ID  
NO:10668, SEQ ID NO:10672, SEQ ID NO:10675, SEQ ID NO:10677, SEQ ID NO:10679,  
25 SEQ ID NO:10681, SEQ ID NO:10684, SEQ ID NO:10686, SEQ ID NO:10688, SEQ ID  
NO:10690, SEQ ID NO:10692, SEQ ID NO:10694, SEQ ID NO:10697, SEQ ID NO:10699,  
SEQ ID NO:10701, SEQ ID NO:10703, SEQ ID NO:10705, SEQ ID NO:10707, SEQ ID  
NO:10709, SEQ ID NO:10712, SEQ ID NO:10714, SEQ ID NO:10716, SEQ ID NO:10719,  
30 SEQ ID NO:10721,  
SEQ ID NO:10724, SEQ ID NO:10726, SEQ ID NO:10729, SEQ ID NO:10731, SEQ ID  
NO:10733, SEQ ID NO:10735, SEQ ID NO:10737, SEQ ID NO:10739, SEQ ID NO:10741,  
SEQ ID NO:10743, SEQ ID NO:10745, SEQ ID NO:10747, SEQ ID NO:10749, SEQ ID  
NO:10751, SEQ ID NO:10755, SEQ ID NO:10759, SEQ ID NO:10762, SEQ ID NO:10764,  
35 SEQ ID NO:10766, SEQ ID NO:10768, SEQ ID NO:10770, SEQ ID NO:10772, SEQ ID  
NO:10775, SEQ ID NO:10777, SEQ ID NO:10779, SEQ ID NO:10782, SEQ ID NO:10784,  
SEQ ID NO:10787, SEQ ID NO:10789, SEQ ID NO:10791, SEQ ID NO:10794, SEQ ID  
NO:10796, SEQ ID NO:10798, SEQ ID NO:10801, SEQ ID NO:10803, SEQ ID NO:10806,  
40 SEQ ID NO:10809, SEQ ID NO:10811, SEQ ID NO:10813, SEQ ID NO:10816, SEQ ID  
NO:10819, SEQ ID NO:10821, SEQ ID NO:10823, SEQ ID NO:10825, SEQ ID NO:10827,  
SEQ ID NO:10829, SEQ ID NO:10833, SEQ ID NO:10835, SEQ ID NO:10837, SEQ ID  
NO:10839, SEQ ID NO:10843, SEQ ID NO:10846, SEQ ID NO:10848, SEQ ID NO:10851,

45

50

55

SEQ ID NO:10853, SEQ ID NO:10855, SEQ ID NO:10857, SEQ ID NO:10860, SEQ ID  
 NO:10863, SEQ ID NO:10865, SEQ ID NO:10867, SEQ ID NO:10869, SEQ ID NO:10871,  
 5 SEQ ID NO:10874, SEQ ID NO:10877, SEQ ID NO:10880, SEQ ID NO:10882, SEQ ID  
 NO:10884, SEQ ID NO:10887, SEQ ID NO:10892, SEQ ID NO:10894, SEQ ID NO:10896,  
 SEQ ID NO:10899, SEQ ID NO:10903, SEQ ID NO:10905, SEQ ID NO:10907, SEQ ID  
 NO:10911, SEQ ID NO:10917, SEQ ID NO:10919, SEQ ID NO:10921, SEQ ID NO:10923,  
 10 SEQ ID NO:10926, SEQ ID NO:10930, SEQ ID NO:10932, SEQ ID NO:10934, SEQ ID  
 NO:10936, SEQ ID NO:10938, SEQ ID NO:10941, SEQ ID NO:10947, SEQ ID NO:10949,  
 SEQ ID NO:10951, SEQ ID NO:10953, SEQ ID NO:10955, SEQ ID NO:10961, SEQ ID  
 NO:10963, SEQ ID NO:10965, SEQ ID NO:10970, SEQ ID NO:10972, SEQ ID NO:10974,  
 SEQ ID NO:10976,  
 SEQ ID NO:10979, SEQ ID NO:10981, SEQ ID NO:10985, SEQ ID NO:10987, SEQ ID  
 NO:10989, SEQ ID NO:10991, SEQ ID NO:10993, SEQ ID NO:10995, SEQ ID NO:10997,  
 15 SEQ ID NO:10999, SEQ ID NO:11002, SEQ ID NO:11004, SEQ ID NO:11008, SEQ ID  
 NO:11010, SEQ ID NO:11013, SEQ ID NO:11015, SEQ ID NO:11017, SEQ ID NO:11020,  
 SEQ ID NO:11022, SEQ ID NO:11024, SEQ ID NO:11026, SEQ ID NO:11028, SEQ ID  
 NO:11031, SEQ ID NO:11033, SEQ ID NO:11037, SEQ ID NO:11039, SEQ ID NO:11041,  
 20 SEQ ID NO:11043, SEQ ID NO:11045, SEQ ID NO:11047, SEQ ID NO:11049, SEQ ID  
 NO:11051, SEQ ID NO:11053, SEQ ID NO:11055, SEQ ID NO:11057, SEQ ID NO:11059,  
 SEQ ID NO:11061, SEQ ID NO:11063, SEQ ID NO:11065, SEQ ID NO:11067, SEQ ID  
 NO:11069, SEQ ID NO:11071, SEQ ID NO:11073, SEQ ID NO:11075, SEQ ID NO:11077,  
 SEQ ID NO:11079, SEQ ID NO:11081, SEQ ID NO:11083, SEQ ID NO:11085, SEQ ID  
 NO:11087, SEQ ID NO:11089, SEQ ID NO:11091, SEQ ID NO:11094, SEQ ID NO:11096,  
 25 SEQ ID NO:11098, SEQ ID NO:11100, SEQ ID NO:11102, SEQ ID NO:11104, SEQ ID  
 NO:11106, SEQ ID NO:11109, SEQ ID NO:11111, SEQ ID NO:11113, SEQ ID NO:11115,  
 SEQ ID NO:11117, SEQ ID NO:11119, SEQ ID NO:11121, SEQ ID NO:11124, SEQ ID  
 NO:11126, SEQ ID NO:11128, SEQ ID NO:11130, SEQ ID NO:11132, SEQ ID NO:11134,  
 30 SEQ ID NO:11136, SEQ ID NO:11138, SEQ ID NO:11140, SEQ ID NO:11142, SEQ ID  
 NO:11144, SEQ ID NO:11146, SEQ ID NO:11149, SEQ ID NO:11151, SEQ ID NO:11153,  
 SEQ ID NO:11155, SEQ ID NO:11157, SEQ ID NO:11159, SEQ ID NO:11161, SEQ ID  
 NO:11163, SEQ ID NO:11166, SEQ ID NO:11169, SEQ ID NO:11171, SEQ ID NO:11173,  
 35 SEQ ID NO:11175, SEQ ID NO:11177, SEQ ID NO:11180, SEQ ID NO:11182, SEQ ID  
 NO:11184, SEQ ID NO:11186, SEQ ID NO:11188, SEQ ID NO:11190, SEQ ID NO:11192,  
 SEQ ID NO:11194,  
 SEQ ID NO:11196, SEQ ID NO:11198, SEQ ID NO:11200, SEQ ID NO:11202, SEQ ID  
 NO:11204, SEQ ID NO:11206, SEQ ID NO:11208, SEQ ID NO:11210, SEQ ID NO:11212,  
 40 SEQ ID NO:11214, SEQ ID NO:11216, SEQ ID NO:11218, SEQ ID NO:11220, SEQ ID  
 NO:11222, SEQ ID NO:11224, SEQ ID NO:11226, SEQ ID NO:11228, SEQ ID NO:11230,  
 SEQ ID NO:11232, SEQ ID NO:11234, SEQ ID NO:11236, SEQ ID NO:11238, SEQ ID  
 NO:11240, SEQ ID NO:11242, SEQ ID NO:11245, SEQ ID NO:11247, SEQ ID NO:11249,  
 SEQ ID NO:11251, SEQ ID NO:11254, SEQ ID NO:11256, SEQ ID NO:11258, SEQ ID  
 NO:11260, SEQ ID NO:11262, SEQ ID NO:11264, SEQ ID NO:11266, SEQ ID NO:11268,  
 45 SEQ ID NO:11270, SEQ ID NO:11272, SEQ ID NO:11274, SEQ ID NO:11276, SEQ ID  
 NO:11278, SEQ ID NO:11280, SEQ ID NO:11282, SEQ ID NO:11284, SEQ ID NO:11286,  
 SEQ ID NO:11288, SEQ ID NO:11290, SEQ ID NO:11292, SEQ ID NO:11294, SEQ ID  
 NO:11296, SEQ ID NO:11298, SEQ ID NO:11300, SEQ ID NO:11302, SEQ ID NO:11305,  
 SEQ ID NO:11307, SEQ ID NO:11309, SEQ ID NO:11311, SEQ ID NO:11313, SEQ ID  
 50 NO:11315, SEQ ID NO:11317, SEQ ID NO:11320, SEQ ID NO:11322, SEQ ID NO:11324,  
 SEQ ID NO:11326, SEQ ID NO:11328, SEQ ID NO:11330, SEQ ID NO:11332, SEQ ID  
 NO:11334, SEQ ID NO:11336, SEQ ID NO:11338, SEQ ID NO:11340, SEQ ID NO:11342,  
 SEQ ID NO:11344, SEQ ID NO:11346, SEQ ID NO:11348, SEQ ID NO:11350, SEQ ID  
 NO:11353, SEQ ID NO:11355, SEQ ID NO:11357, SEQ ID NO:11359, SEQ ID NO:11361,

5           SEQ ID NO:11363, SEQ ID NO:11365, SEQ ID NO:11367, SEQ ID NO:11371, SEQ ID  
 NO:11373, SEQ ID NO:11375, SEQ ID NO:11377, SEQ ID NO:11379, SEQ ID NO:11381,  
 SEQ ID NO:11383, SEQ ID NO:11385, SEQ ID NO:11387, SEQ ID NO:11389, SEQ ID  
 NO:11391, SEQ ID NO:11393, SEQ ID NO:11395, SEQ ID NO:11398, SEQ ID NO:11400,  
 SEQ ID NO:11402,  
 10          SEQ ID NO:11404, SEQ ID NO:11406, SEQ ID NO:11408, SEQ ID NO:11410, SEQ ID  
 NO:11412, SEQ ID NO:11414, SEQ ID NO:11417, SEQ ID NO:11420, SEQ ID NO:11422,  
 SEQ ID NO:11424, SEQ ID NO:11426, SEQ ID NO:11428, SEQ ID NO:11431, SEQ ID  
 NO:11433, SEQ ID NO:11435, SEQ ID NO:11438, SEQ ID NO:11440, SEQ ID NO:11442,  
 SEQ ID NO:11444, SEQ ID NO:11446, SEQ ID NO:11448, SEQ ID NO:11450, SEQ ID  
 NO:11452, SEQ ID NO:11454, SEQ ID NO:11456, SEQ ID NO:11458, SEQ ID NO:11460,  
 SEQ ID NO:11462, SEQ ID NO:11464, SEQ ID NO:11466, SEQ ID NO:11468, SEQ ID  
 NO:11471, SEQ ID NO:11473, SEQ ID NO:11475, SEQ ID NO:11477, SEQ ID NO:11479,  
 15          SEQ ID NO:11481, SEQ ID NO:11483, SEQ ID NO:11486, SEQ ID NO:11488, SEQ ID  
 NO:11490, SEQ ID NO:11492, SEQ ID NO:11494, SEQ ID NO:11497, SEQ ID NO:11499,  
 SEQ ID NO:11501, SEQ ID NO:11503, SEQ ID NO:11505, SEQ ID NO:11508, SEQ ID  
 NO:11510, SEQ ID NO:11512, SEQ ID NO:11514, SEQ ID NO:11516, SEQ ID NO:11518,  
 20          SEQ ID NO:11520, SEQ ID NO:11522, SEQ ID NO:11525, SEQ ID NO:11527, SEQ ID  
 NO:11529, SEQ ID NO:11531, SEQ ID NO:11533, SEQ ID NO:11535, SEQ ID NO:11537,  
 SEQ ID NO:11539, SEQ ID NO:11542, SEQ ID NO:11544, SEQ ID NO:11546, SEQ ID  
 NO:11548, SEQ ID NO:11550, SEQ ID NO:11552, SEQ ID NO:11554, SEQ ID NO:11556,  
 25          SEQ ID NO:11558, SEQ ID NO:11563, SEQ ID NO:11565, SEQ ID NO:11567, SEQ ID  
 NO:11570, SEQ ID NO:11572, SEQ ID NO:11574, SEQ ID NO:11576, SEQ ID NO:11578,  
 SEQ ID NO:11580, SEQ ID NO:11583, SEQ ID NO:11585, SEQ ID NO:11587, SEQ ID  
 NO:11589, SEQ ID NO:11591, SEQ ID NO:11593, SEQ ID NO:11595, SEQ ID NO:11597,  
 30          SEQ ID NO:11599, SEQ ID NO:11601, SEQ ID NO:11603, SEQ ID NO:11605, SEQ ID  
 NO:11607, SEQ ID NO:11610, SEQ ID NO:11612, SEQ ID NO:11614, SEQ ID NO:11616,  
 SEQ ID NO:11618,  
 35          SEQ ID NO:11621, SEQ ID NO:11623, SEQ ID NO:11625, SEQ ID NO:11627, SEQ ID  
 NO:11629, SEQ ID NO:11631, SEQ ID NO:11633, SEQ ID NO:11635, SEQ ID NO:11637,  
 SEQ ID NO:11640, SEQ ID NO:11642, SEQ ID NO:11644, SEQ ID NO:11646, SEQ ID  
 NO:11648, SEQ ID NO:11650, SEQ ID NO:11652, SEQ ID NO:11655, SEQ ID NO:11657,  
 40          SEQ ID NO:11660, SEQ ID NO:11662, SEQ ID NO:11664, SEQ ID NO:11667, SEQ ID  
 NO:11669, SEQ ID NO:11671, SEQ ID NO:11673, SEQ ID NO:11676, SEQ ID NO:11679,  
 SEQ ID NO:11681, SEQ ID NO:11683, SEQ ID NO:11686, SEQ ID NO:11688, SEQ ID  
 NO:11690, SEQ ID NO:11692, SEQ ID NO:11694, SEQ ID NO:11696, SEQ ID NO:11698,  
 45          SEQ ID NO:11700, SEQ ID NO:11702, SEQ ID NO:11704, SEQ ID NO:11706, SEQ ID  
 NO:11708, SEQ ID NO:11710, SEQ ID NO:11712, SEQ ID NO:11714, SEQ ID NO:11716,  
 SEQ ID NO:11719, SEQ ID NO:11721, SEQ ID NO:11723, SEQ ID NO:11725, SEQ ID  
 NO:11727, SEQ ID NO:11729, SEQ ID NO:11731, SEQ ID NO:11733, SEQ ID NO:11735,  
 50          SEQ ID NO:11737, SEQ ID NO:11741, SEQ ID NO:11743, SEQ ID NO:11745, SEQ ID  
 NO:11747, SEQ ID NO:11749, SEQ ID NO:11751, SEQ ID NO:11753, SEQ ID NO:11755,  
 SEQ ID NO:11757, SEQ ID NO:11760, SEQ ID NO:11762, SEQ ID NO:11764, SEQ ID  
 NO:11766, SEQ ID NO:11769, SEQ ID NO:11771, SEQ ID NO:11773, SEQ ID NO:11775,  
 SEQ ID NO:11777, SEQ ID NO:11779, SEQ ID NO:11781, SEQ ID NO:11783, SEQ ID  
 NO:11785, SEQ ID NO:11787, SEQ ID NO:11789, SEQ ID NO:11791, SEQ ID NO:11793,  
 SEQ ID NO:11795, SEQ ID NO:11797, SEQ ID NO:11799, SEQ ID NO:11801, SEQ ID  
 NO:11803, SEQ ID NO:11805, SEQ ID NO:11807, SEQ ID NO:11809, SEQ ID NO:11812,  
 SEQ ID NO:11814, SEQ ID NO:11816, SEQ ID NO:11818, SEQ ID NO:11821, SEQ ID  
 NO:11823, SEQ ID NO:11825, SEQ ID NO:11827, SEQ ID NO:11829, SEQ ID NO:11831,  
 55          SEQ ID NO:11834,



SEQ ID NO:12312, SEQ ID NO:12314, SEQ ID NO:12316, SEQ ID NO:12318, SEQ ID  
NO:12320, SEQ ID NO:12322, SEQ ID NO:12324, SEQ ID NO:12326, SEQ ID NO:12328,  
SEQ ID NO:12330, SEQ ID NO:12332, SEQ ID NO:12334, SEQ ID NO:12336, SEQ ID  
NO:12338, SEQ ID NO:12340, SEQ ID NO:12342, SEQ ID NO:12344, SEQ ID NO:12346,  
SEQ ID NO:12348, SEQ ID NO:12350, SEQ ID NO:12352, SEQ ID NO:12355, SEQ ID  
NO:12357, SEQ ID NO:12359, SEQ ID NO:12361, SEQ ID NO:12363, SEQ ID NO:12365,  
SEQ ID NO:12367, SEQ ID NO:12369, SEQ ID NO:12371, SEQ ID NO:12373, SEQ ID  
NO:12375, SEQ ID NO:12377, SEQ ID NO:12379, SEQ ID NO:12381, SEQ ID NO:12383,  
SEQ ID NO:12385, SEQ ID NO:12387, SEQ ID NO:12389, SEQ ID NO:12391, SEQ ID  
NO:12393, SEQ ID NO:12395, SEQ ID NO:12397, SEQ ID NO:12399, SEQ ID NO:12401,  
SEQ ID NO:12404, SEQ ID NO:12406, SEQ ID NO:12408, SEQ ID NO:12411, SEQ ID  
NO:12413, SEQ ID NO:12415, SEQ ID NO:12418, SEQ ID NO:12420, SEQ ID NO:12422,  
SEQ ID NO:12424, SEQ ID NO:12426, SEQ ID NO:12428, SEQ ID NO:12430, SEQ ID  
NO:12432, SEQ ID NO:12434, SEQ ID NO:12437, SEQ ID NO:12439, SEQ ID NO:12441,  
SEQ ID NO:12443, SEQ ID NO:12445, SEQ ID NO:12447, SEQ ID NO:12449, SEQ ID  
NO:12451, SEQ ID NO:12453, SEQ ID NO:12455, SEQ ID NO:12457, SEQ ID NO:12459,  
SEQ ID NO:12462,  
SEQ ID NO:12464, SEQ ID NO:12466, SEQ ID NO:12468, SEQ ID NO:12470, SEQ ID  
NO:12472, SEQ ID NO:12474, SEQ ID NO:12476, SEQ ID NO:12478, SEQ ID NO:12480,  
SEQ ID NO:12484, SEQ ID NO:12487, SEQ ID NO:12489, SEQ ID NO:12492, SEQ ID  
NO:12494, SEQ ID NO:12497, SEQ ID NO:12499, SEQ ID NO:12501, SEQ ID NO:12504,  
SEQ ID NO:12506, SEQ ID NO:12508, SEQ ID NO:12510, SEQ ID NO:12512, SEQ ID  
NO:12515, SEQ ID NO:12517, SEQ ID NO:12519, SEQ ID NO:12521, SEQ ID NO:12523,  
SEQ ID NO:12525, SEQ ID NO:12527, SEQ ID NO:12530, SEQ ID NO:12532, SEQ ID  
NO:12536, SEQ ID NO:12538, SEQ ID NO:12540, SEQ ID NO:12542, SEQ ID NO:12544,  
SEQ ID NO:12547, SEQ ID NO:12549, SEQ ID NO:12551, SEQ ID NO:12553, SEQ ID  
NO:12558, SEQ ID NO:12560, SEQ ID NO:12562, SEQ ID NO:12564, SEQ ID NO:12566,  
SEQ ID NO:12568, SEQ ID NO:12570, SEQ ID NO:12573, SEQ ID NO:12575, SEQ ID  
NO:12577, SEQ ID NO:12579, SEQ ID NO:12582, SEQ ID NO:12584, SEQ ID NO:12586,  
SEQ ID NO:12588, SEQ ID NO:12590, SEQ ID NO:12594, SEQ ID NO:12596, SEQ ID  
NO:12598, SEQ ID NO:12600, SEQ ID NO:12602, SEQ ID NO:12604, SEQ ID NO:12606,  
SEQ ID NO:12610, SEQ ID NO:12612, SEQ ID NO:12614, SEQ ID NO:12616, SEQ ID  
NO:12618, SEQ ID NO:12620, SEQ ID NO:12624, SEQ ID NO:12626, SEQ ID NO:12629,  
SEQ ID NO:12631, SEQ ID NO:12633, SEQ ID NO:12635, SEQ ID NO:12637, SEQ ID  
NO:12639, SEQ ID NO:12641, SEQ ID NO:12643, SEQ ID NO:12645, SEQ ID NO:12647,  
SEQ ID NO:12650, SEQ ID NO:12652, SEQ ID NO:12654, SEQ ID NO:12656, SEQ ID  
NO:12658, SEQ ID NO:12661, SEQ ID NO:12663, SEQ ID NO:12666, SEQ ID NO:12668,  
SEQ ID NO:12670, SEQ ID NO:12672, SEQ ID NO:12674, SEQ ID NO:12676, SEQ ID  
NO:12678, SEQ ID NO:12680, SEQ ID NO:12682, SEQ ID NO:12684, SEQ ID NO:12686,  
SEQ ID NO:12688,  
SEQ ID NO:12690, SEQ ID NO:12692, SEQ ID NO:12694, SEQ ID NO:12696, SEQ ID  
NO:12699, SEQ ID NO:12701, SEQ ID NO:12704, SEQ ID NO:12706, SEQ ID NO:12708,  
SEQ ID NO:12712, SEQ ID NO:12714, SEQ ID NO:12716, SEQ ID NO:12718, SEQ ID  
NO:12720, SEQ ID NO:12722, SEQ ID NO:12724, SEQ ID NO:12727, SEQ ID NO:12729,  
SEQ ID NO:12732, SEQ ID NO:12734, SEQ ID NO:12736, SEQ ID NO:12738, SEQ ID  
NO:12740, SEQ ID NO:12742, SEQ ID NO:12744, SEQ ID NO:12746, SEQ ID NO:12748,  
SEQ ID NO:12750, SEQ ID NO:12752, SEQ ID NO:12755, SEQ ID NO:12757, SEQ ID  
NO:12759, SEQ ID NO:12761, SEQ ID NO:12766, SEQ ID NO:12768, SEQ ID NO:12772,  
SEQ ID NO:12774, SEQ ID NO:12777, SEQ ID NO:12779, SEQ ID NO:12782, SEQ ID  
NO:12784, SEQ ID NO:12786, SEQ ID NO:12788, SEQ ID NO:12790, SEQ ID NO:12792,  
SEQ ID NO:12794, SEQ ID NO:12796, SEQ ID NO:12802, SEQ ID NO:12804, SEQ ID  
NO:12807, SEQ ID NO:12809, SEQ ID NO:12811, SEQ ID NO:12814, SEQ ID NO:12816.

SEQ ID NO:12818, SEQ ID NO:12820, SEQ ID NO:12822, SEQ ID NO:12824, SEQ ID  
 NO:12826, SEQ ID NO:12828, SEQ ID NO:12830, SEQ ID NO:12832, SEQ ID NO:12834,  
 5 SEQ ID NO:12836, SEQ ID NO:12838, SEQ ID NO:12840, SEQ ID NO:12842, SEQ ID  
 NO:12844, SEQ ID NO:12846, SEQ ID NO:12849, SEQ ID NO:12851, SEQ ID NO:12853,  
 SEQ ID NO:12855, SEQ ID NO:12857, SEQ ID NO:12859, SEQ ID NO:12861, SEQ ID  
 NO:12863, SEQ ID NO:12865, SEQ ID NO:12869, SEQ ID NO:12872, SEQ ID NO:12875,  
 10 SEQ ID NO:12877, SEQ ID NO:12879, SEQ ID NO:12882, SEQ ID NO:12884, SEQ ID  
 NO:12886, SEQ ID NO:12888, SEQ ID NO:12890, SEQ ID NO:12893, SEQ ID NO:12895,  
 SEQ ID NO:12898, SEQ ID NO:12900, SEQ ID NO:12902, SEQ ID NO:12904, SEQ ID  
 NO:12906, SEQ ID NO:12908, SEQ ID NO:12910, SEQ ID NO:12912, SEQ ID NO:12914,  
 SEQ ID NO:12917,  
 SEQ ID NO:12919, SEQ ID NO:12921, SEQ ID NO:12924, SEQ ID NO:12926, SEQ ID  
 15 NO:12928, SEQ ID NO:12930, SEQ ID NO:12932, SEQ ID NO:12935, SEQ ID NO:12937,  
 SEQ ID NO:12939, SEQ ID NO:12942, SEQ ID NO:12944, SEQ ID NO:12946, SEQ ID  
 NO:12948, SEQ ID NO:12951, SEQ ID NO:12954, SEQ ID NO:12957, SEQ ID NO:12959,  
 SEQ ID NO:12962, SEQ ID NO:12964, SEQ ID NO:12968, SEQ ID NO:12970, SEQ ID  
 NO:12972, SEQ ID NO:12974, SEQ ID NO:12976, SEQ ID NO:12978, SEQ ID NO:12980,  
 20 SEQ ID NO:12982, SEQ ID NO:12984, SEQ ID NO:12986, SEQ ID NO:12988, SEQ ID  
 NO:12990, SEQ ID NO:12992, SEQ ID NO:12994, SEQ ID NO:12996, SEQ ID NO:12998,  
 SEQ ID NO:13000, SEQ ID NO:13002, SEQ ID NO:13004, SEQ ID NO:13006, SEQ ID  
 NO:13008, SEQ ID NO:13010, SEQ ID NO:13012, SEQ ID NO:13014, SEQ ID NO:13016,  
 25 SEQ ID NO:13019, SEQ ID NO:13022, SEQ ID NO:13024, SEQ ID NO:13026, SEQ ID  
 NO:13028, SEQ ID NO:13030, SEQ ID NO:13032, SEQ ID NO:13034, SEQ ID NO:13036,-  
 SEQ ID NO:13038, SEQ ID NO:13041, SEQ ID NO:13043, SEQ ID NO:13045, SEQ ID  
 NO:13047, SEQ ID NO:13049, SEQ ID NO:13051, SEQ ID NO:13054, SEQ ID NO:13056,  
 30 SEQ ID NO:13059, SEQ ID NO:13062, SEQ ID NO:13064, SEQ ID NO:13066, SEQ ID  
 NO:13068, SEQ ID NO:13070, SEQ ID NO:13073, SEQ ID NO:13075, SEQ ID NO:13078,  
 SEQ ID NO:13080, SEQ ID NO:13082, SEQ ID NO:13084, SEQ ID NO:13086, SEQ ID  
 NO:13090, SEQ ID NO:13093, SEQ ID NO:13095, SEQ ID NO:13098, SEQ ID NO:13100,  
 35 SEQ ID NO:13102, SEQ ID NO:13104, SEQ ID NO:13106, SEQ ID NO:13111, SEQ ID  
 NO:13113, SEQ ID NO:13115, SEQ ID NO:13117, SEQ ID NO:13121, SEQ ID NO:13123,  
 SEQ ID NO:13126, SEQ ID NO:13128, SEQ ID NO:13130, SEQ ID NO:13132, SEQ ID  
 NO:13134, SEQ ID NO:13136, SEQ ID NO:13138, SEQ ID NO:13140, SEQ ID NO:13142,  
 40 SEQ ID NO:13146,  
 SEQ ID NO:13148, SEQ ID NO:13150, SEQ ID NO:13153, SEQ ID NO:13155, SEQ ID  
 NO:13157, SEQ ID NO:13159, SEQ ID NO:13161, SEQ ID NO:13163, SEQ ID NO:13165,  
 SEQ ID NO:13167, SEQ ID NO:13169, SEQ ID NO:13171, SEQ ID NO:13173, SEQ ID  
 NO:13175, SEQ ID NO:13179, SEQ ID NO:13182, SEQ ID NO:13184, SEQ ID NO:13186,  
 45 SEQ ID NO:13188, SEQ ID NO:13190, SEQ ID NO:13192, SEQ ID NO:13194, SEQ ID  
 NO:13196, SEQ ID NO:13199, SEQ ID NO:13202, SEQ ID NO:13204, SEQ ID NO:13206,  
 SEQ ID NO:13208, SEQ ID NO:13210, SEQ ID NO:13212, SEQ ID NO:13214, SEQ ID  
 NO:13217, SEQ ID NO:13220, SEQ ID NO:13223, SEQ ID NO:13225, SEQ ID NO:13227,  
 SEQ ID NO:13229, SEQ ID NO:13231, SEQ ID NO:13233, SEQ ID NO:13236, SEQ ID  
 NO:13240, SEQ ID NO:13244, SEQ ID NO:13247, SEQ ID NO:13249, SEQ ID NO:13251,  
 50 SEQ ID NO:13253, SEQ ID NO:13255, SEQ ID NO:13258, SEQ ID NO:13262, SEQ ID  
 NO:13265, SEQ ID NO:13267, SEQ ID NO:13269, SEQ ID NO:13272, SEQ ID NO:13274,  
 SEQ ID NO:13277, SEQ ID NO:13281, SEQ ID NO:13283, SEQ ID NO:13285, SEQ ID  
 NO:13287, SEQ ID NO:13289,  
 55 SEQ ID NO:13295, SEQ ID NO:13297, SEQ ID NO:13299, SEQ ID NO:13301, SEQ ID  
 NO:13303, SEQ ID NO:13305, SEQ ID NO:13308, SEQ ID NO:13311, SEQ ID NO:13313,  
 SEQ ID NO:13315, SEQ ID NO:13317, SEQ ID NO:13320, SEQ ID NO:13323, SEQ ID  
 NO:13326, SEQ ID NO:13329, SEQ ID NO:13331, SEQ ID NO:13335, SEQ ID NO:13340,



SEQ ID NO:13987, SEQ ID NO:13991, SEQ ID NO:13993, SEQ ID NO:13995, SEQ ID  
 NO:13997, SEQ ID NO:14000, SEQ ID NO:14002, SEQ ID NO:14004, SEQ ID NO:14007,  
 5 SEQ ID NO:14009, SEQ ID NO:14011, SEQ ID NO:14017, SEQ ID NO:14020, SEQ ID  
 NO:14022, SEQ ID NO:14024, SEQ ID NO:14027, SEQ ID NO:14029, SEQ ID NO:14032,  
 SEQ ID NO:14034, SEQ ID NO:14036, SEQ ID NO:14038, SEQ ID NO:14040, SEQ ID  
 NO:14043, SEQ ID NO:14046, SEQ ID NO:14048, SEQ ID NO:14051, SEQ ID NO:14055,  
 10 SEQ ID NO:14057, SEQ ID NO:14059, SEQ ID NO:14061, SEQ ID NO:14063, SEQ ID  
 NO:14065, SEQ ID NO:14068, SEQ ID NO:14070, SEQ ID NO:14074, SEQ ID NO:14078,  
 SEQ ID NO:14080, SEQ ID NO:14082, SEQ ID NO:14087, SEQ ID NO:14089, SEQ ID  
 NO:14091, SEQ ID NO:14093, SEQ ID NO:14095, SEQ ID NO:14097, SEQ ID NO:14099,  
 15 SEQ ID NO:14101, SEQ ID NO:14103, SEQ ID NO:14105, SEQ ID NO:14107, SEQ ID  
 NO:14109, SEQ ID NO:14111, SEQ ID NO:14113, SEQ ID NO:14115, SEQ ID NO:14117,  
 SEQ ID NO:14119,  
 SEQ ID NO:14121, SEQ ID NO:14123, SEQ ID NO:14125, SEQ ID NO:14127, SEQ ID  
 NO:14130, SEQ ID NO:14132, SEQ ID NO:14134, SEQ ID NO:14136, SEQ ID NO:14138,  
 20 SEQ ID NO:14140, SEQ ID NO:14142, SEQ ID NO:14144, SEQ ID NO:14147, SEQ ID  
 NO:14149, SEQ ID NO:14151, SEQ ID NO:14153, SEQ ID NO:14155, SEQ ID NO:14157,  
 SEQ ID NO:14159, SEQ ID NO:14161, SEQ ID NO:14163, SEQ ID NO:14166, SEQ ID  
 NO:14170, SEQ ID NO:14172, SEQ ID NO:14174, SEQ ID NO:14176, SEQ ID NO:14178,  
 SEQ ID NO:14180, SEQ ID NO:14182, SEQ ID NO:14184, SEQ ID NO:14186, SEQ ID  
 NO:14189, SEQ ID NO:14191, SEQ ID NO:14193, SEQ ID NO:14195, SEQ ID NO:14197,  
 25 SEQ ID NO:14199, SEQ ID NO:14201, SEQ ID NO:14203, SEQ ID NO:14205, SEQ ID  
 NO:14207, SEQ ID NO:14209, SEQ ID NO:14211, SEQ ID NO:14213, SEQ ID NO:14215,  
 SEQ ID NO:14218, SEQ ID NO:14220, SEQ ID NO:14222, SEQ ID NO:14224, SEQ ID  
 NO:14226, SEQ ID NO:14228, SEQ ID NO:14230, SEQ ID NO:14232, SEQ ID NO:14234,  
 30 SEQ ID NO:14236, SEQ ID NO:14238, SEQ ID NO:14240, SEQ ID NO:14242, SEQ ID  
 NO:14244, SEQ ID NO:14246, SEQ ID NO:14248, SEQ ID NO:14250, SEQ ID NO:14252,  
 SEQ ID NO:14254, SEQ ID NO:14256, SEQ ID NO:14258, SEQ ID NO:14260, SEQ ID  
 NO:14262, SEQ ID NO:14264, SEQ ID NO:14267, SEQ ID NO:14269, SEQ ID NO:14271,  
 35 SEQ ID NO:14273, SEQ ID NO:14275, SEQ ID NO:14277, SEQ ID NO:14279, SEQ ID  
 NO:14281, SEQ ID NO:14283, SEQ ID NO:14285, SEQ ID NO:14288, SEQ ID NO:14290,  
 SEQ ID NO:14292, SEQ ID NO:14294, SEQ ID NO:14296, SEQ ID NO:14298, SEQ ID  
 NO:14301, SEQ ID NO:14303, SEQ ID NO:14306, SEQ ID NO:14308, SEQ ID NO:14310,  
 40 SEQ ID NO:14312, SEQ ID NO:14314, SEQ ID NO:14316, SEQ ID NO:14318, SEQ ID  
 NO:14320, SEQ ID NO:14322, SEQ ID NO:14324, SEQ ID NO:14326, SEQ ID NO:14328,  
 SEQ ID NO:14331,  
 SEQ ID NO:14334, SEQ ID NO:14337, SEQ ID NO:14340, SEQ ID NO:14342, SEQ ID  
 NO:14346, SEQ ID NO:14348, SEQ ID NO:14350, SEQ ID NO:14352, SEQ ID NO:14354,  
 45 SEQ ID NO:14356, SEQ ID NO:14358, SEQ ID NO:14360, SEQ ID NO:14362, SEQ ID  
 NO:14364, SEQ ID NO:14366, SEQ ID NO:14368, SEQ ID NO:14370, SEQ ID NO:14372,  
 SEQ ID NO:14374, SEQ ID NO:14376, SEQ ID NO:14379, SEQ ID NO:14381, SEQ ID  
 NO:14383, SEQ ID NO:14385, SEQ ID NO:14387, SEQ ID NO:14389, SEQ ID NO:14391,  
 SEQ ID NO:14393, SEQ ID NO:14396, SEQ ID NO:14398, SEQ ID NO:14401, SEQ ID  
 NO:14404, SEQ ID NO:14406, SEQ ID NO:14408, SEQ ID NO:14410, SEQ ID NO:14412,  
 50 SEQ ID NO:14414, SEQ ID NO:14416, SEQ ID NO:14418, SEQ ID NO:14420, SEQ ID  
 NO:14423, SEQ ID NO:14425, SEQ ID NO:14427, SEQ ID NO:14429, SEQ ID NO:14431,  
 SEQ ID NO:14433, SEQ ID NO:14435, SEQ ID NO:14437, SEQ ID NO:14440, SEQ ID  
 NO:14442, SEQ ID NO:14444, SEQ ID NO:14446, SEQ ID NO:14448, SEQ ID NO:14450,  
 SEQ ID NO:14452, SEQ ID NO:14454, SEQ ID NO:14456, SEQ ID NO:14458, SEQ ID  
 NO:14460, SEQ ID NO:14462, SEQ ID NO:14466, SEQ ID NO:14468, SEQ ID NO:14470,  
 55 SEQ ID NO:14472, SEQ ID NO:14474, SEQ ID NO:14476, SEQ ID NO:14478, SEQ ID  
 NO:14480, SEQ ID NO:14482, SEQ ID NO:14484, SEQ ID NO:14486, SEQ ID NO:14488,

SEQ ID NO:14490, SEQ ID NO:14492, SEQ ID NO:14494, SEQ ID NO:14496, SEQ ID  
NO:14498, SEQ ID NO:14500, SEQ ID NO:14502, SEQ ID NO:14505, SEQ ID NO:14507,  
SEQ ID NO:14509, SEQ ID NO:14511, SEQ ID NO:14514, SEQ ID NO:14516, SEQ ID  
NO:14518, SEQ ID NO:14520, SEQ ID NO:14522, SEQ ID NO:14524, SEQ ID NO:14526,  
SEQ ID NO:14530, SEQ ID NO:14532, SEQ ID NO:14534, SEQ ID NO:14536, SEQ ID  
NO:14538, SEQ ID NO:14541, SEQ ID NO:14543, SEQ ID NO:14546, SEQ ID NO:14548,  
SEQ ID NO:14550,  
10 SEQ ID NO:14553, SEQ ID NO:14555, SEQ ID NO:14557, SEQ ID NO:14559, SEQ ID  
NO:14561, SEQ ID NO:14563, SEQ ID NO:14565, SEQ ID NO:14567, SEQ ID NO:14569,  
SEQ ID NO:14571, SEQ ID NO:14573, SEQ ID NO:14575, SEQ ID NO:14577, SEQ ID  
NO:14579, SEQ ID NO:14581, SEQ ID NO:14583, SEQ ID NO:14585, SEQ ID NO:14587,  
SEQ ID NO:14589, SEQ ID NO:14591, SEQ ID NO:14593, SEQ ID NO:14596, SEQ ID  
NO:14598, SEQ ID NO:14600, SEQ ID NO:14602, SEQ ID NO:14604, SEQ ID NO:14606,  
15 SEQ ID NO:14608, SEQ ID NO:14612, SEQ ID NO:14614, SEQ ID NO:14616, SEQ ID  
NO:14618, SEQ ID NO:14621, SEQ ID NO:14623, SEQ ID NO:14625, SEQ ID NO:14627,  
SEQ ID NO:14629, SEQ ID NO:14631, SEQ ID NO:14634, SEQ ID NO:14636, SEQ ID  
NO:14638, SEQ ID NO:14640, SEQ ID NO:14642, SEQ ID NO:14645, SEQ ID NO:14647,  
20 SEQ ID NO:14649, SEQ ID NO:14651, SEQ ID NO:14653, SEQ ID NO:14655, SEQ ID  
NO:14657, SEQ ID NO:14659, SEQ ID NO:14661, SEQ ID NO:14663, SEQ ID NO:14665,  
SEQ ID NO:14667, SEQ ID NO:14669, SEQ ID NO:14671, SEQ ID NO:14673, SEQ ID  
NO:14675, SEQ ID NO:14677, SEQ ID NO:14680, SEQ ID NO:14682, SEQ ID NO:14684,  
25 SEQ ID NO:14687, SEQ ID NO:14689, SEQ ID NO:14691, SEQ ID NO:14694, SEQ ID  
NO:14696, SEQ ID NO:14698, SEQ ID NO:14701, SEQ ID NO:14703, SEQ ID NO:14705,  
SEQ ID NO:14707, SEQ ID NO:14709, SEQ ID NO:14711, SEQ ID NO:14714, SEQ ID  
NO:14716, SEQ ID NO:14718, SEQ ID NO:14720, SEQ ID NO:14723, SEQ ID NO:14726,  
SEQ ID NO:14728, SEQ ID NO:14730, SEQ ID NO:14733, SEQ ID NO:14736, SEQ ID  
NO:14739, SEQ ID NO:14741, SEQ ID NO:14743, SEQ ID NO:14745, SEQ ID NO:14747,  
30 SEQ ID NO:14749, SEQ ID NO:14751, SEQ ID NO:14753, SEQ ID NO:14756, SEQ ID  
NO:14759, SEQ ID NO:14761, SEQ ID NO:14763, SEQ ID NO:14765, SEQ ID NO:14767,  
SEQ ID NO:14769,  
SEQ ID NO:14771, SEQ ID NO:14773, SEQ ID NO:14775, SEQ ID NO:14777, SEQ ID  
NO:14779, SEQ ID NO:14781, SEQ ID NO:14783, SEQ ID NO:14785, SEQ ID NO:14787,  
35 SEQ ID NO:14789, SEQ ID NO:14791, SEQ ID NO:14793, SEQ ID NO:14795, SEQ ID  
NO:14797, SEQ ID NO:14799, SEQ ID NO:14801, SEQ ID NO:14803, SEQ ID NO:14805,  
SEQ ID NO:14807, SEQ ID NO:14810, SEQ ID NO:14813, SEQ ID NO:14815, SEQ ID  
NO:14817, SEQ ID NO:14819, SEQ ID NO:14821, SEQ ID NO:14825, SEQ ID NO:14827,  
40 SEQ ID NO:14829, SEQ ID NO:14832, SEQ ID NO:14834, SEQ ID NO:14836, SEQ ID  
NO:14838, SEQ ID NO:14840, SEQ ID NO:14842, SEQ ID NO:14844, SEQ ID NO:14846,  
SEQ ID NO:14848, SEQ ID NO:14851, SEQ ID NO:14853, SEQ ID NO:14855, SEQ ID  
NO:14857, SEQ ID NO:14859, SEQ ID NO:14861, SEQ ID NO:14863, SEQ ID NO:14866,  
45 SEQ ID NO:14868, SEQ ID NO:14870, SEQ ID NO:14873, SEQ ID NO:14875, SEQ ID  
NO:14877, SEQ ID NO:14879, SEQ ID NO:14881, SEQ ID NO:14883, SEQ ID NO:14885,  
SEQ ID NO:14887, SEQ ID NO:14889, SEQ ID NO:14891, SEQ ID NO:14893, SEQ ID  
NO:14895, SEQ ID NO:14897, SEQ ID NO:14899, SEQ ID NO:14901, SEQ ID NO:14903,  
50 SEQ ID NO:14905, SEQ ID NO:14907, SEQ ID NO:14909, SEQ ID NO:14911, SEQ ID  
NO:14913, SEQ ID NO:14915, SEQ ID NO:14917, SEQ ID NO:14920, SEQ ID NO:14922,  
SEQ ID NO:14926, SEQ ID NO:14928, SEQ ID NO:14930, SEQ ID NO:14932, SEQ ID  
NO:14934, SEQ ID NO:14936, SEQ ID NO:14939, SEQ ID NO:14941, SEQ ID NO:14943,  
SEQ ID NO:14945, SEQ ID NO:14947, SEQ ID NO:14949, SEQ ID NO:14951, SEQ ID  
NO:14953, SEQ ID NO:14955, SEQ ID NO:14957, SEQ ID NO:14959, SEQ ID NO:14962,  
55 SEQ ID NO:14964, SEQ ID NO:14966, SEQ ID NO:14968, SEQ ID NO:14970, SEQ ID

NO:14972, SEQ ID NO:14974, SEQ ID NO:14976, SEQ ID NO:14978, SEQ ID NO:14980,  
SEQ ID NO:14983,  
SEQ ID NO:14985, SEQ ID NO:14989, SEQ ID NO:14991, SEQ ID NO:14995, SEQ ID  
5 NO:14997, SEQ ID NO:14999, SEQ ID NO:15001, SEQ ID NO:15003, SEQ ID NO:15008,  
SEQ ID NO:15010, SEQ ID NO:15014, SEQ ID NO:15016, SEQ ID NO:15018, SEQ ID  
NO:15020, SEQ ID NO:15022, SEQ ID NO:15024, SEQ ID NO:15027, SEQ ID NO:15030,  
SEQ ID NO:15032, SEQ ID NO:15034, SEQ ID NO:15036, SEQ ID NO:15038, SEQ ID  
10 NO:15041, SEQ ID NO:15043, SEQ ID NO:15045, SEQ ID NO:15047, SEQ ID NO:15049,  
SEQ ID NO:15052, SEQ ID NO:15054, SEQ ID NO:15056, SEQ ID NO:15058, SEQ ID  
NO:15061, SEQ ID NO:15063, SEQ ID NO:15065, SEQ ID NO:15068, SEQ ID NO:15070,  
SEQ ID NO:15072, SEQ ID NO:15074, SEQ ID NO:15076, SEQ ID NO:15079, SEQ ID  
15 NO:15081, SEQ ID NO:15083, SEQ ID NO:15085, SEQ ID NO:15087, SEQ ID NO:15089,  
SEQ ID NO:15092, SEQ ID NO:15094, SEQ ID NO:15097, SEQ ID NO:15100, SEQ ID  
NO:15102, SEQ ID NO:15104, SEQ ID NO:15106, SEQ ID NO:15108, SEQ ID NO:15110,  
SEQ ID NO:15112, SEQ ID NO:15114, SEQ ID NO:15116, SEQ ID NO:15118, SEQ ID  
20 NO:15120, SEQ ID NO:15122, SEQ ID NO:15124, SEQ ID NO:15126, SEQ ID NO:15128,  
SEQ ID NO:15131, SEQ ID NO:15133, SEQ ID NO:15135, SEQ ID NO:15137, SEQ ID  
NO:15139, SEQ ID NO:15141, SEQ ID NO:15143, SEQ ID NO:15145, SEQ ID NO:15149,  
SEQ ID NO:15151, SEQ ID NO:15153, SEQ ID NO:15156, SEQ ID NO:15158, SEQ ID  
NO:15160, SEQ ID NO:15162, SEQ ID NO:15164, SEQ ID NO:15166, SEQ ID NO:15170,  
SEQ ID NO:15172, SEQ ID NO:15174, SEQ ID NO:15176, SEQ ID NO:15178, SEQ ID  
25 NO:15180, SEQ ID NO:15182, SEQ ID NO:15184, SEQ ID NO:15186, SEQ ID NO:15188,  
SEQ ID NO:15190, SEQ ID NO:15193, SEQ ID NO:15195, SEQ ID NO:15197, SEQ ID  
NO:15199, SEQ ID NO:15202, SEQ ID NO:15204, SEQ ID NO:15206, SEQ ID NO:15208,  
SEQ ID NO:15210,  
SEQ ID NO:15212, SEQ ID NO:15214, SEQ ID NO:15216, SEQ ID NO:15218, SEQ ID  
30 NO:15221, SEQ ID NO:15223, SEQ ID NO:15225, SEQ ID NO:15227, SEQ ID NO:15229,  
SEQ ID NO:15231, SEQ ID NO:15233, SEQ ID NO:15235, SEQ ID NO:15237, SEQ ID  
NO:15239, SEQ ID NO:15241, SEQ ID NO:15243, SEQ ID NO:15245, SEQ ID NO:15247,  
SEQ ID NO:15249, SEQ ID NO:15251, SEQ ID NO:15253, SEQ ID NO:15255, SEQ ID  
NO:15257, SEQ ID NO:15260, SEQ ID NO:15262, SEQ ID NO:15264, SEQ ID NO:15266,  
SEQ ID NO:15268, SEQ ID NO:15270, SEQ ID NO:15273, SEQ ID NO:15275, SEQ ID  
35 NO:15277, SEQ ID NO:15279, SEQ ID NO:15281, SEQ ID NO:15284, SEQ ID NO:15286,  
SEQ ID NO:15288, SEQ ID NO:15290, SEQ ID NO:15293, SEQ ID NO:15296, SEQ ID  
NO:15299, SEQ ID NO:15303, SEQ ID NO:15306, SEQ ID NO:15308, SEQ ID NO:15310,  
SEQ ID NO:15312, SEQ ID NO:15314, SEQ ID NO:15317, SEQ ID NO:15320, SEQ ID  
40 NO:15322, SEQ ID NO:15324, SEQ ID NO:15326, SEQ ID NO:15328, SEQ ID NO:15330,  
SEQ ID NO:15332, SEQ ID NO:15335, SEQ ID NO:15337, SEQ ID NO:15339, SEQ ID  
NO:15341, SEQ ID NO:15343, SEQ ID NO:15345, SEQ ID NO:15347, SEQ ID NO:15349,  
SEQ ID NO:15351, SEQ ID NO:15353, SEQ ID NO:15356, SEQ ID NO:15358, SEQ ID  
45 NO:15360, SEQ ID NO:15362, SEQ ID NO:15365, SEQ ID NO:15367, SEQ ID NO:15369,  
SEQ ID NO:15371, SEQ ID NO:15373, SEQ ID NO:15375, SEQ ID NO:15377, SEQ ID  
NO:15379, SEQ ID NO:15381, SEQ ID NO:15383, SEQ ID NO:15385, SEQ ID NO:15387,  
SEQ ID NO:15389, SEQ ID NO:15392, SEQ ID NO:15394, SEQ ID NO:15398, SEQ ID  
NO:15400, SEQ ID NO:15402, SEQ ID NO:15405, SEQ ID NO:15408, SEQ ID NO:15410,  
SEQ ID NO:15413, SEQ ID NO:15415, SEQ ID NO:15418, SEQ ID NO:15420, SEQ ID  
50 NO:15422, SEQ ID NO:15424, SEQ ID NO:15426, SEQ ID NO:15428, SEQ ID NO:15430,  
SEQ ID NO:15432,  
SEQ ID NO:15434, SEQ ID NO:15437, SEQ ID NO:15440, SEQ ID NO:15444, SEQ ID  
NO:15452, SEQ ID NO:15454, SEQ ID NO:15456, SEQ ID NO:15458, SEQ ID NO:15460,  
SEQ ID NO:15462, SEQ ID NO:15464, SEQ ID NO:15466, SEQ ID NO:15468, SEQ ID  
55 NO:15470, SEQ ID NO:15472, SEQ ID NO:15474, SEQ ID NO:15476, SEQ ID NO:15479,



5           SEQ ID NO:16034, SEQ ID NO:16036, SEQ ID NO:16038, SEQ ID NO:16040, SEQ ID  
           NO:16042, SEQ ID NO:16044, SEQ ID NO:16046, SEQ ID NO:16050, SEQ ID NO:16053,  
           SEQ ID NO:16055, SEQ ID NO:16058, SEQ ID NO:16060, SEQ ID NO:16062, SEQ ID  
           NO:16064, SEQ ID NO:16066, SEQ ID NO:16068, SEQ ID NO:16070, SEQ ID NO:16072,  
           SEQ ID NO:16074, SEQ ID NO:16076, SEQ ID NO:16078, SEQ ID NO:16080, SEQ ID  
           NO:16082, SEQ ID NO:16084, SEQ ID NO:16086, SEQ ID NO:16088, SEQ ID NO:16090,  
           SEQ ID NO:16092, SEQ ID NO:16094, SEQ ID NO:16096, SEQ ID NO:16098, SEQ ID  
           NO:16100, SEQ ID NO:16102, SEQ ID NO:16104, SEQ ID NO:16106, SEQ ID NO:16108,  
           SEQ ID NO:16110,  
 10          SEQ ID NO:16221, SEQ ID NO:16223, SEQ ID NO:16227, SEQ ID NO:16231, SEQ ID  
           NO:16234, SEQ ID NO:16237, SEQ ID NO:16239, SEQ ID NO:16241, SEQ ID NO:16244,  
           SEQ ID NO:16256, SEQ ID NO:16263, SEQ ID NO:16271, SEQ ID NO:16288, SEQ ID  
 15          NO:16290, SEQ ID NO:16292, SEQ ID NO:16296, SEQ ID NO:16298, SEQ ID NO:16300,  
           SEQ ID NO:16302, SEQ ID NO:16305, SEQ ID NO:16311, SEQ ID NO:16313, SEQ ID  
           NO:16326, SEQ ID NO:16329, SEQ ID NO:16335, SEQ ID NO:16342, SEQ ID NO:16344,  
           SEQ ID NO:16349, SEQ ID NO:16355, SEQ ID NO:16357, SEQ ID NO:16361, SEQ ID  
           NO:16366, SEQ ID NO:16368, SEQ ID NO:16370, SEQ ID NO:16375, SEQ ID NO:16382,  
 20          SEQ ID NO:16386, SEQ ID NO:16388, SEQ ID NO:16390, SEQ ID NO:16392, SEQ ID  
           NO:16397, SEQ ID NO:16399, SEQ ID NO:16405, SEQ ID NO:16407, SEQ ID NO:16410,  
           SEQ ID NO:16413, SEQ ID NO:16415, SEQ ID NO:16417, SEQ ID NO:16419, SEQ ID  
           NO:16430, SEQ ID NO:16432, SEQ ID NO:16434, SEQ ID NO:16439, SEQ ID NO:16442,  
           SEQ ID NO:16444, SEQ ID NO:16446, SEQ ID NO:16463, SEQ ID NO:16466, SEQ ID  
 25          NO:16468, SEQ ID NO:16470, SEQ ID NO:16472, SEQ ID NO:16475, SEQ ID NO:16477,  
           SEQ ID NO:16480, SEQ ID NO:16482, SEQ ID NO:16485, SEQ ID NO:16488, SEQ ID  
           NO:16491, SEQ ID NO:16493, SEQ ID NO:16495, SEQ ID NO:16498, SEQ ID NO:16502,  
           SEQ ID NO:16504, SEQ ID NO:16507, SEQ ID NO:16510, SEQ ID NO:16521, SEQ ID  
 30          NO:16523, SEQ ID NO:16525, SEQ ID NO:16528, SEQ ID NO:16530, SEQ ID NO:16533,  
           SEQ ID NO:16538, SEQ ID NO:16541, SEQ ID NO:16543, SEQ ID NO:16545, SEQ ID  
           NO:16549, SEQ ID NO:16551, SEQ ID NO:16554, SEQ ID NO:16556, SEQ ID NO:16558,  
           SEQ ID NO:16560, SEQ ID NO:16562, SEQ ID NO:16566, SEQ ID NO:16572, SEQ ID  
           NO:16582, SEQ ID NO:16584, SEQ ID NO:16587, SEQ ID NO:16590, SEQ ID NO:16592,  
           SEQ ID NO:16595,  
 35          SEQ ID NO:16599, SEQ ID NO:16602, SEQ ID NO:16605, SEQ ID NO:16610, SEQ ID  
           NO:16616, SEQ ID NO:16619, SEQ ID NO:16621, SEQ ID NO:16623, SEQ ID NO:16625,  
           SEQ ID NO:16630, SEQ ID NO:16632, SEQ ID NO:16634, SEQ ID NO:16638, SEQ ID  
           NO:16641, SEQ ID NO:16644, SEQ ID NO:16663, SEQ ID NO:16665, SEQ ID NO:16674,  
 40          SEQ ID NO:16680, SEQ ID NO:16685, SEQ ID NO:16688, SEQ ID NO:16690, SEQ ID  
           NO:16693, SEQ ID NO:16699, SEQ ID NO:16702, SEQ ID NO:16704, SEQ ID NO:16708,  
           SEQ ID NO:16712, SEQ ID NO:16714, SEQ ID NO:16723, SEQ ID NO:16726, SEQ ID  
           NO:16728, SEQ ID NO:16730, SEQ ID NO:16732, SEQ ID NO:16741, SEQ ID NO:16743,  
           SEQ ID NO:16745, SEQ ID NO:16747, SEQ ID NO:16752, SEQ ID NO:16763, SEQ ID  
 45          NO:16765, SEQ ID NO:16767, SEQ ID NO:16771, SEQ ID NO:16776, SEQ ID NO:16781,  
           SEQ ID NO:16784, SEQ ID NO:16786, SEQ ID NO:16788, SEQ ID NO:16791, SEQ ID  
           NO:16793, SEQ ID NO:16795, SEQ ID NO:16797, SEQ ID NO:16801, SEQ ID NO:16804,  
           SEQ ID NO:16807, SEQ ID NO:16809, SEQ ID NO:16813, SEQ ID NO:16815, SEQ ID  
           NO:16818, SEQ ID NO:16822, SEQ ID NO:16825, SEQ ID NO:16845, SEQ ID NO:16847,  
 50          SEQ ID NO:16849, SEQ ID NO:16853, SEQ ID NO:16855, SEQ ID NO:16857, SEQ ID  
           NO:16863, SEQ ID NO:16865, SEQ ID NO:16870, SEQ ID NO:16876, SEQ ID NO:16879,  
           SEQ ID NO:16884, SEQ ID NO:16892, SEQ ID NO:16896, SEQ ID NO:16901, SEQ ID  
           NO:16903, SEQ ID NO:16909, SEQ ID NO:16921, SEQ ID NO:16925, SEQ ID NO:16928,  
           SEQ ID NO:16935, SEQ ID NO:16937, SEQ ID NO:16939, SEQ ID NO:16941, SEQ ID  
           NO:16943, SEQ ID NO:16947, SEQ ID NO:16954, SEQ ID NO:16956, SEQ ID NO:16960,

SEQ ID NO:16963, SEQ ID NO:16965, SEQ ID NO:16968, SEQ ID NO:16971, SEQ ID  
 NO:16976, SEQ ID NO:16980, SEQ ID NO:16987, SEQ ID NO:16990, SEQ ID NO:16999,  
 SEQ ID NO:17003,  
 5 SEQ ID NO:17019, SEQ ID NO:17025, SEQ ID NO:17028, SEQ ID NO:17032, SEQ ID  
 NO:17038, SEQ ID NO:17040, SEQ ID NO:17042, SEQ ID NO:17051, SEQ ID NO:17053,  
 SEQ ID NO:17058, SEQ ID NO:17060, SEQ ID NO:17062, SEQ ID NO:17064, SEQ ID  
 NO:17072, SEQ ID NO:17074, SEQ ID NO:17076, SEQ ID NO:17079, SEQ ID NO:17081,  
 10 SEQ ID NO:17083, SEQ ID NO:17085, SEQ ID NO:17087, SEQ ID NO:17089, SEQ ID  
 NO:17091, SEQ ID NO:17093, SEQ ID NO:17095, SEQ ID NO:17097, SEQ ID NO:17099,  
 SEQ ID NO:17101, SEQ ID NO:17104, SEQ ID NO:17106, SEQ ID NO:17109, SEQ ID  
 15 NO:17111, SEQ ID NO:17113, SEQ ID NO:17115, SEQ ID NO:17117, SEQ ID NO:17120,  
 SEQ ID NO:17122, SEQ ID NO:17124, SEQ ID NO:17127, SEQ ID NO:17129, SEQ ID  
 NO:17131, SEQ ID NO:17133, SEQ ID NO:17135, SEQ ID NO:17137, SEQ ID NO:17140,  
 20 SEQ ID NO:17142, SEQ ID NO:17144, SEQ ID NO:17146, SEQ ID NO:17148, SEQ ID  
 NO:17150, SEQ ID NO:17152, SEQ ID NO:17154, SEQ ID NO:17156, SEQ ID NO:17158,  
 SEQ ID NO:17161, SEQ ID NO:17163, SEQ ID NO:17165, SEQ ID NO:17167, SEQ ID  
 NO:17169, SEQ ID NO:17171, SEQ ID NO:17173, SEQ ID NO:17175, SEQ ID NO:17177,  
 25 SEQ ID NO:17179, SEQ ID NO:17181, SEQ ID NO:17184, SEQ ID NO:17186, SEQ ID  
 NO:17188, SEQ ID NO:17191, SEQ ID NO:17194, SEQ ID NO:17196, SEQ ID NO:17198,  
 SEQ ID NO:17200, SEQ ID NO:17203, SEQ ID NO:17205, SEQ ID NO:17207, SEQ ID  
 NO:17211, SEQ ID NO:17215, SEQ ID NO:17217, SEQ ID NO:17219, SEQ ID NO:17221,  
 30 SEQ ID NO:17223, SEQ ID NO:17225, SEQ ID NO:17227, SEQ ID NO:17229, SEQ ID  
 NO:17231, SEQ ID NO:17233, SEQ ID NO:17235, SEQ ID NO:17237, SEQ ID NO:17239,  
 SEQ ID NO:17241, SEQ ID NO:17243, SEQ ID NO:17245, SEQ ID NO:17247, SEQ ID  
 NO:17250, SEQ ID NO:17252, SEQ ID NO:17254, SEQ ID NO:17257, SEQ ID NO:17260,  
 35 SEQ ID NO:17262,  
 SEQ ID NO:17266, SEQ ID NO:17269, SEQ ID NO:17271, SEQ ID NO:17273, SEQ ID  
 NO:17276, SEQ ID NO:17278, SEQ ID NO:17280, SEQ ID NO:17282, SEQ ID NO:17284,  
 SEQ ID NO:17286, SEQ ID NO:17288, SEQ ID NO:17291, SEQ ID NO:17293, SEQ ID  
 NO:17295, SEQ ID NO:17298, SEQ ID NO:17301, SEQ ID NO:17303, SEQ ID NO:17306,  
 40 SEQ ID NO:17308, SEQ ID NO:17311, SEQ ID NO:17313, SEQ ID NO:17317, SEQ ID  
 NO:17319, SEQ ID NO:17321, SEQ ID NO:17323, SEQ ID NO:17325, SEQ ID NO:17327,  
 SEQ ID NO:17329, SEQ ID NO:17331, SEQ ID NO:17333, SEQ ID NO:17335, SEQ ID  
 NO:17337, SEQ ID NO:17339, SEQ ID NO:17342, SEQ ID NO:17346, SEQ ID NO:17348,  
 45 SEQ ID NO:17350, SEQ ID NO:17352, SEQ ID NO:17354, SEQ ID NO:17357, SEQ ID  
 NO:17359, SEQ ID NO:17361, SEQ ID NO:17363, SEQ ID NO:17367, SEQ ID NO:17369,  
 SEQ ID NO:17373, SEQ ID NO:17375, SEQ ID NO:17379, SEQ ID NO:17382, SEQ ID  
 NO:17384, SEQ ID NO:17386, SEQ ID NO:17389, SEQ ID NO:17391, SEQ ID NO:17394,  
 50 SEQ ID NO:17396, SEQ ID NO:17400, SEQ ID NO:17403, SEQ ID NO:17405, SEQ ID  
 NO:17407, SEQ ID NO:17409, SEQ ID NO:17411, SEQ ID NO:17413, SEQ ID NO:17415,  
 SEQ ID NO:17417, SEQ ID NO:17419, SEQ ID NO:17421, SEQ ID NO:17423, SEQ ID  
 NO:17425, SEQ ID NO:17428, SEQ ID NO:17431, SEQ ID NO:17435, SEQ ID NO:17439,  
 55 SEQ ID NO:17441, SEQ ID NO:17444, SEQ ID NO:17446, SEQ ID NO:17448, SEQ ID  
 NO:17451, SEQ ID NO:17453, SEQ ID NO:17455, SEQ ID NO:17458, SEQ ID NO:17462,  
 SEQ ID NO:17464, SEQ ID NO:17466, SEQ ID NO:17469, SEQ ID NO:17471, SEQ ID  
 NO:17473, SEQ ID NO:17476, SEQ ID NO:17478, SEQ ID NO:17481, SEQ ID NO:17483,  
 SEQ ID NO:17486, SEQ ID NO:17488, SEQ ID NO:17491, SEQ ID NO:17493, SEQ ID  
 NO:17495, SEQ ID NO:17497, SEQ ID NO:17499, SEQ ID NO:17501, SEQ ID NO:17503,  
 SEQ ID NO:17505,  
 SEQ ID NO:17507, SEQ ID NO:17509, SEQ ID NO:17511, SEQ ID NO:17513, SEQ ID  
 NO:17515, SEQ ID NO:17517, SEQ ID NO:17519, SEQ ID NO:17521, SEQ ID NO:17523,  
 60 SEQ ID NO:17525, SEQ ID NO:17528, SEQ ID NO:17530, SEQ ID NO:17534, SEQ ID

NO:17536, SEQ ID NO:17538, SEQ ID NO:17540, SEQ ID NO:17542, SEQ ID NO:17544,  
SEQ ID NO:17546, SEQ ID NO:17548, SEQ ID NO:17550, SEQ ID NO:17552, SEQ ID  
NO:17554, SEQ ID NO:17556, SEQ ID NO:17558, SEQ ID NO:17560, SEQ ID NO:17562,  
SEQ ID NO:17564, SEQ ID NO:17566, SEQ ID NO:17568, SEQ ID NO:17570, SEQ ID  
NO:17573, SEQ ID NO:17575, SEQ ID NO:17577, SEQ ID NO:17580, SEQ ID NO:17582,  
SEQ ID NO:17584, SEQ ID NO:17587, SEQ ID NO:17590, SEQ ID NO:17592, SEQ ID  
NO:17595, SEQ ID NO:17597, SEQ ID NO:17599, SEQ ID NO:17601, SEQ ID NO:17603,  
SEQ ID NO:17605, SEQ ID NO:17607, SEQ ID NO:17609, SEQ ID NO:17611, SEQ ID  
NO:17613, SEQ ID NO:17615, SEQ ID NO:17617, SEQ ID NO:17619, SEQ ID NO:17621,  
SEQ ID NO:17623, SEQ ID NO:17625, SEQ ID NO:17627, SEQ ID NO:17629, SEQ ID  
NO:17631, SEQ ID NO:17633, SEQ ID NO:17635, SEQ ID NO:17637, SEQ ID NO:17639,  
SEQ ID NO:17641, SEQ ID NO:17643, SEQ ID NO:17645, SEQ ID NO:17647, SEQ ID  
NO:17651, SEQ ID NO:17653, SEQ ID NO:17655, SEQ ID NO:17658, SEQ ID NO:17661,  
SEQ ID NO:17664, SEQ ID NO:17667, SEQ ID NO:17669, SEQ ID NO:17671, SEQ ID  
NO:17673, SEQ ID NO:17675, SEQ ID NO:17677, SEQ ID NO:17679, SEQ ID NO:17684,  
SEQ ID NO:17686, SEQ ID NO:17688, SEQ ID NO:17690, SEQ ID NO:17692, SEQ ID  
NO:17694, SEQ ID NO:17696, SEQ ID NO:17698, SEQ ID NO:17700, SEQ ID NO:17702,  
SEQ ID NO:17704, SEQ ID NO:17707, SEQ ID NO:17709, SEQ ID NO:17711, SEQ ID  
NO:17713, SEQ ID NO:17715, SEQ ID NO:17719, SEQ ID NO:17725, SEQ ID NO:17727,  
SEQ ID NO:17731,  
SEQ ID NO:17734, SEQ ID NO:17736, SEQ ID NO:17738, SEQ ID NO:17741, SEQ ID  
NO:17743, SEQ ID NO:17745, SEQ ID NO:17749, SEQ ID NO:17752, SEQ ID NO:17755,  
SEQ ID NO:17757, SEQ ID NO:17760, SEQ ID NO:17766, SEQ ID NO:17772, SEQ ID  
NO:17775, SEQ ID NO:17777, SEQ ID NO:17779, SEQ ID NO:17782, SEQ ID NO:17784,  
SEQ ID NO:17786, SEQ ID NO:17788, SEQ ID NO:17791, SEQ ID NO:17793, SEQ ID  
NO:17796, SEQ ID NO:17798, SEQ ID NO:17800, SEQ ID NO:17804, SEQ ID NO:17808,  
SEQ ID NO:17810, SEQ ID NO:17812, SEQ ID NO:17814, SEQ ID NO:17816, SEQ ID  
NO:17819, SEQ ID NO:17821, SEQ ID NO:17823, SEQ ID NO:17825, SEQ ID NO:17827,  
SEQ ID NO:17829, SEQ ID NO:17833, SEQ ID NO:17835, SEQ ID NO:17838, SEQ ID  
NO:17840, SEQ ID NO:17842, SEQ ID NO:17844, SEQ ID NO:17846, SEQ ID NO:17854,  
SEQ ID NO:17857, SEQ ID NO:17862, SEQ ID NO:17864, SEQ ID NO:17866, SEQ ID  
NO:17868, SEQ ID NO:17873, SEQ ID NO:17879, SEQ ID NO:17882, SEQ ID NO:17884,  
SEQ ID NO:17887, SEQ ID NO:17889, SEQ ID NO:17891, SEQ ID NO:17893, SEQ ID  
NO:17897, SEQ ID NO:17899, SEQ ID NO:17901, SEQ ID NO:17905, SEQ ID NO:17908,  
SEQ ID NO:17910, SEQ ID NO:17913, SEQ ID NO:17915, SEQ ID NO:17921, SEQ ID  
NO:17923, SEQ ID NO:17927, SEQ ID NO:17930, SEQ ID NO:17933, SEQ ID NO:17935,  
SEQ ID NO:17937, SEQ ID NO:17939, SEQ ID NO:17944, SEQ ID NO:17948, SEQ ID  
NO:17950, SEQ ID NO:17953, SEQ ID NO:17955, SEQ ID NO:17957, SEQ ID NO:17960,  
SEQ ID NO:17963, SEQ ID NO:17968, SEQ ID NO:17970, SEQ ID NO:17972, SEQ ID  
NO:17975, SEQ ID NO:17977, SEQ ID NO:17983, SEQ ID NO:17988, SEQ ID NO:17992,  
SEQ ID NO:17994, SEQ ID NO:17996, SEQ ID NO:17998, SEQ ID NO:18002, SEQ ID  
NO:18007, SEQ ID NO:18009, SEQ ID NO:18011, SEQ ID NO:18014, SEQ ID NO:18018,  
SEQ ID NO:18020,  
SEQ ID NO:18023, SEQ ID NO:18025, SEQ ID NO:18027, SEQ ID NO:18029, SEQ ID  
NO:18031, SEQ ID NO:18033, SEQ ID NO:18035, SEQ ID NO:18037, SEQ ID NO:18039,  
SEQ ID NO:18041, SEQ ID NO:18047, SEQ ID NO:18049, SEQ ID NO:18051, SEQ ID  
NO:18053, SEQ ID NO:18055, SEQ ID NO:18057, SEQ ID NO:18060, SEQ ID NO:18062,  
SEQ ID NO:18064, SEQ ID NO:18067, SEQ ID NO:18069, SEQ ID NO:18073, SEQ ID  
NO:18075, SEQ ID NO:18077, SEQ ID NO:18079, SEQ ID NO:18081, SEQ ID NO:18083,  
SEQ ID NO:18085, SEQ ID NO:18087, SEQ ID NO:18089, SEQ ID NO:18091, SEQ ID  
NO:18093, SEQ ID NO:18097, SEQ ID NO:18100, SEQ ID NO:18102, SEQ ID NO:18106,  
SEQ ID NO:18108, SEQ ID NO:18111, SEQ ID NO:18113, SEQ ID NO:18115, SEQ ID

5 NO:18118, SEQ ID NO:18122, SEQ ID NO:18126, SEQ ID NO:18128, SEQ ID NO:18130,  
SEQ ID NO:18132, SEQ ID NO:18134, SEQ ID NO:18136, SEQ ID NO:18138, SEQ ID  
NO:18141, SEQ ID NO:18143, SEQ ID NO:18145, SEQ ID NO:18147, SEQ ID NO:18149,  
SEQ ID NO:18155, SEQ ID NO:18158, SEQ ID NO:18160, SEQ ID NO:18164, SEQ ID  
NO:18167, SEQ ID NO:18169, SEQ ID NO:18171, SEQ ID NO:18173, SEQ ID NO:18175,  
SEQ ID NO:18177, SEQ ID NO:18179, SEQ ID NO:18181, SEQ ID NO:18183, SEQ ID  
NO:18185, SEQ ID NO:18187, SEQ ID NO:18189, SEQ ID NO:18191, SEQ ID NO:18193,  
SEQ ID NO:18195, SEQ ID NO:18197, SEQ ID NO:18199, SEQ ID NO:18202, SEQ ID  
NO:18204, SEQ ID NO:18206, SEQ ID NO:18208, SEQ ID NO:18211, SEQ ID NO:18213,  
SEQ ID NO:18215, SEQ ID NO:18217, SEQ ID NO:18219, SEQ ID NO:18221, SEQ ID  
NO:18223, SEQ ID NO:18225, SEQ ID NO:18228, SEQ ID NO:18230, SEQ ID NO:18232,  
SEQ ID NO:18234, SEQ ID NO:18237, SEQ ID NO:18239, SEQ ID NO:18241, SEQ ID  
NO:18244, SEQ ID NO:18246, SEQ ID NO:18248, SEQ ID NO:18250, SEQ ID NO:18252,  
SEQ ID NO:18255,  
10 SEQ ID NO:18257, SEQ ID NO:18262, SEQ ID NO:18267, SEQ ID NO:18269, SEQ ID  
NO:18271, SEQ ID NO:18273, SEQ ID NO:18275, SEQ ID NO:18277, SEQ ID NO:18279,  
SEQ ID NO:18281, SEQ ID NO:18283, SEQ ID NO:18285, SEQ ID NO:18287, SEQ ID  
NO:18290, SEQ ID NO:18292, SEQ ID NO:18294, SEQ ID NO:18296, SEQ ID NO:18299,  
SEQ ID NO:18301, SEQ ID NO:18304, SEQ ID NO:18306, SEQ ID NO:18311, SEQ ID  
NO:18313, SEQ ID NO:18315, SEQ ID NO:18317, SEQ ID NO:18319, SEQ ID NO:18322,  
SEQ ID NO:18324, SEQ ID NO:18326, SEQ ID NO:18328, SEQ ID NO:18330, SEQ ID  
NO:18333, SEQ ID NO:18336, SEQ ID NO:18338, SEQ ID NO:18340, SEQ ID NO:18342,  
SEQ ID NO:18344, SEQ ID NO:18346, SEQ ID NO:18348, SEQ ID NO:18350, SEQ ID  
NO:18352, SEQ ID NO:18354, SEQ ID NO:18356, SEQ ID NO:18359, SEQ ID NO:18361,  
25 SEQ ID NO:18363, SEQ ID NO:18365, SEQ ID NO:18367, SEQ ID NO:18369, SEQ ID  
NO:18371, SEQ ID NO:18373  
30 SEQ ID NO:18376, SEQ ID NO:18380, SEQ ID NO:18382, SEQ ID NO:18384, SEQ ID  
NO:18386, SEQ ID NO:18388, SEQ ID NO:18391, SEQ ID NO:18393, SEQ ID NO:18396,  
SEQ ID NO:18400, SEQ ID NO:18403, SEQ ID NO:18405, SEQ ID NO:18407, SEQ ID  
NO:18409, SEQ ID NO:18411, SEQ ID NO:18415, SEQ ID NO:18417, SEQ ID NO:18419,  
SEQ ID NO:18423, SEQ ID NO:18425, SEQ ID NO:18429, SEQ ID NO:18431, SEQ ID  
NO:18434, SEQ ID NO:18436, SEQ ID NO:18438, SEQ ID NO:18440, SEQ ID NO:18442,  
35 SEQ ID NO:18445, SEQ ID NO:18448, SEQ ID NO:18450, SEQ ID NO:18452, SEQ ID  
NO:18455, SEQ ID NO:18457, SEQ ID NO:18459, SEQ ID NO:18461, SEQ ID NO:18463,  
SEQ ID NO:18466, SEQ ID NO:18469, SEQ ID NO:18471, SEQ ID NO:18473, SEQ ID  
NO:18475, SEQ ID NO:18477, SEQ ID NO:18479, SEQ ID NO:18481, SEQ ID NO:18483,  
40 SEQ ID NO:18485, SEQ ID NO:18487, SEQ ID NO:18490, SEQ ID NO:18492, SEQ ID  
NO:18494, SEQ ID NO:18498, SEQ ID NO:18506, SEQ ID NO:18508, SEQ ID NO:18510,  
SEQ ID NO:18512, SEQ ID NO:18514, SEQ ID NO:18516, SEQ ID NO:18518, SEQ ID  
NO:18520, SEQ ID NO:18522, SEQ ID NO:18524, SEQ ID NO:18526, SEQ ID NO:18529,  
45 SEQ ID NO:18532, SEQ ID NO:18536, SEQ ID NO:18538, SEQ ID NO:18541, SEQ ID  
NO:18546, SEQ ID NO:18550, SEQ ID NO:18552, SEQ ID NO:18554, SEQ ID NO:18556,  
SEQ ID NO:18558, SEQ ID NO:18562, SEQ ID NO:18568, SEQ ID NO:18572, SEQ ID  
NO:18574, SEQ ID NO:18576, SEQ ID NO:18580, SEQ ID NO:18582, SEQ ID NO:18587,  
SEQ ID NO:18590, SEQ ID NO:18592, SEQ ID NO:18594, SEQ ID NO:18596, SEQ ID  
NO:18598, SEQ ID NO:18600, SEQ ID NO:18602, SEQ ID NO:18604, SEQ ID NO:18606,  
50 SEQ ID NO:18608, SEQ ID NO:18611, SEQ ID NO:18613, SEQ ID NO:18615, SEQ ID  
NO:18617, SEQ ID NO:18619, SEQ ID NO:18623, SEQ ID NO:18625, SEQ ID NO:18627,  
SEQ ID NO:18629,  
55 SEQ ID NO:18631, SEQ ID NO:18633, SEQ ID NO:18635, SEQ ID NO:18637, SEQ ID  
NO:18639, SEQ ID NO:18644, SEQ ID NO:18646, SEQ ID NO:18649, SEQ ID NO:18651,  
SEQ ID NO:18653, SEQ ID NO:18655, SEQ ID NO:18657, SEQ ID NO:18660, SEQ ID

NO:18662, SEQ ID NO:18665, SEQ ID NO:18668, SEQ ID NO:18672, SEQ ID NO:18674,  
 5 SEQ ID NO:18676, SEQ ID NO:18678, SEQ ID NO:18680, SEQ ID NO:18682, SEQ ID  
 NO:18686, SEQ ID NO:18688, SEQ ID NO:18691, SEQ ID NO:18693, SEQ ID NO:18695,  
 SEQ ID NO:18697, SEQ ID NO:18699, SEQ ID NO:18701, SEQ ID NO:18703, SEQ ID  
 10 NO:18705, SEQ ID NO:18709, SEQ ID NO:18711, SEQ ID NO:18713, SEQ ID NO:18715,  
 SEQ ID NO:18717, SEQ ID NO:18720, SEQ ID NO:18722, SEQ ID NO:18724, SEQ ID  
 NO:18726, SEQ ID NO:18729, SEQ ID NO:18731, SEQ ID NO:18733, SEQ ID NO:18735,  
 15 SEQ ID NO:18737, SEQ ID NO:18739, SEQ ID NO:18741, SEQ ID NO:18743, SEQ ID  
 NO:18745, SEQ ID NO:18747, SEQ ID NO:18749, SEQ ID NO:18751, SEQ ID NO:18753,  
 SEQ ID NO:18759, SEQ ID NO:18763, SEQ ID NO:18765, SEQ ID NO:18770, SEQ ID  
 20 NO:18773, SEQ ID NO:18775, SEQ ID NO:18777, SEQ ID NO:18779, SEQ ID NO:18781,  
 SEQ ID NO:18783, SEQ ID NO:18785, SEQ ID NO:18787, SEQ ID NO:18790, SEQ ID  
 NO:18793, SEQ ID NO:18795, SEQ ID NO:18797, SEQ ID NO:18800, SEQ ID NO:18802,  
 25 SEQ ID NO:18804, SEQ ID NO:18806, SEQ ID NO:18809, SEQ ID NO:18811, SEQ ID  
 NO:18813, SEQ ID NO:18815, SEQ ID NO:18817, SEQ ID NO:18819, SEQ ID NO:18822,  
 SEQ ID NO:18824, SEQ ID NO:18826, SEQ ID NO:18828, SEQ ID NO:18830, SEQ ID  
 30 NO:18832, SEQ ID NO:18834, SEQ ID NO:18836, SEQ ID NO:18840, SEQ ID NO:18843,  
 SEQ ID NO:18847, SEQ ID NO:18850, SEQ ID NO:18853, SEQ ID NO:18855, SEQ ID  
 NO:18857, SEQ ID NO:18859, SEQ ID NO:18862, SEQ ID NO:18865, SEQ ID NO:18868,  
 35 SEQ ID NO:18870,  
 SEQ ID NO:18874, SEQ ID NO:18876, SEQ ID NO:18879, SEQ ID NO:18882, SEQ ID  
 NO:18884, SEQ ID NO:18888, SEQ ID NO:18891, SEQ ID NO:18894, SEQ ID NO:18896,  
 SEQ ID NO:18898, SEQ ID NO:18900, SEQ ID NO:18902, SEQ ID NO:18906, SEQ ID  
 40 NO:18908, SEQ ID NO:18910, SEQ ID NO:18912, SEQ ID NO:18914, SEQ ID NO:18916,  
 SEQ ID NO:18918, SEQ ID NO:18920, SEQ ID NO:18922, SEQ ID NO:18924, SEQ ID  
 NO:18926, SEQ ID NO:18929, SEQ ID NO:18931, SEQ ID NO:18933, SEQ ID NO:18935,  
 SEQ ID NO:18937, SEQ ID NO:18939, SEQ ID NO:18942, SEQ ID NO:18945, SEQ ID  
 45 NO:18948, SEQ ID NO:18950, SEQ ID NO:18952, SEQ ID NO:18954, SEQ ID NO:18961,  
 SEQ ID NO:18963, SEQ ID NO:18965, SEQ ID NO:18967, SEQ ID NO:18971, SEQ ID  
 NO:18974, SEQ ID NO:18977, SEQ ID NO:18979,  
 SEQ ID NO:18991, SEQ ID NO:18994, SEQ ID NO:18996, SEQ ID NO:19003, SEQ ID  
 NO:19005  
 SEQ ID NO:19008, SEQ ID NO:19010, SEQ ID NO:19015, SEQ ID NO:19017, SEQ ID  
 50 NO:19019, SEQ ID NO:19021, and SEQ ID NO:19023

- (c) a polynucleotide comprising a nucleotide sequence encoding a protein comprising an amino acid sequence selected from the amino acid sequences of (b), in which one or more amino acids are substituted, deleted, inserted, and/or added, wherein said protein is functionally equivalent to the protein comprising said amino acid sequence selected from the amino acid sequences of (b);
- (d) a polynucleotide that hybridizes with a polynucleotide comprising a nucleotide sequence selected from the nucleotide sequences of (a), and that comprises a nucleotide sequence encoding a protein functionally equivalent to the protein encoded by the nucleotide sequence selected from the nucleotide sequences of (a);
- (e) a polynucleotide comprising a nucleotide sequence encoding a partial amino acid sequence of a protein encoded by the polynucleotide of (a) to (d);
- (f) a polynucleotide comprising a nucleotide sequence with at least 70% identity to the nucleotide sequence of (a).

55 9. A substantially pure protein encoded by the polynucleotide of claim 8.

10. An antibody against the protein or peptide of any one of claims 6, 7, and 9.

11. A vector comprising the polynucleotide of claim 5 or 8.
12. A transformant carrying the polynucleotide of claim 5 or 8, or the vector of claim 11.
- 5 13. A transformant expressively carrying the polynucleotide of claim 5 or 8, or the vector of claim 11.
14. A method for producing the protein or peptide of any one of claims 6, 7, and 9, comprising culturing the transformant of claim 13 and recovering the expression product.
- 10 15. An oligonucleotide comprising the nucleotide sequence of claim 8 (a) or the nucleotide sequence complementary to the complementary strand thereof, wherein said oligonucleotide comprises 15 nucleotides or more.
16. Use of the oligonucleotide of claim 15 as a primer for synthesizing a polynucleotide.
- 15 17. Use of the oligonucleotide of claim 15 as a probe for detecting a gene.
18. An antisense polynucleotide against the polynucleotide of claim 8, or the portion thereof.
19. A method for synthesizing a polynucleotide, the method comprising:  
20
  - a) synthesizing a complementary strand using a cDNA library as a template, and using the primer set of claim 2 or 3, or the primer of claim 16; and
  - b) recovering the synthesized product.
- 25 20. The method of claim 19, wherein the cDNA library is obtainable by oligo-capping method.
21. The method of claim 19, wherein the complementary strand is obtainable by PCR.
22. A method for detecting the polynucleotide of claim 8, the method comprising:  
30
  - a) incubating a target polynucleotide with the oligonucleotide of claim 15 under the conditions where hybridization occurs, and
  - b) detecting the hybridization of the target polynucleotide with the oligonucleotide of claim 15.
- 35 23. A database of polynucleotides and/or proteins, the database comprising information on at least one sequence selected from the nucleotide sequences of claim 8 (a) and/or the amino acid sequences of claim 8 (b), or a medium on which the database is stored.

40

45

50

55

Figure 1

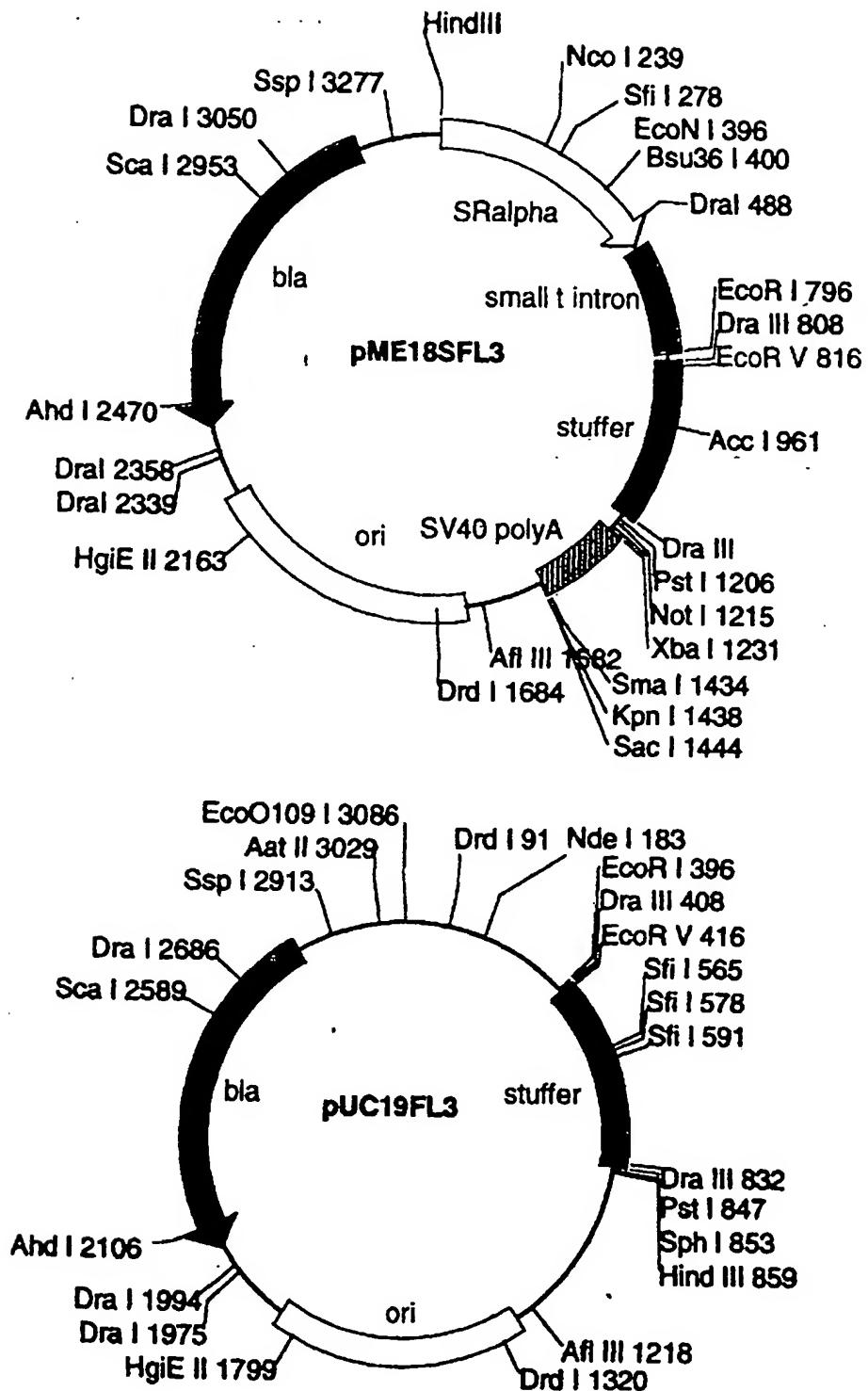


Figure 2

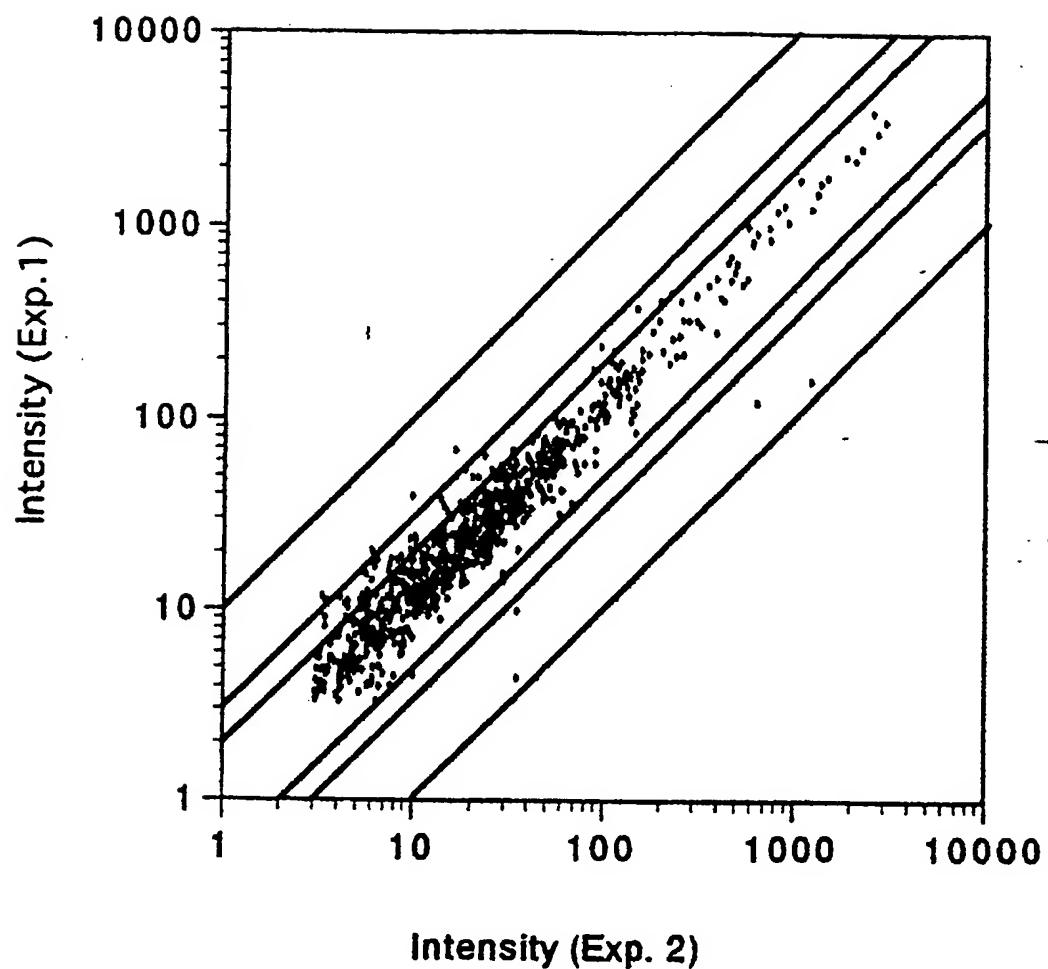
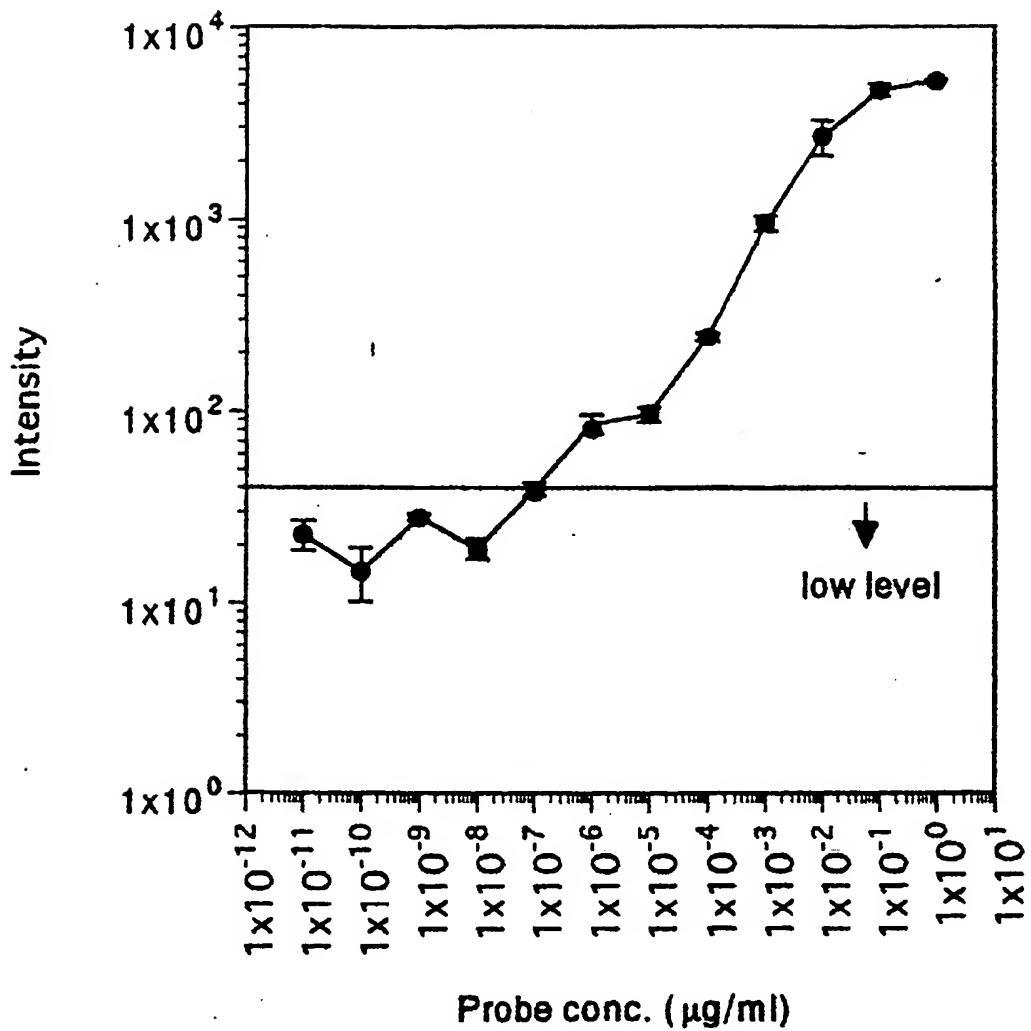


Figure 3





(19) Europäisches Patentamt  
European Patent Office  
Office européen des brevets



(11) EP 1 074 617 A3

(12)

## EUROPEAN PATENT APPLICATION

(88) Date of publication A3:  
21.04.2004 Bulletin 2004/17

(51) Int Cl.7: C12N 15/12, C12N 15/11,  
C07K 14/47, C07K 16/18,  
C12Q 1/68

(43) Date of publication A2:  
07.02.2001 Bulletin 2001/06

(21) Application number: 00116126.4

(22) Date of filing: 28.07.2000

(84) Designated Contracting States:  
AT BE CH CY DE DK ES FI FR GB GR IE IT LI LU  
MC NL PT SE

Designated Extension States:  
AL LT LV MK RO SI

(30) Priority: 29.07.1999 JP 24803699  
27.08.1999 JP 30025399  
11.01.2000 JP 2000118776  
02.05.2000 JP 2000183767  
09.06.2000 JP 2000241899

(71) Applicant: Research Association for  
Biotechnology  
Tokyo 105-0003 (JP)

(72) Inventors:  
• Ota, Toshio  
Fujisawa-shi, Kanagawa 251-0042 (JP)  
• Isogai, Takao  
Inashiki-gun, Ibaraki 300-0303 (JP)

- Nishikawa, Tetsuo  
Itabashi-ku, Tokyo 173-0013 (JP)
- Hayashi, Kohji  
Ichihara-shi, Chiba 292-0056 (JP)
- Saito, Kaoru  
Kisarazu-shi, Chiba 292-0056 (JP)
- Yamamoto, Junichi  
Kisarazu-shi, Chiba 292-0041 (JP)
- Ishii, Shizuko  
Kisarazu-shi, Chiba 292-0812 (JP)
- Sugiyama, Tomoyasu  
Kisarazu-shi, Chiba 292-0045 (JP)
- Wakamatsu, Ai  
Kisarazu-shi, Chiba 292-0014 (JP)
- Nagai, Keiichi  
Higashiyamato-shi, Tokyo 207-0022 (JP)
- Otsuki, Tetsuji  
Kisarazu-shi, Chiba 292-0045 (JP)

(74) Representative: VOSSIUS & PARTNER  
Siebertstrasse 4  
81675 München (DE)

(54) Primers for synthesising full-length cDNA and their use

(57) Primers for synthesizing full-length cDNAs and their use are provided.

5602 cDNA encoding a human protein has been isolated and nucleotide sequences of 5'-, and 3' -ends of the cDNA have been determined. Furthermore, primers for synthesizing the full-length cDNA have been pro-

vided to clarify the function of the protein encoded by the cDNA. The full-length cDNA of the present invention containing the translation start site provides information useful for analyzing the functions of the protein.



European Patent  
Office

## PARTIAL EUROPEAN SEARCH REPORT

Application Number

which under Rule 45 of the European Patent Convention EP 00 11 6126  
shall be considered, for the purposes of subsequent  
proceedings, as the European search report

DOCUMENTS CONSIDERED TO BE RELEVANT			
Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	CLASSIFICATION OF THE APPLICATION (Int.Cl.7)
X	BRIGHTMAN S E ET AL: "Isolation of a mouse cDNA encoding MTJ1, a new murine member of the Dnaj family of proteins" GENE, ELSEVIER BIOMEDICAL PRESS. AMSTERDAM, NL, vol. 153, no. 2, 14 February 1995 (1995-02-14), pages 249-254, XP004042536 ISSN: 0378-1119 * abstract; figures 1,3,5 *	1-22	C12N15/12 C12N15/11 C07K14/47 C07K16/18 C12Q1/68
X	DATABASE EMBL [Online] 23 November 1998 (1998-11-23), STRAUSBERG: "q171b04.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE: I877743-3 similar to SW:MTJ1 MOUSE Q61712 Dnaj PROTEIN HOMOLOG MTJ1. ;, mRNA" XP002270645 accession no. EBI Database accession no. AI276458 * the whole document *	1-22 ---- ---- -/-	
			TECHNICAL FIELDS SEARCHED (Int.Cl.7) C07K C12N
INCOMPLETE SEARCH			
<p>The Search Division considers that the present application, or one or more of its claims, does/do not comply with the EPC to such an extent that a meaningful search into the state of the art cannot be carried out, or can only be carried out partially, for these claims.</p> <p>Claims searched completely :</p> <p>Claims searched incompletely :</p> <p>Claims not searched :</p> <p>Reason for the limitation of the search: see sheet C</p>			
Place of search	Date of completion of the search	Examiner	
The Hague	18 February 2004	Gurdjian, D	
CATEGORY OF CITED DOCUMENTS			
<p>X : particularly relevant if taken alone Y : particularly relevant if combined with another document of the same category A : technological background O : non-written disclosure P : intermediate document</p> <p>T : theory or principle underlying the invention E : earlier patent document, but published on, or after the filing date D : document cited in the application L : document cited for other reasons &amp; : member of the same patent family, corresponding document</p>			



European Patent  
Office

INCOMPLETE SEARCH  
SHEET C

Application Number

EP 00 11 6126

Claim(s) not searched:  
23

Reason for the limitation of the search (non-patentable invention(s)):

Article 52 (2)(d) EPC - Presentation of information



European Patent  
Office

## PARTIAL EUROPEAN SEARCH REPORT

Application Number

EP 00 11 6126

Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	CLASSIFICATION OF THE APPLICATION (Int.Cl.7)
			TECHNICAL FIELDS , SEARCHED (Int.Cl.7)
X	<p>DATABASE EMBL [Online]            31 December 1998 (1998-12-31),            STRAUSBERG: "tb98c06.x1 NCI CGAP_Co16 Homo            sapiens cDNA clone IMAGE:2062378_3'            similar to SW:MTJ1 MOUSE Q61712 DNAJ            PROTEIN HOMOLOG MTJ1. ;, mRNA sequence."            XP002270646 accession no. EBI            Database accession no. AI337322            * the whole document *</p> <p>-----</p>	1-22	
D,A	<p>CARNINCI P ET AL: "High-efficiency            full-length cDNA cloning by biotinylated            CAP trapper"            GENOMICS, ACADEMIC PRESS, SAN DIEGO, US,            vol. 37, no. 3,            1 November 1996 (1996-11-01), pages            327-336, XP002081729            ISSN: 0888-7543            * abstract *</p> <p>-----</p>	1-22	
A	<p>KATO S ET AL: "Construction of a human            full-length cDNA bank"            GENE, ELSEVIER BIOMEDICAL PRESS.            AMSTERDAM, NL,            vol. 150, 1994, pages 243-250, XP002081364            ISSN: 0378-1119            * abstract *</p> <p>-----</p>	1-22	
X	<p>DATABASE EMBL [Online]            16 March 1999 (1999-03-16),            STRAUSBERG: "tk01b12.x1 NCI CGAP_Lu24 Homo            sapiens cDNA clone IMAGE:2149727_3', mRNA"            XP002270647 accession no. EBI            Database accession no. AI457194            * the whole document *</p> <p>-----</p> <p>-/-</p>	1-22	



European Patent  
Office

## PARTIAL EUROPEAN SEARCH REPORT

Application Number

EP 00 11 6126

Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	CLASSIFICATION OF THE APPLICATION (Int.Cl.7)
			TECHNICAL FIELDS SEARCHED (Int.Cl.7)
X	DATABASE EMBL [Online] 23 August 1999 (1999-08-23), STRAUSBERG: "wx91e11.x1 NCI CGAP Lu27 Homo sapiens cDNA clone IMAGE:2551052-3', mRNA" XP002270648 accession no. EBI Database accession no. AI954939 * the whole document * -----	1-22	
E	WO 00/58513 A (HUMAN GENOME SCIENCES INC ;ROSEN CRAIG A (US); RUBEN STEVEN M (US)) 5 October 2000 (2000-10-05) * claims 1-23; figure SEQ.14 * -----	1-22	
P,X	DATABASE EMBL [Online] 22 February 2000 (2000-02-22), ISOGAI T.: "Homo sapiens cDNA FLJ10199 fis, clone HEMBA1004850." XP002270649 accession no. EBI Database accession no. AK001061. * the whole document * -----	1-22	
T	DATABASE SWALL [Online] 28 February 2003 (2003-02-28), ISOGAI,T. ET AL.: "DnaJ homolog subfamily C member 1." XP002260362 accession no. EBI Database accession no. Q96KC8 * the whole document * -----	1-22	
T	WO 02/31111 A (HYSEQ INC ;WEHRMAN TOM (US); YANG YONGHONG (US); ZHANG JIE (US); Z) 18 April 2002 (2002-04-18) * page 115; claim 20; figure SEQ.461; table 2 * -----	1-22	



European Patent  
Office

Application Number

EP 00 11 6126

#### CLAIMS INCURRING FEES

The present European patent application comprised at the time of filing more than ten claims.

Only part of the claims have been paid within the prescribed time limit. The present European search report has been drawn up for the first ten claims and for those claims for which claims fees have been paid, namely claim(s):

No claims fees have been paid within the prescribed time limit. The present European search report has been drawn up for the first ten claims.

#### LACK OF UNITY OF INVENTION

The Search Division considers that the present European patent application does not comply with the requirements of unity of invention and relates to several inventions or groups of inventions, namely:

see sheet B

All further search fees have been paid within the fixed time limit. The present European search report has been drawn up for all claims.

As all searchable claims could be searched without effort justifying an additional fee, the Search Division did not invite payment of any additional fee.

Only part of the further search fees have been paid within the fixed time limit. The present European search report has been drawn up for those parts of the European patent application which relate to the inventions in respect of which search fees have been paid, namely claims:

1-22

None of the further search fees have been paid within the fixed time limit. The present European search report has been drawn up for those parts of the European patent application which relate to the invention first mentioned in the claims, namely claims:

European Patent  
OfficeLACK OF UNITY OF INVENTION  
SHEET BApplication Number  
EP 00 11 6126

The Search Division considers that the present European patent application does not comply with the requirements of unity of invention and relates to several inventions or groups of inventions, namely:

## 1. claims: 1-23 partly

## Invention 1 :

A primer set for synthesizing polynucleotides, the primer set comprising oligonucleotide complementary to the complementary strand of the polynucleotide comprising the nucleotide sequences set forth in of SEQ ID N0:1,5548 where seq.1 is corresponding to the 5'end of polynucleotide of clone HEMBA1000005 having seq.id.10468 ,corresponding coding region in the polynucleotide with corresponding protein with amino acid sequence with seq.id.10469 , and method for synthesizing a polynucleotide.

---

## 2. claims: 1-23 partly

## Inventions 2-5602 :

A primer set for synthesizing polynucleotides, the primer set comprising oligonucleotide complementary to the complementary strand of the polynucleotide probably corresponding to the 5'end and 3' end of polynucleotide of the 5601 clones as disclosed on tables 1 and 2 of the present application , or as disclosed on pages 127 line 33-page 130 line 47 combined with example 11 of the present application , the polynucleotide of this clone, corresponding coding region in the polynucleotide with corresponding protein , and method for synthesizing a polynucleotide.

---

**ANNEX TO THE EUROPEAN SEARCH REPORT  
ON EUROPEAN PATENT APPLICATION NO.**

EP 00 11 6126

This annex lists the patent family members relating to the patent documents cited in the above-mentioned European search report.  
 The members are as contained in the European Patent Office EDP file on  
 The European Patent Office is in no way liable for these particulars which are merely given for the purpose of information.

18-02-2004

Patent document cited in search report	Publication date	Patent family member(s)		Publication date
WO 0058513 A 05-10-2000	AU	4174500	A	16-10-2000
	CA	2368700	A1	05-10-2000
	EP	1185694	A1	13-03-2002
	JP	2002539847	T	26-11-2002
	WO	0058513	A1	05-10-2000
WO 0231111 A 18-04-2002	AU	9623501	A	22-04-2002
	CA	2425827	A1	18-04-2002
	EP	1325120	A2	09-07-2003
	WO	0231111	A2	18-04-2002
	US	2004022786	A1	05-02-2004
	US	2004023870	A1	05-02-2004